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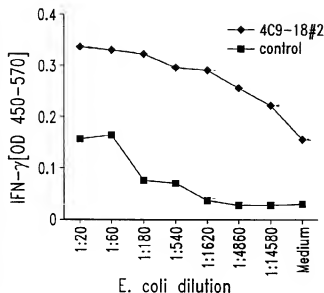
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(54) Title: COMPOUNDS AND METHODS FOR TREATMENT AND DIAGNOSIS OF CHLAMYDIAL INFECTION

(57) Abstract: Compounds and methods for the diagnosis and treatment of Chlamydial infection are disclosed. The compounds provided include polypeptides that contain at least one antigenic portion of a *Chlamydia* antigen and DNA sequences encoding such polypeptides. Pharmaceutical compositions and vaccines comprising such polypeptides or DNA sequences are also provided, together with antibodies directed against such polypeptides. Diagnostic kits containing such polypeptides or DNA sequences and a suitable detection reagent may be used for the detection of Chlamydial infection in patients and in biological samples.

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COMPOUNDS AND METHODS FOR TREATMENT AND DIAGNOSIS OF CHLAMYDIAL INFECTION

TECHNICAL FIELD

5 The present invention relates generally to the detection and treatment of Chlamydial infection. In particular, the invention is related to polypeptides comprising a *Chlamydia* antigen and the use of such polypeptides for the serodiagnosis and treatment of Chlamydial infection.

10 BACKGROUND OF THE INVENTION

 Chlamydiae are intracellular bacterial pathogens that are responsible for a wide variety of important human and animal infections. *Chlamydia trachomatis* is one of the most common causes of sexually transmitted diseases and can lead to pelvic inflammatory disease (PID), resulting in tubal obstruction and infertility. *Chlamydia trachomatis* may also play a role in male infertility. In 1990, the cost of treating PID in the US was estimated to be \$4 billion. Trachoma, due to ocular infection with *Chlamydia trachomatis*, is the leading cause of preventable blindness worldwide. *Chlamydia pneumonia* is a major cause of acute respiratory tract infections in humans and is also believed to play a role in the pathogenesis of atherosclerosis and, in particular, coronary heart disease. Individuals with a high titer of antibodies to *Chlamydia pneumonia* have been shown to be at least twice as likely to suffer from coronary heart disease as seronegative individuals. Chlamydial infections thus constitute a significant health problem both in the US and worldwide.

 Chlamydial infection is often asymptomatic. For example, by the time a woman seeks medical attention for PID, irreversible damage may have already occurred resulting in infertility. There thus remains a need in the art for improved vaccines and pharmaceutical compositions for the prevention and treatment of *Chlamydia* infections. The present invention fulfills this need and further provides other related advantages.

30 SUMMARY OF THE INVENTION

 The present invention provides compositions and methods for the diagnosis and therapy of *Chlamydia* infection. In one aspect, the present invention

provides polypeptides comprising an immunogenic portion of a *Chlamydia* antigen, or a variant of such an antigen. Certain portions and other variants are immunogenic, such that the ability of the variant to react with antigen-specific antisera is not substantially diminished. Within certain embodiments,, the polypeptide comprises an amino acid
5 sequence encoded by a polynucleotide sequence selected from the group consisting of (a) a sequence of SEQ ID NO: 358-361, 366-385, 406-430, 455-489, 516-517, 523-559, and 582-596; (b) the complements of said sequences; and (c) sequences that hybridize to a sequence of (a) or (b) under moderate to highly stringent conditions. In specific embodiments, the polypeptides of the present invention comprise at least a portion of a
10 *Chlamydial* protein that includes an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NO:362-365, 386-405, 431-454, 490-515, 518-522, 560-581, and 597-599 and variants thereof.

The present invention further provides polynucleotides that encode a polypeptide as described above, or a portion thereof (such as a portion encoding at least
15 15 amino acid residues of a *Chlamydial* protein), expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

In a related aspect, polynucleotide sequences encoding the above polypeptides, recombinant expression vectors comprising one or more of these polynucleotide sequences and host cells transformed or transfected with such expression
20 vectors are also provided.

In another aspect, the present invention provides fusion proteins comprising an inventive polypeptide, or, alternatively, an inventive polypeptide and a known *Chlamydia* antigen, as well as polynucleotides encoding such fusion proteins, in combination with a physiologically acceptable carrier or immunostimulant for use as
25 pharmaceutical compositions and vaccines thereof.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody, both polyclonal and monoclonal, or antigen-binding fragment thereof that specifically binds to a *Chlamydial* protein; and (b) a physiologically acceptable carrier. Within other aspects, the present invention provides
30 pharmaceutical compositions that comprise one or more *Chlamydia* polypeptides disclosed herein, e.g., a polypeptide according to SEQ ID NO:362-365, 386-405, 431-454, 490-515, 518-522, 560-581, and 597-599, or a polynucleotide molecule encoding

such a polypeptide, such as a polynucleotide according to SEQ ID NO:358-361, 366-385, 406-430, 455-489, 516-517, 523-559, and 582-596, and a physiologically acceptable carrier. The invention also provides vaccines for prophylactic and therapeutic purposes comprising one or more of the disclosed polypeptides and an immunostimulant, as defined herein, together with vaccines comprising one or more polynucleotide sequences encoding such polypeptides and an immunostimulant.

In yet another aspect, methods are provided for inducing protective immunity in a patient, comprising administering to a patient an effective amount of one or more of the above pharmaceutical compositions or vaccines.

In yet a further aspect, methods for the treatment of *Chlamydia* infection in a patient are provided, the methods comprising obtaining peripheral blood mononuclear cells (PBMC) from the patient, incubating the PBMC with a polypeptide of the present invention (or a polynucleotide that encodes such a polypeptide) to provide incubated T cells and administering the incubated T cells to the patient. The present invention additionally provides methods for the treatment of *Chlamydia* infection that comprise incubating antigen presenting cells with a polypeptide of the present invention (or a polynucleotide that encodes such a polypeptide) to provide incubated antigen presenting cells and administering the incubated antigen presenting cells to the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient. In certain embodiments, the antigen presenting cells are selected from the group consisting of dendritic cells, macrophages, monocytes, B-cells, and fibroblasts. Compositions for the treatment of *Chlamydia* infection comprising T cells or antigen presenting cells that have been incubated with a polypeptide or polynucleotide of the present invention are also provided. Within related aspects, vaccines are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) an immunostimulant.

The present invention further provides, within other aspects, methods for removing *Chlamydia*-infected cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a *Chlamydia* protein, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of *Chlamydial* infection in a patient, comprising administering to a patient a biological sample treated as described above. In further aspects of the subject invention, methods and diagnostic kits are provided for detecting *Chlamydia* infection in a patient. In one embodiment, the method comprises: (a) contacting a biological sample with at least one of the polypeptides or fusion proteins disclosed herein; and (b) detecting in the sample the presence of binding agents that bind to the polypeptide or fusion protein, thereby detecting *Chlamydia* infection in the biological sample. Suitable biological samples include whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid and urine. In one embodiment, the diagnostic kits comprise one or more of the polypeptides or fusion proteins disclosed herein in combination with a detection reagent. In yet another embodiment, the diagnostic kits comprise either a monoclonal antibody or a polyclonal antibody that binds with a polypeptide of the present invention.

The present invention also provides methods for detecting *Chlamydia* infection comprising: (a) obtaining a biological sample from a patient; (b) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, at least one of the oligonucleotide primers being specific for a polynucleotide sequence disclosed herein; and (c) detecting in the sample a polynucleotide sequence that amplifies in the presence of the oligonucleotide primers. In one embodiment, the oligonucleotide primer comprises at least about 10 contiguous nucleotides of a polynucleotide sequence disclosed herein, or of a sequence that hybridizes thereto.

In a further aspect, the present invention provides a method for detecting *Chlamydia* infection in a patient comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with an oligonucleotide probe specific for a polynucleotide sequence disclosed herein; and (c) detecting in the sample a polynucleotide sequence that hybridizes to the oligonucleotide probe. In one embodiment, the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a polynucleotide sequence disclosed herein, or a sequence that hybridizes thereto.

These and other aspects of the present invention will become apparent upon reference to the following detailed description. All references disclosed herein are

hereby incorporated by reference in their entirety as if each was incorporated individually.

SEQUENCE IDENTIFIERS

- 5 SEQ ID NO: 1 is the determined DNA sequence for the *C. trachomatis* clone 1-B1-66.
- SEQ ID NO: 2 is the determined DNA sequence for the *C. trachomatis* clone 4-D7-28.
- SEQ ID NO: 3 is the determined DNA sequence for the *C. trachomatis* clone 3-G3-10.
- 10 SEQ ID NO: 4 is the determined DNA sequence for the *C. trachomatis* clone 10-C10-31.
- SEQ ID NO: 5 is the predicted amino acid sequence for 1-B1-66.
- SEQ ID NO: 6 is the predicted amino acid sequence for 4-D7-28.
- 15 SEQ ID NO: 7 is a first predicted amino acid sequence for 3-G3-10.
- SEQ ID NO: 8 is a second predicted amino acid sequence for 3-G3-10.
- SEQ ID NO: 9 is a third predicted amino acid sequence for 3-G3-10.
- SEQ ID NO: 10 is a fourth predicted amino acid sequence for 3-G3-10.
- SEQ ID NO: 11 is a fifth predicted amino acid sequence for 3-G3-10.
- 20 SEQ ID NO: 12 is the predicted amino acid sequence for 10-C10-31.
- SEQ ID NO: 13 is the amino acid sequence of the synthetic peptide 1-B1-66/48-67.
- SEQ ID NO: 14 is the amino acid sequence of the synthetic peptide 1-B1-66/58-77.
- 25 SEQ ID NO: 15 is the determined DNA sequence for the *C. trachomatis* serovar LGV II clone 2C7-8
- SEQ ID NO: 16 is a DNA sequence of a putative open reading frame from a region of the *C. trachomatis* serovar D genome to which 2C7-8 maps
- SEQ ID NO: 17 is the predicted amino acid sequence encoded by the DNA sequence of SEQ ID NO: 16
- 30 SEQ ID NO: 18 is the amino acid sequence of the synthetic peptide CtC7.8-12

SEQ ID NO: 19 is the amino acid sequence of the synthetic peptide
CtC7.8-13

SEQ ID NO: 20 is the predicted amino acid sequence encoded by a
second putative open reading from *C. trachomatis* serovar D

5 SEQ ID NO: 21 is the determined DNA sequence for clone 4C9-18 from
C. trachomatis LGV II

SEQ ID NO: 22 is the determined DNA sequence homologous to
Lipoamide Dehydrogenase from *C. trachomatis* LGV II

10 SEQ ID NO: 23 is the determined DNA sequence homologous to
Hypothetical protein from *C. trachomatis* LGV II

SEQ ID NO: 24 is the determined DNA sequence homologous to
Ubiquinone Methyltransferase from *C. trachomatis* LGV II

SEQ ID NO: 25 is the determined DNA sequence for clone 4C9-18#2
BL21 pLysS from *C. trachomatis* LGV II

15 SEQ ID NO: 26 is the predicted amino acid sequence for 4C9-18#2 from
C. trachomatis LGV II

SEQ ID NO: 27 is the determined DNA sequence for Cp-SWIB from *C.*
pneumonia strain TWAR

20 SEQ ID NO: 28 is the predicted amino acid sequence for Cp-SWIB from
C. pneumonia strain TWAR

SEQ ID NO: 29 is the determined DNA sequence for Cp-S13 (CT509)
from *C. pneumonia* strain TWAR

SEQ ID NO: 30 is the predicted amino acid sequence for Cp-S13 from
C. pneumonia strain TWAR

25 SEQ ID NO: 31 is the amino acid sequence for a 10mer consensus
peptide from CtC7.8-12 and CtC7.8-13

SEQ ID NO: 32 is the predicted amino acid sequence for clone 2C7-8
from *C. trachomatis* LGV II

30 SEQ ID NO: 33 is the DNA sequence corresponding to nucleotides
597304-597145 of the *C. trachomatis* serovar D genome (NCBI, BLASTN search),
which shows homology to clone 2C7-8

SEQ ID NO: 34 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 33

SEQ ID NO: 35 is the DNA sequence for C.p. SWIB Nde (5' primer) from *C. pneumonia*

5 SEQ ID NO: 36 is the DNA sequence for C.p. SWIB EcoRI (3' primer) from *C. pneumonia*

SEQ ID NO : 37 is the DNA sequence for C.p. S13 Nde (5' primer) from *C. pneumonia*

10 SEQ ID NO: 38 is the DNA sequence for C.p. S13 EcoRI (3' primer) from *C. pneumonia*

SEQ ID NO: 39 is the amino acid sequence for CtSwib 52-67 peptide from *C. trachomatis* LGV II

SEQ ID NO: 40 is the amino acid sequence for CpSwib 53-68 peptide from *C. pneumonia*

15 SEQ ID NO: 41 is the amino acid sequence for HuSwib 288-302 peptide from Human SWI domain

SEQ ID NO: 42 is the amino acid sequence for CtSWI-T 822-837 peptide from the topoisomerase-SWIB fusion of *C. trachomatis*

20 SEQ ID NO: 43 is the amino acid sequence for CpSWI-T 828-842 peptide from the topoisomerase-SWIB fusion of *C. pneumonia*

SEQ ID NO: 44 is a first determined DNA sequence for the *C. trachomatis* LGV II clone 19783.3.jen.seq(1>509)CTL2#11-3', representing the 3' end.

SEQ ID NO: 45 is a second determined DNA sequence for the *C. trachomatis* LGV II clone 19783.4.jen.seq(1>481)CTL2#11-5', representing the 5' end.

25 SEQ ID NO: 46 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19784CTL2_12consensus.seq(1>427)CTL2#12.

SEQ ID NO: 47 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19785.4.jen.seq(1>600)CTL2#16-5', representing the 5' end.

30 SEQ ID NO: 48 is a first determined DNA sequence for the *C. trachomatis* LGV II clone 19786.3.jen.seq(1>600)CTL2#18-3', representing the 3' end.

SEQ ID NO: 49 is a second determined DNA sequence for the *C. trachomatis* LGV II clone 19786.4.jen.seq(1>600)CTL2#18-5', representing the 5' end.

- SEQ ID NO: 50 is the determined DNA sequence for the *C. trachomatis*
LGV II clone 19788CTL2_21consensus.seq(1>406)CTL2#21.
- SEQ ID NO: 51 is the determined DNA sequence for the *C. trachomatis*
LGV II clone 19790CTL2_23consensus.seq(1>602)CTL2#23.
- 5 SEQ ID NO: 52 is the determined DNA sequence for the *C. trachomatis*
LGV II clone 19791CTL2_24consensus.seq(1>145)CTL2#24.
- SEQ ID NO: 53 is the determined DNA sequence for the *C. trachomatis*
LGV II clone CTL2#4.
- SEQ ID NO: 54 is the determined DNA sequence for the *C. trachomatis*
10 LGV II clone CTL2#8b.
- SEQ ID NO: 55 is the determined DNA sequence for the *C. trachomatis*
LGV II clone 15-G1-89, sharing homology to the lipoamide dehydrogenase gene CT557.
- SEQ ID NO: 56 is the determined DNA sequence for the *C. trachomatis*
LGV II clone 14-H1-4, sharing homology to the thiol specific antioxidant gene CT603.
- 15 SEQ ID NO: 57 is the determined DNA sequence for the *C. trachomatis*
LGV II clone 12-G3-83, sharing homology to the hypothetical protein CT622.
- SEQ ID NO: 58 is the determined DNA sequence for the *C. trachomatis*
LGV II clone 12-B3-95, sharing homology to the lipoamide dehydrogenase gene
CT557.
- 20 SEQ ID NO: 59 is the determined DNA sequence for the *C. trachomatis*
LGV II clone 11-H4-28, sharing homology to the dnaK gene CT396.
- SEQ ID NO: 60 is the determined DNA sequence for the *C. trachomatis*
LGV II clone 11-H3-68, sharing partial homology to the PGP6-D virulence protein and
L1 ribosomal gene CT318.
- 25 SEQ ID NO: 61 is the determined DNA sequence for the *C. trachomatis*
LGV II clone 11-G1-34, sharing partial homology to the malate dehydrogenase gene
CT376 and to the glycogen hydrolase gene CT042.
- SEQ ID NO: 62 is the determined DNA sequence for the *C. trachomatis*
LGV II clone 11-G10-46, sharing homology to the hypothetical protein CT610.
- 30 SEQ ID NO: 63 is the determined DNA sequence for the *C. trachomatis*
LGV II clone 11-C12-91, sharing homology to the OMP2 gene CT443.

SEQ ID NO: 64 is the determined DNA sequence for the *C. trachomatis* LGV II clone 11-A3-93, sharing homology to the HAD superfamily gene CT103.

SEQ ID NO: 65 is the determined amino acid sequence for the *C. trachomatis* LGV II clone 14-H1-4, sharing homology to the thiol specific antioxidant gene CT603.

SEQ ID NO: 66 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#9.

SEQ ID NO: 67 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#7.

SEQ ID NO: 68 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#6.

SEQ ID NO: 69 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#5.

SEQ ID NO: 70 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#2.

SEQ ID NO: 71 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#1.

SEQ ID NO: 72 is a first determined DNA sequence for the *C. trachomatis* LGV II clone 23509.2CtL2#3-5', representing the 5' end.

SEQ ID NO: 73 is a second determined DNA sequence for the *C. trachomatis* LGV II clone 23509.1CtL2#3-3', representing the 3' end.

SEQ ID NO: 74 is a first determined DNA sequence for the *C. trachomatis* LGV II clone 22121.2CtL2#10-5', representing the 5' end.

SEQ ID NO: 75 is a second determined DNA sequence for the *C. trachomatis* LGV II clone 22121.1CtL2#10-3', representing the 3' end.

SEQ ID NO: 76 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19787.6CtL2#19-5', representing the 5' end.

SEQ ID NO: 77 is the determined DNA sequence for the *C. pneumoniae* LGV II clone CpS13-His.

SEQ ID NO: 78 is the determined DNA sequence for the *C. pneumoniae* LGV II clone Cp_SWIB-His.

SEQ ID NO: 79 is the determined DNA sequence for the *C. trachomatis* LGV II clone 23-G7-68, sharing partial homology to the L11, L10 and L1 ribosomal protein.

SEQ ID NO: 80 is the determined DNA sequence for the *C. trachomatis* LGV II clone 22-F8-91, sharing homology to the pmpC gene.

SEQ ID NO: 81 is the determined DNA sequence for the *C. trachomatis* LGV II clone 21-E8-95, sharing homology to the CT610-CT613 genes.

SEQ ID NO: 82 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19-F12-57, sharing homology to the CT858 and recA genes.

10 SEQ ID NO: 83 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19-F12-53, sharing homology to the CT445 gene encoding glutamyl tRNA synthetase.

SEQ ID NO: 84 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19-A5-54, sharing homology to the cryptic plasmid gene.

15 SEQ ID NO: 85 is the determined DNA sequence for the *C. trachomatis* LGV II clone 17-E11-72, sharing partial homology to the OppC_2 and pmpD genes.

SEQ ID NO: 86 is the determined DNA sequence for the *C. trachomatis* LGV II clone 17-C1-77, sharing partial homology to the CT857 and CT858 open reading frames.

20 SEQ ID NO: 87 is the determined DNA sequence for the *C. trachomatis* LGV II clone 15-H2-76, sharing partial homology to the pmpD and SycE genes, and to the CT089 ORF.

SEQ ID NO: 88 is the determined DNA sequence for the *C. trachomatis* LGV II clone 15-A3-26, sharing homology to the CT858 ORF.

25 SEQ ID NO: 89 is the determined amino acid sequence for the *C. pneumoniae* clone Cp_SWIB-His.

SEQ ID NO: 90 is the determined amino acid sequence for the *C. trachomatis* LGV II clone CtL2_LPDA_FL.

30 SEQ ID NO: 91 is the determined amino acid sequence for the *C. pneumoniae* clone CpS13-His.

SEQ ID NO: 92 is the determined amino acid sequence for the *C. trachomatis* LGV II clone CtL2_TSA_FL.

SEQ ID NO: 93 is the amino acid sequence for Ct-Swib 43-61 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 94 is the amino acid sequence for Ct-Swib 48-67 peptide from *C. trachomatis* LGV II.

5 SEQ ID NO: 95 is the amino acid sequence for Ct-Swib 52-71 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 96 is the amino acid sequence for Ct-Swib 58-77 peptide from *C. trachomatis* LGV II.

10 SEQ ID NO: 97 is the amino acid sequence for Ct-Swib 63-82 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 98 is the amino acid sequence for Ct-Swib 51-66 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 99 is the amino acid sequence for Cp-Swib 52-67 peptide from *C. pneumonia*.

15 SEQ ID NO: 100 is the amino acid sequence for Cp-Swib 37-51 peptide from *C. pneumonia*.

SEQ ID NO: 101 is the amino acid sequence for Cp-Swib 32-51 peptide from *C. pneumonia*.

20 SEQ ID NO: 102 is the amino acid sequence for Cp-Swib 37-56 peptide from *C. pneumonia*.

SEQ ID NO: 103 is the amino acid sequence for Ct-Swib 36-50 peptide from *C. trachomatis*.

SEQ ID NO: 104 is the amino acid sequence for Ct-S13 46-65 peptide from *C. trachomatis*.

25 SEQ ID NO: 105 is the amino acid sequence for Ct-S13 60-80 peptide from *C. trachomatis*.

SEQ ID NO: 106 is the amino acid sequence for Ct-S13 1-20 peptide from *C. trachomatis*.

30 SEQ ID NO: 107 is the amino acid sequence for Ct-S13 46-65 peptide from *C. trachomatis*.

SEQ ID NO: 108 is the amino acid sequence for Ct-S13 56-75 peptide from *C. trachomatis*.

SEQ ID NO: 109 is the amino acid sequence for Cp-S13 56-75 peptide from *C. pneumoniae*.

SEQ ID NO: 110 is the determined DNA sequence for the *C. trachomatis* LGV II clone 21-G12-60, containing partial open reading frames for
5 hypothetical proteins CT875, CT229 and CT228.

SEQ ID NO: 111 is the determined DNA sequence for the *C. trachomatis* LGV II clone 22-B3-53, sharing homology to the CT110 ORF of GroEL.

SEQ ID NO: 112 is the determined DNA sequence for the *C. trachomatis* LGV II clone 22-A1-49, sharing partial homology to the CT660 and CT659
10 ORFs.

SEQ ID NO: 113 is the determined DNA sequence for the *C. trachomatis* LGV II clone 17-E2-9, sharing partial homology to the CT611 and CT 610 ORFs.

SEQ ID NO: 114 is the determined DNA sequence for the *C. trachomatis* LGV II clone 17-C10-31, sharing partial homology to the CT858 ORF.
15

SEQ ID NO: 115 is the determined DNA sequence for the *C. trachomatis* LGV II clone 21-C7-8, sharing homology to the dnaK-like gene.

SEQ ID NO: 116 is the determined DNA sequence for the *C. trachomatis* LGV II clone 20-G3-45, containing part of the pmpB gene CT413.
20

SEQ ID NO: 117 is the determined DNA sequence for the *C. trachomatis* LGV II clone 18-C5-2, sharing homology to the S1 ribosomal protein ORF.

SEQ ID NO: 118 is the determined DNA sequence for the *C. trachomatis* LGV II clone 17-C5-19, containing part of the ORFs for CT431 and CT430.

SEQ ID NO: 119 is the determined DNA sequence for the *C. trachomatis* LGV II clone 16-D4-22, contains partial sequences of ORF3 and ORF4 of the plasmid for growth within mammalian cells.
25

SEQ ID NO: 120 is the determined full-length DNA sequence for the *C. trachomatis* serovar LGV II Cap1 gene CT529.

SEQ ID NO: 121 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar LGV II Cap1 gene CT529.
30

SEQ ID NO: 122 is the determined full-length DNA sequence for the *C. trachomatis* serovar E Cap1 gene CT529.

SEQ ID NO: 123 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar E Cap1 gene CT529.

5 SEQ ID NO: 124 is the determined full-length DNA sequence for the *C. trachomatis* serovar 1A Cap1 gene CT529.

SEQ ID NO: 125 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar 1A Cap1 gene CT529.

10 SEQ ID NO: 126 is the determined full-length DNA sequence for the *C. trachomatis* serovar G Cap1 gene CT529.

SEQ ID NO: 127 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar G Cap1 gene CT529.

SEQ ID NO: 128 is the determined full-length DNA sequence for the *C. trachomatis* serovar F1 NII Cap1 gene CT529.

15 SEQ ID NO: 129 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar F1 NII Cap1 gene CT529.

SEQ ID NO: 130 is the determined full-length DNA sequence for the *C. trachomatis* serovar L1 Cap1 gene CT529.

20 SEQ ID NO: 131 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar L1 Cap1 gene CT529.

SEQ ID NO: 132 is the determined full-length DNA sequence for the *C. trachomatis* serovar L3 Cap1 gene CT529.

SEQ ID NO: 133 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar L3 Cap1 gene CT529.

25 SEQ ID NO: 134 is the determined full-length DNA sequence for the *C. trachomatis* serovar Ba Cap1 gene CT529.

SEQ ID NO: 135 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar Ba Cap1 gene CT529.

30 SEQ ID NO: 136 is the determined full-length DNA sequence for the *C. trachomatis* serovar MOPN Cap1 gene CT529.

SEQ ID NO: 137 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar MOPN Cap1 gene CT529.

- SEQ ID NO: 138 is the determined amino acid sequence for the Cap1
CT529 ORF peptide #124-139 of *C. trachomatis* serovar L2.
- SEQ ID NO: 139 is the determined amino acid sequence for the Cap1
CT529 ORF peptide #132-147 of *C. trachomatis* serovar L2.
- 5 SEQ ID NO: 140 is the determined amino acid sequence for the Cap1
CT529 ORF peptide #138-155 of *C. trachomatis* serovar L2.
- SEQ ID NO: 141 is the determined amino acid sequence for the Cap1
CT529 ORF peptide #146-163 of *C. trachomatis* serovar L2.
- SEQ ID NO: 142 is the determined amino acid sequence for the Cap1
10 CT529 ORF peptide #154-171 of *C. trachomatis* serovar L2.
- SEQ ID NO: 143 is the determined amino acid sequence for the Cap1
CT529 ORF peptide #162-178 of *C. trachomatis* serovar L2.
- SEQ ID NO: 144 is the determined amino acid sequence for the Cap1
CT529 ORF peptide #138-147 of *C. trachomatis* serovar L2.
- 15 SEQ ID NO: 145 is the determined amino acid sequence for the Cap1
CT529 ORF peptide #139-147 of *C. trachomatis* serovar L2.
- SEQ ID NO: 146 is the determined amino acid sequence for the Cap1
CT529 ORF peptide #140-147 of *C. trachomatis* serovar L2.
- SEQ ID NO: 147 is the determined amino acid sequence for the Cap1
20 CT529 ORF peptide #138-146 of *C. trachomatis* serovar L2.
- SEQ ID NO: 148 is the determined amino acid sequence for the Cap1
CT529 ORF peptide #138-145 of *C. trachomatis* serovar L2.
- SEQ ID NO: 149 is the determined amino acid sequence for the Cap1
CT529 ORF peptide # F140->I of *C. trachomatis* serovar L2.
- 25 SEQ ID NO: 150 is the determined amino acid sequence for the Cap1
CT529 ORF peptide # #S139>Ga of *C. trachomatis* serovar L2.
- SEQ ID NO: 151 is the determined amino acid sequence for the Cap1
CT529 ORF peptide # #S139>Gb of *C. trachomatis* serovar L2.
- SEQ ID NO: 152 is the determined amino acid sequence for the peptide
30 # 2 C7.8-6 of the 216aa ORF of *C. trachomatis* serovar L2.
- SEQ ID NO: 153 is the determined amino acid sequence for the peptide
2 C7.8-7 of the 216aa ORF of *C. trachomatis* serovar L2.

SEQ ID NO: 154 is the determined amino acid sequence for the peptide
2 C7.8-8 of the 216aa ORF of *C. trachomatis* serovar L2.

SEQ ID NO: 155 is the determined amino acid sequence for the peptide
2 C7.8-9 of the 216aa ORF of *C. trachomatis* serovar L2.

5 SEQ ID NO: 156 is the determined amino acid sequence for the peptide
2 C7.8-10 of the 216aa ORF of *C. trachomatis* serovar L2.

SEQ ID NO: 157 is the determined amino acid sequence for the 53
amino acid residue peptide of the 216aa ORF within clone 2C7.8 of *C. trachomatis*
serovar L2.

10 SEQ ID NO: 158 is the determined amino acid sequence for the 52
amino acid residue peptide of the CT529 ORF within clone 2C7.8 of *C. trachomatis*
serovar L2.

SEQ ID NO: 159 is the determined DNA sequence for the 5' (forward)
primer for cloning full-length CT529 serovar L2.

15 SEQ ID NO: 160 is the determined DNA sequence for the 5' (reverse)
primer for cloning full-length CT529 serovar L2.

SEQ ID NO: 161 is the determined DNA sequence for the 5' (forward)
primer for cloning full-length CT529 for serovars other than L2 and MOPN.

20 SEQ ID NO: 162 is the determined DNA sequence for the 5' (reverse)
primer for cloning full-length CT529 serovars other than L2 and MOPN.

SEQ ID NO: 163 is the determined DNA sequence for the 5' (forward)
primer for cloning full-length CT529 serovar MOPN.

SEQ ID NO: 164 is the determined DNA sequence for the 5' (reverse)
primer for cloning full-length CT529 serovar MOPN.

25 SEQ ID NO: 165 is the determined DNA sequence for the 5' (forward)
primer for pBIB-KS.

SEQ ID NO: 166 is the determined DNA sequence for the 5' (reverse)
primer for pBIB-KS.

30 SEQ ID NO: 167 is the determined amino acid sequence for the 9-mer
epitope peptide Cap1#139-147 from serovar L2.

SEQ ID NO: 168 is the determined amino acid sequence for the 9-mer
epitope peptide Cap1#139-147 from serovar D.

SEQ ID NO: 169 is the determined full-length DNA sequence for the *C. trachomatis* pmpI (CT874) gene.

SEQ ID NO: 170 is the determined full-length DNA sequence for the *C. trachomatis* pmpG gene.

5 SEQ ID NO: 171 is the determined full-length DNA sequence for the *C. trachomatis* pmpE gene.

SEQ ID NO: 172 is the determined full-length DNA sequence for the *C. trachomatis* pmpD gene.

10 SEQ ID NO: 173 is the determined full-length DNA sequence for the *C. trachomatis* pmpC gene.

SEQ ID NO: 174 is the determined full-length DNA sequence for the *C. trachomatis* pmpB gene.

SEQ ID NO: 175 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpI gene.

15 SEQ ID NO: 176 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpG gene.

SEQ ID NO: 177 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpE gene.

20 SEQ ID NO: 178 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpD gene.

SEQ ID NO: 179 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpC gene.

SEQ ID NO: 180 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpB gene.

25 SEQ ID NO: 181 is the determined DNA sequence minus the signal sequence for the *C. trachomatis* pmpI gene.

SEQ ID NO: 182 is a subsequently determined full-length DNA sequence for the *C. trachomatis* pmpG gene.

30 SEQ ID NO: 183 is the determined DNA sequence minus the signal sequence for the *C. trachomatis* pmpE gene.

SEQ ID NO: 184 is a first determined DNA sequence representing the carboxy terminus for the *C. trachomatis* pmpD gene.

SEQ ID NO: 185 is a second determined DNA sequence representing the amino terminus minus the signal sequence for the *C. trachomatis* pmpD gene.

SEQ ID NO: 186 is a first determined DNA sequence representing the carboxy terminus for the *C. trachomatis* pmpC gene.

5 SEQ ID NO: 187 is a second determined DNA sequence representing the amino terminus minus the signal sequence for the *C. trachomatis* pmpC gene.

SEQ ID NO: 188 is the determined DNA sequence representing the *C. pneumoniae* serovar MOMPS pmp gene in a fusion molecule with Ra12.

10 SEQ ID NO: 189 is the predicted amino acid sequence minus the signal sequence for the *C. trachomatis* pmpI gene.

SEQ ID NO: 190 is subsequently predicted amino acid sequence for the *C. trachomatis* pmpG gene.

SEQ ID NO: 191 is the predicted amino acid sequence minus the signal sequence for the *C. trachomatis* pmpE gene.

15 SEQ ID NO: 192 is a first predicted amino acid sequence representing the carboxy terminus for the *C. trachomatis* pmpD gene.

SEQ ID NO: 193 is a second predicted amino acid sequence representing the Amino terminus minus the signal sequence for the *C. trachomatis* pmpD gene.

20 SEQ ID NO: 194 is a first predicted amino acid sequence representing the Carboxy terminus for the *C. trachomatis* pmpC gene.

SEQ ID NO: 195 is a second predicted amino acid sequence representing the Amino terminus for the *C. trachomatis* pmpC gene.

SEQ ID NO: 196 is the predicted amino acid sequence representing the *C. pneumoniae* serovar MOMPS pmp gene in a fusion molecule with Ra12.

25 SEQ ID NO: 197 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpC gene in the SKB vaccine vector.

SEQ ID NO: 198 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpC gene in the SKB vaccine vector.

30 SEQ ID NO: 199 is the determined DNA sequence for the insertion sequence for cloning the *C. trachomatis* pmpC gene in the SKB vaccine vector.

SEQ ID NO: 200 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpD gene in the SKB vaccine vector.

SEQ ID NO: 201 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpD gene in the SKB vaccine vector.

SEQ ID NO: 202 is the determined DNA sequence for the insertion sequence for cloning the *C. trachomatis* pmpD gene in the SKB vaccine vector.

5 SEQ ID NO: 203 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpE gene in the SKB vaccine vector.

SEQ ID NO: 204 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpE gene in the SKB vaccine vector.

10 SEQ ID NO: 205 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpG gene in the SKB vaccine vector.

SEQ ID NO: 206 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpG gene in the SKB vaccine vector.

15 SEQ ID NO: 207 is the determined DNA sequence for the 5' oligo primer for cloning the amino terminus portion of the *C. trachomatis* pmpC gene in the pET17b vector.

SEQ ID NO: 208 is the determined DNA sequence for the 3' oligo primer for cloning the amino terminus portion of the *C. trachomatis* pmpC gene in the pET17b vector.

20 SEQ ID NO: 209 is the determined DNA sequence for the 5' oligo primer for cloning the carboxy terminus portion of the *C. trachomatis* pmpC gene in the pET17b vector.

SEQ ID NO: 210 is the determined DNA sequence for the 3' oligo primer for cloning the carboxy terminus portion of the *C. trachomatis* pmpC gene in the pET17b vector.

25 SEQ ID NO: 211 is the determined DNA sequence for the 5' oligo primer for cloning the amino terminus portion of the *C. trachomatis* pmpD gene in the pET17b vector.

30 SEQ ID NO: 212 is the determined DNA sequence for the 3' oligo primer for cloning the amino terminus portion of the *C. trachomatis* pmpD gene in the pET17b vector.

SEQ ID NO: 213 is the determined DNA sequence for the 5' oligo primer for cloning the carboxy terminus portion of the *C. trachomatis* pmpD gene in the pET17b vector.

SEQ ID NO: 214 is the determined DNA sequence for the 3' oligo primer for cloning the carboxy terminus portion of the *C. trachomatis* pmpD gene in the pET17b vector.

SEQ ID NO: 215 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpE gene in the pET17b vector.

SEQ ID NO: 216 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpE gene in the pET17b vector.

SEQ ID NO: 217 is the determined DNA sequence for the insertion sequence for cloning the *C. trachomatis* pmpE gene in the pET17b vector.

SEQ ID NO: 218 is the amino acid sequence for the insertion sequence for cloning the *C. trachomatis* pmpE gene in the pET17b vector.

SEQ ID NO: 219 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpG gene in the pET17b vector.

SEQ ID NO: 220 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpG gene in the pET17b vector.

SEQ ID NO: 221 is the amino acid sequence for the insertion sequence for cloning the *C. trachomatis* pmpG gene in the pET17b vector.

SEQ ID NO: 222 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpI gene in the pET17b vector.

SEQ ID NO: 223 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpI gene in the pET17b vector.

SEQ ID NO: 224 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 1-20.

SEQ ID NO: 225 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 6-25.

SEQ ID NO: 226 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 12-31.

SEQ ID NO: 227 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 17-36.

SEQ ID NO: 228 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 22-41.

SEQ ID NO: 229 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 27-46.

5 SEQ ID NO: 230 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 42-61.

SEQ ID NO: 231 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 46-65.

10 SEQ ID NO: 232 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 51-70.

SEQ ID NO: 233 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 56-75.

SEQ ID NO: 234 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 61-80.

15 SEQ ID NO: 235 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 66-87.

SEQ ID NO: 236 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 103-122.

20 SEQ ID NO: 237 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 108-127.

SEQ ID NO: 238 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 113-132.

SEQ ID NO: 239 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 118-137.

25 SEQ ID NO: 240 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 123-143.

SEQ ID NO: 241 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 128-147.

30 SEQ ID NO: 242 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 133-152.

SEQ ID NO: 243 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 137-156.

SEQ ID NO: 244 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 142-161.

SEQ ID NO: 245 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 147-166.

5 SEQ ID NO: 246 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 152-171.

SEQ ID NO: 247 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 157-176.

10 SEQ ID NO: 248 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 162-181.

SEQ ID NO: 249 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 167-186.

SEQ ID NO: 250 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 171-190.

15 SEQ ID NO: 251 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 171-186.

SEQ ID NO: 252 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 175-186.

20 SEQ ID NO: 252 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 175-186.

SEQ ID NO: 253 is the determined amino acid sequence for the *C. pneumoniae* OMCB peptide 185-198.

SEQ ID NO: 254 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 96-115.

25 SEQ ID NO: 255 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 101-120.

SEQ ID NO: 256 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 106-125.

30 SEQ ID NO: 257 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 111-130.

SEQ ID NO: 258 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 116-135.

SEQ ID NO: 259 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 121-140.

SEQ ID NO: 260 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 126-145.

5 SEQ ID NO: 261 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 131-150.

SEQ ID NO: 262 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 136-155.

10 SEQ ID NO: 263 is the determined full-length DNA sequence for the *C. trachomatis* CT529/Cap 1 gene serovar I.

SEQ ID NO: 264 is the predicted full-length amino sequence for the *C. trachomatis* CT529/Cap 1 gene serovar I.

SEQ ID NO: 265 is the determined full-length DNA sequence for the *C. trachomatis* CT529/Cap 1 gene serovar K.

15 SEQ ID NO: 266 is the predicted full-length amino sequence for the *C. trachomatis* CT529/Cap 1 gene serovar K.

SEQ ID NO: 267 is the determined DNA sequence for the *C. trachomatis* clone 17-G4-36 sharing homology to part of the ORF of DNA-directed RNA polymerase beta subunit-CT315 in serD.

20 SEQ ID NO: 268 is the determined DNA sequence for the partial sequence of the *C. trachomatis* CT016 gene in clone 2E10.

SEQ ID NO: 269 is the determined DNA sequence for the partial sequence of the *C. trachomatis* tRNA synthase gene in clone 2E10.

25 SEQ ID NO: 270 is the determined DNA sequence for the partial sequence for the *C. trachomatis* clpX gene in clone 2E10.

SEQ ID NO: 271 is a first determined DNA sequence for the *C. trachomatis* clone Ctl2gam-30 representing the 5'end.

SEQ ID NO: 272 is a second determined DNA sequence for the *C. trachomatis* clone Ctl2gam-30 representing the 3'end.

30 SEQ ID NO: 273 is the determined DNA sequence for the *C. trachomatis* clone Ctl2gam-28.

- SEQ ID NO: 274 is the determined DNA sequence for the *C. trachomatis* clone Ctl2gam-27.
- SEQ ID NO: 275 is the determined DNA sequence for the *C. trachomatis* clone Ctl2gam-26.
- 5 SEQ ID NO: 276 is the determined DNA sequence for the *C. trachomatis* clone Ctl2gam-24.
- SEQ ID NO: 277 is the determined DNA sequence for the *C. trachomatis* clone Ctl2gam-23.
- 10 SEQ ID NO: 278 is the determined DNA sequence for the *C. trachomatis* clone Ctl2gam-21.
- SEQ ID NO: 279 is the determined DNA sequence for the *C. trachomatis* clone Ctl2gam-18.
- SEQ ID NO: 280 is the determined DNA sequence for the *C. trachomatis* clone Ctl2gam-17.
- 15 SEQ ID NO: 281 is a first determined DNA sequence for the *C. trachomatis* clone Ctl2gam-15 representing the 5' end.
- SEQ ID NO: 282 is a second determined DNA sequence for the *C. trachomatis* clone Ctl2gam-15 representing the 3' end.
- SEQ ID NO: 283 is the determined DNA sequence for the *C. trachomatis* clone Ctl2gam-13.
- 20 SEQ ID NO: 284 is the determined DNA sequence for the *C. trachomatis* clone Ctl2gam-10.
- SEQ ID NO: 285 is the determined DNA sequence for the *C. trachomatis* clone Ctl2gam-8.
- 25 SEQ ID NO: 286 is a first determined DNA sequence for the *C. trachomatis* clone Ctl2gam-6 representing the 5' end.
- SEQ ID NO: 287 is a second determined DNA sequence for the *C. trachomatis* clone Ctl2gam-6 representing the 3' end.
- SEQ ID NO: 288 is the determined DNA sequence for the *C. trachomatis* clone Ctl2gam-5.
- 30 SEQ ID NO: 289 is the determined DNA sequence for the *C. trachomatis* clone Ctl2gam-2.

SEQ ID NO: 290 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-1.

SEQ ID NO: 291 is the determined full-length DNA sequence for the *C. pneumoniae* homologue of the CT529 gene.

5 SEQ ID NO: 292 is the predicted full-length amino acid sequence for the *C. pneumoniae* homologue of the CT529 gene.

SEQ ID NO: 293 is the determined DNA sequence for the insertion sequence for cloning the *C. trachomatis* pmpG gene in the SKB vaccine vector.

10 SEQ ID NO: 294 is the amino acid sequence of an open reading frame of clone CT603.

SEQ ID NO: 295 is the amino acid sequence of a first open reading frame of clone CT875.

SEQ ID NO: 296 is the amino acid sequence of a second open reading frame of clone CT875.

15 SEQ ID NO: 297 is the amino acid sequence of a first open reading frame of clone CT858.

SEQ ID NO: 298 is the amino acid sequence of a second open reading frame of clone CT858.

20 SEQ ID NO: 299 is the amino acid sequence of an open reading frame of clone CT622.

SEQ ID NO: 300 is the amino acid sequence of an open reading frame of clone CT610.

SEQ ID NO: 301 is the amino acid sequence of an open reading frame of clone CT396.

25 SEQ ID NO: 302 is the amino acid sequence of an open reading frame of clone CT318.

SEQ ID NO: 304 is the amino acid sequence for *C. trachomatis*, serovar L2 rCt529c1-125 having a modified N-terminal sequence (6-His tag).

30 SEQ ID NO: 305 is the amino acid sequence for *C. trachomatis*, serovar L2 rCt529c1-125.

SEQ ID NO: 306 is the sense primer used in the synthesis of the PmpA(N-term) fusion protein.

SEQ ID NO: 307 is the antisense primer used in the synthesis of the PmpA(N-term) fusion protein.

SEQ ID NO: 308 is the DNA sequence encoding the PmpA(N-term) fusion protein.

5 SEQ ID NO: 309 is the amino acid sequence of the PmpA(N-term) fusion protein.

SEQ ID NO: 310 is the sense primer used in the synthesis of the PmpA(C-term) fusion protein.

10 SEQ ID NO: 311 is the antisense primer used in the synthesis of the PmpA(C-term) fusion protein.

SEQ ID NO: 312 is the DNA sequence encoding the PmpA(C-term) fusion protein.

SEQ ID NO: 313 is the amino acid sequence of the PmpA(C-term) fusion protein.

15 SEQ ID NO: 314 is the sense primer used in the synthesis of the PmpF(N-term) fusion protein.

SEQ ID NO: 315 is the antisense primer used in the synthesis of the PmpF(N-term) fusion protein.

20 SEQ ID NO: 316 is the DNA sequence encoding the PmpF(N-term) fusion protein.

SEQ ID NO: 317 is the amino acid sequence of the PmpF(N-term) fusion protein.

SEQ ID NO: 318 is the sense primer used in the synthesis of the PmpF(C-term) fusion protein.

25 SEQ ID NO: 319 is the antisense primer used in the synthesis of the PmpF(C-term) fusion protein.

SEQ ID NO: 320 is the DNA sequence encoding the PmpF(C-term) fusion protein.

30 SEQ ID NO: 321 is the amino acid sequence of the PmpF(C-term) fusion protein.

SEQ ID NO: 322 is the sense primer used in the synthesis of the PmpH (CT412) (N-term) fusion protein.

SEQ ID NO: 323 is the antisense primer used in the synthesis of the PmpH(N-term) fusion protein.

SEQ ID NO: 324 is the DNA sequence encoding the PmpH(N-term) fusion protein.

5 SEQ ID NO: 325 is the amino acid sequence of the PmpH(N-term) fusion protein.

SEQ ID NO: 326 is the sense primer used in the synthesis of the PmpH(C-term) fusion protein.

10 SEQ ID NO: 327 is the antisense primer used in the synthesis of the PmpH(C-term) fusion protein.

SEQ ID NO: 328 is the DNA sequence encoding the PmpH(C-term) fusion protein.

SEQ ID NO: 329 is the amino acid sequence of the PmpH(C-term) fusion protein.

15 SEQ ID NO: 330 is the sense primer used in the synthesis of the PmpB(1) fusion protein.

SEQ ID NO: 331 is the antisense primer used in the synthesis of the PmpB(1) fusion protein.

20 SEQ ID NO: 332 is the DNA sequence encoding the PmpB(1) fusion protein.

SEQ ID NO: 333 is the amino acid sequence of the PmpB(1) fusion protein.

SEQ ID NO: 334 is the sense primer used in the synthesis of the PmpB(2) fusion protein.

25 SEQ ID NO: 335 is the antisense primer used in the synthesis of the PmpB(2) fusion protein.

SEQ ID NO: 336 is the DNA sequence encoding the PmpB(2) fusion protein.

30 SEQ ID NO: 337 is the amino acid sequence of the PmpB(2) fusion protein.

SEQ ID NO: 338 is the sense primer used in the synthesis of the PmpB(3) fusion protein.

SEQ ID NO: 339 is the antisense primer used in the synthesis of the PmpB(3) fusion protein.

SEQ ID NO: 340 is the DNA sequence encoding the PmpB(3) fusion protein.

5 SEQ ID NO: 341 is the amino acid sequence of the PmpB(3) fusion protein.

SEQ ID NO: 342 is the sense primer used in the synthesis of the PmpB(4) fusion protein.

10 SEQ ID NO: 343 is the antisense primer used in the synthesis of the PmpB(4) fusion protein.

SEQ ID NO: 344 is the DNA sequence encoding the PmpB(4) fusion protein.

SEQ ID NO: 345 is the amino acid sequence of the PmpB(4) fusion protein.

15 SEQ ID NO: 346 is the sense primer used in the synthesis of the PmpC(1) fusion protein.

SEQ ID NO: 347 is the antisense primer used in the synthesis of the PmpC(1) fusion protein.

20 SEQ ID NO: 348 is the DNA sequence encoding the PmpC(1) fusion protein.

SEQ ID NO: 349 is the amino acid sequence of the PmpC(1) fusion protein.

SEQ ID NO: 350 is the sense primer used in the synthesis of the PmpC(2) fusion protein.

25 SEQ ID NO: 351 is the antisense primer used in the synthesis of the PmpC(2) fusion protein.

SEQ ID NO: 352 is the DNA sequence encoding the PmpC(2) fusion protein.

30 SEQ ID NO: 353 is the amino acid sequence of the PmpC(2) fusion protein.

SEQ ID NO: 354 is the sense primer used in the synthesis of the PmpC(3) fusion protein.

SEQ ID NO: 355 is the antisense primer used in the synthesis of the PmpC(3) fusion protein.

SEQ ID NO: 356 is the DNA sequence encoding the PmpC(3) fusion protein.

5 SEQ ID NO: 357 is the amino acid sequence of the PmpC(3) fusion protein.

SEQ ID NO: 358 is the DNA sequence of the oppA1 protein, devoid of the first trans-membrane domain.

SEQ ID NO: 359 is the full length DNA sequence of CT139.

10 SEQ ID NO: 360 is the full length DNA sequence of ORF-3.

SEQ ID NO: 361 is the full length DNA sequence of CT611.

SEQ ID NO: 362 is the amino acid sequence of oppA1 starting from amino acid 22.

SEQ ID NO: 363 is the amino acid sequence of CT139.

15 SEQ ID NO: 364 is the amino acid sequence of ORF-3.

SEQ ID NO: 365 is the amino acid sequence of CT611.

SEQ ID NO: 366 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0275, of the Chlamydia trachomatis gene CT190.

20 SEQ ID NO: 367 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0407, of the Chlamydia trachomatis gene CT103.

SEQ ID NO: 368 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0720, of the Chlamydia trachomatis gene CT659.

SEQ ID NO: 369 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0716, of the Chlamydia trachomatis gene CT660.

25 SEQ ID NO: 370 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0519, of the Chlamydia trachomatis gene CT430.

SEQ ID NO: 371 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0520, of the Chlamydia trachomatis gene CT431.

30 SEQ ID NO: 372 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0078, of the Chlamydia trachomatis gene CT318.

SEQ ID NO: 373 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0628, of the Chlamydia trachomatis gene CT509.

SEQ ID NO: 374 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0540, of the Chlamydia trachomatis gene CT414.

SEQ ID NO: 375 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, pmp20, of the Chlamydia trachomatis gene CT413.

5 SEQ ID NO: 376 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0081, of the Chlamydia trachomatis gene CT315.

SEQ ID NO: 377 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0761, of the Chlamydia trachomatis gene CT610.

10 SEQ ID NO: 378 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0557, of the Chlamydia trachomatis gene CT443.

SEQ ID NO: 379 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0833, of the Chlamydia trachomatis gene CT557.

SEQ ID NO: 380 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0134, of the Chlamydia trachomatis gene CT604.

15 SEQ ID NO: 381 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0388, of the Chlamydia trachomatis gene CT042.

SEQ ID NO: 382 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn1028, of the Chlamydia trachomatis gene CT376.

20 SEQ ID NO: 383 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0875, of the Chlamydia trachomatis gene CT734.

SEQ ID NO: 384 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0908, of the Chlamydia trachomatis gene CT764.

SEQ ID NO: 385 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0728, of the Chlamydia trachomatis gene CT622.

25 SEQ ID NO: 386 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0275, of the Chlamydia trachomatis gene CT190.

SEQ ID NO: 387 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0407, of the Chlamydia trachomatis gene CT103.

30 SEQ ID NO: 388 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0720, of the Chlamydia trachomatis gene CT659.

SEQ ID NO: 389 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0716, of the Chlamydia trachomatis gene CT660.

SEQ ID NO: 390 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0519, of the Chlamydia trachomatis gene CT430.

SEQ ID NO: 391 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0520, of the Chlamydia trachomatis gene CT431.

5 SEQ ID NO: 392 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0078, of the Chlamydia trachomatis gene CT318.

SEQ ID NO: 393 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0628, of the Chlamydia trachomatis gene CT509.

10 SEQ ID NO: 394 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0540, of the Chlamydia trachomatis gene CT414.

SEQ ID NO: 395 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, pmp20, of the Chlamydia trachomatis gene CT413.

SEQ ID NO: 396 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0081, of the Chlamydia trachomatis gene CT315.

15 SEQ ID NO: 397 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0761, of the Chlamydia trachomatis gene CT610.

SEQ ID NO: 398 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0557, of the Chlamydia trachomatis gene CT443.

20 SEQ ID NO: 399 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0833, of the Chlamydia trachomatis gene CT557.

SEQ ID NO: 400 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0134, of the Chlamydia trachomatis gene CT604.

SEQ ID NO: 401 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0388, of the Chlamydia trachomatis gene CT042.

25 SEQ ID NO: 402 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn1028, of the Chlamydia trachomatis gene CT376.

SEQ ID NO: 403 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0875, of the Chlamydia trachomatis gene CT734.

30 SEQ ID NO: 404 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0908, of the Chlamydia trachomatis gene CT764.

SEQ ID NO: 405 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0728, of the Chlamydia trachomatis gene CT622.

SEQ ID NO: 406 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT287.

SEQ ID NO: 407 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT858.

5 SEQ ID NO: 408 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT764.

SEQ ID NO: 409 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT734.

10 SEQ ID NO: 410 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT660.

SEQ ID NO: 411 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT659.

SEQ ID NO: 412 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT622.

15 SEQ ID NO: 413 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT610.

SEQ ID NO: 414 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT604.

20 SEQ ID NO: 415 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT557.

SEQ ID NO: 416 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT509.

SEQ ID NO: 417 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT443.

25 SEQ ID NO: 418 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT431.

SEQ ID NO: 419 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT430.

30 SEQ ID NO: 420 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT414.

SEQ ID NO: 421 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT413.

SEQ ID NO: 422 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT396.

SEQ ID NO: 423 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT376.

5 SEQ ID NO: 424 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT318.

SEQ ID NO: 425 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT315.

10 SEQ ID NO: 426 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT104.

SEQ ID NO: 427 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT103.

SEQ ID NO: 428 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT102.

15 SEQ ID NO: 429 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT098.

SEQ ID NO: 430 sets forth the full-length serovar D DNA sequence of the *Chlamydia trachomatis* gene CT042.

20 SEQ ID NO: 431 sets forth the full-length serovar D amino acid sequence of the *Chlamydia trachomatis* gene CT858.

SEQ ID NO: 432 sets forth the full-length serovar D amino acid sequence of the *Chlamydia trachomatis* gene CT764.

SEQ ID NO: 433 sets forth the full-length serovar D amino acid sequence of the *Chlamydia trachomatis* gene CT734.

25 SEQ ID NO: 434 sets forth the full-length serovar D amino acid sequence of the *Chlamydia trachomatis* gene CT660.

SEQ ID NO: 435 sets forth the full-length serovar D amino acid sequence of the *Chlamydia trachomatis* gene CT659.

30 SEQ ID NO: 436 sets forth the full-length serovar D amino acid sequence of the *Chlamydia trachomatis* gene CT622.

SEQ ID NO: 437 sets forth the full-length serovar D amino acid sequence of the *Chlamydia trachomatis* gene CT610.

SEQ ID NO: 438 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT604.

SEQ ID NO: 439 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT557.

5 SEQ ID NO: 440 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT509.

SEQ ID NO: 441 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT443.

10 SEQ ID NO: 442 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT431.

SEQ ID NO: 443 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT430.

SEQ ID NO: 444 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT414.

15 SEQ ID NO: 445 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT413.

SEQ ID NO: 446 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT396.

20 SEQ ID NO: 447 sets forth the full length serovar D amino acid sequence of the Chlamydia trachomatis gene CT376.

SEQ ID NO: 448 sets forth the full length serovar D amino acid sequence of the Chlamydia trachomatis gene CT318.

SEQ ID NO: 449 sets forth the full length serovar D amino acid sequence of the Chlamydia trachomatis gene CT315.

25 SEQ ID NO: 450 sets forth the full length serovar D amino acid sequence of the Chlamydia trachomatis gene CT104.

SEQ ID NO: 451 sets forth the full length serovar D amino acid sequence of the Chlamydia trachomatis gene CT103.

30 SEQ ID NO: 452 sets forth the full length serovar D amino acid sequence of the Chlamydia trachomatis gene CT102.

SEQ ID NO: 453 sets forth the full length serovar D amino acid sequence of the Chlamydia trachomatis gene CT098.

SEQ ID NO: 454 sets forth the full length serovar D amino acid sequence of the *Chlamydia trachomatis* gene CT042.

SEQ ID NO: 455 corresponds to the DNA sequence of CPn0894, which is the CP homologue of CT751 (amn), which was identified in clones CTL2-1, and CTL2-5.

SEQ ID NO: 456 corresponds to the DNA sequence of CPn0074, which is the CP homologue of CT322 (tuf), which was identified in clone CTL2-2.

SEQ ID NO: 457 corresponds to the DNA sequence of CPn0122, which is the CP homologue of CT032 (metG), which was identified in clones CTL2gam2, CTL2-3(5') and CTL2-4.

SEQ ID NO: 458 corresponds to the DNA sequence of CPn0121, which is the CP homologue of CT031, which was identified in clone CTL2-3(5')(3').

SEQ ID NO: 459 corresponds to the DNA sequence of CPn0120, which is the CP homologue of CT030 (gmK), which was identified in clones CTL2-3(3') and CTL2-21.

SEQ ID NO: 460 corresponds to the DNA sequence of CPn0359, which is the CP homologue of CT064 (lepA), which was identified in clone CTL2gam5.

SEQ ID NO: 461 corresponds to the DNA sequence of CPn0414, which is the CP homologue of CT265 (accA), which was identified in clone CTL2-6.

SEQ ID NO: 462 corresponds to the DNA sequence of CPn0413, which is the CP homologue of CT264 (msbA), which was identified in clone CTL2-6.

SEQ ID NO: 463 corresponds to the DNA sequence of CPn0394, which is the CP homologue of CT256 which was identified in clones CTL2gam6(5') and CTL2-11(5').

SEQ ID NO: 464 corresponds to the DNA sequence of CPn0395, which is the CP homologue of CT257 which was identified in clones CTL2gam6(5') and CTL2-11(5').

SEQ ID NO: 465 corresponds to the DNA sequence of CPn0487, which is the CP homologue of CT384 which was identified in clones CTL2gam6(3') and CTL2-11(3').

SEQ ID NO: 466 corresponds to the DNA sequence of CPn0592, which is the CP homologue of CT473, which was identified in clone CTL2-8b.

SEQ ID NO: 467 corresponds to the DNA sequence of CPn0593, which is the CP homologue of CT474, which was identified in clone CTL2-8b.

5 SEQ ID NO: 468 corresponds to the DNA sequence of CPn0197, which is the CP homologue of CT139 (oppA1), which was identified in clone CTL2-8b.

SEQ ID NO: 469 corresponds to the DNA sequence of CPn0363, which is the CP homologue of CT060 (flhA), which was identified in clone CTL2-8b.

10 SEQ ID NO: 470 corresponds to the DNA sequence of CPn0301, which is the CP homologue of CT242, which was identified in clone CTL2gam8.

SEQ ID NO: 471 corresponds to the DNA sequence of CPn0302, which is the CP homologue of CT243 (lpxD), which was identified in clone CTL2gam8.

15 SEQ ID NO: 472 corresponds to the DNA sequence of CPn0324, which is the CP homologue of CT089 (lcrE), which was identified in clones CTL2-9, CTL2gam1, CTL2gam17 and CTL2-19(5').

SEQ ID NO: 473 corresponds to the DNA sequence of CPn0761, which is the CP homologue of CT610, which was identified in clone CTL2-10(5')(3').

20 SEQ ID NO: 474 corresponds to the DNA sequence of CPn0760, which is the CP homologue of CT611, which was identified in clone CTL2-10(5').

SEQ ID NO: 475 corresponds to the DNA sequence of CPn0329, which is the CP homologue of CT154, which was identified in clones CTL2gam10 and CTL2gam21.

25 SEQ ID NO: 476 corresponds to the DNA sequence of CPn0990, which is the CP homologue of CT833 (infC), which was identified in clone CTL2-12.

SEQ ID NO: 477 corresponds to the DNA sequence of CPn0984, which is the CP homologue of CT827 (nrdA), which was identified in clones CTL2-16(3') and CTL2gam15(3').

30 SEQ ID NO: 478 corresponds to the DNA sequence of CPn0985 which is the CP homologue of CT828 (nrdB) which was identified in clones CTL2-16(3') CTL2gam15(3').

SEQ ID NO: 479 corresponds to the DNA sequence of CPn0349, which is the CP homologue of CT067 (ytgA), which was identified in clone CTL2gam18.

5 SEQ ID NO: 480 corresponds to the DNA sequence of CPn0325, which is the CP homologue of CT088 (sycE), which was identified in clone CTL2-19(5').

SEQ ID NO: 481 corresponds to the DNA sequence of CPn0326, which is the CP homologue of CT087 (malQ), which was identified in clone CTL2-19(5').

10 SEQ ID NO: 482 corresponds to the DNA sequence of CPn0793, which is the CP homologue of CT588 (rbsu), which was identified in clone CTL2gam23.

SEQ ID NO: 483 corresponds to the DNA sequence of CPn0199, which is the CP homologue of CT199 (oppB1), which was identified in clone
15 CTL2gam24.

SEQ ID NO: 484 corresponds to the DNA sequence of CPn0666, which is the CP homologue of CT545 (dnaE), which was identified in clone CTL2-24.

SEQ ID NO: 485 corresponds to the DNA sequence of CPn0065, which is the CP homologue of CT288, which was identified in clone CTL2gam27.

20 SEQ ID NO: 486 corresponds to the DNA sequence of CPn0444, which is the CP homologue of CT413 (pmpB), which was identified in clone CTL2gam30(5')(3').

SEQ ID NO: 487 corresponds to the DNA sequence of CPn-ORF5, which is the CP homologue of CT-ORF3, which was identified in clones
25 CTL2gam15(5'), CTL2-16(5'), CTL2-18(5'), and CTL2-23.

SEQ ID NO: 488 corresponds to the DNA sequence of CPn-ORF6, which is the CP homologue of CT-ORF4, which was identified in clone CTL2-18(3').

30 SEQ ID NO: 489 corresponds to the DNA sequence of CP-ORF7, which is the CP homologue of CT-ORF5, which was identified in clone CTL2-18(3').

SEQ ID NO: 490 corresponds to the amino acid sequence of CPn0894, which is the CP homologue of CT1751 (amn), which was identified in clones CTL2-1 and CTL2-5.

5 SEQ ID NO: 491 corresponds to the amino acid sequence of CPn0074, which is the CP homologue of CT332 (tuf), which was identified in clone CTL2-2.

 SEQ ID NO: 492 corresponds to the amino acid sequence of CPn0122, which is the CP homologue of CT032 (metG), which was identified in clones CTL2gam2, CTL2-3(5') and CTL2-4.

10 SEQ ID NO: 493 corresponds to the amino acid sequence of CPn0121, which is the CP homologue of CT031, which was identified in clone CTL2-3(5')(3').

 SEQ ID NO: 494 corresponds to the amino acid sequence of CPn0120 which is the CP homologue of CT030 (gmK) which was identified in clones
15 CTL2-3 (3') and CTL2-21.

 SEQ ID NO: 495 corresponds to the amino acid sequence of CPn0359, which is the CP homologue of CT064 (lepA), which was identified in clone CTL2gam5.

20 SEQ ID NO: 496 corresponds to the amino acid sequence of CPn0414, which is the CP homologue of CT265 (accA), which was identified in clone CTL2-6.

 SEQ ID NO: 497 corresponds to the amino acid sequence of CPn0413, which is the CP homologue of CT264 (msbA), which was identified in clone CTL2-6.

25 SEQ ID NO: 498 corresponds to the amino acid sequence of CPn0394, which is the CP homologue of CT256, which was identified in clones CTL2gam6(5') and CTL2-11(5').

30 SEQ ID NO: 499 corresponds to the amino acid sequence of CPn0395, which is the CP homologue of CT257, which was identified in clones CTL2gam6(5') and CTL2-11(5').

SEQ ID NO: 500 corresponds to the amino acid sequence of CPn0487, which is the CP homologue of CT384, which was identified in clones CTL2gam6(3') and CTL2-11(3').

5 SEQ ID NO: 501 corresponds to the amino acid sequence of CPn0592, which is the CP homologue of CT473, which was identified in clone CTL2-8b.

SEQ ID NO: 502 corresponds to the amino acid sequence of CPn0593, which is the CP homologue of CT474, which was identified in clone CTL2-8b.

10 SEQ ID NO: 503 corresponds to the amino acid sequence of CPn0197, which is the CP homologue of CT139 (oppA1), which was identified in clone CTL2-8b.

SEQ ID NO: 504 corresponds to the amino acid sequence of CPn0363, which is the CP homologue of CT060 (flhA), which was identified in clone CTL2-8b.

15 SEQ ID NO: 505 corresponds to the amino acid sequence of CPn0301, which is the CP homologue of CT242, which was identified in clone CTL2gam8.

SEQ ID NO: 506 corresponds to the amino acid sequence of CPn0302, which is the CP homologue of CT243 (lpxD), which was identified in clone CTL2gam8.

20 SEQ ID NO: 507 corresponds to the amino acid sequence of CPn0324, which is the CP homologue of CT089 (lcrE), which was identified in clones CTL2-9, CTL2gam1, CTL2gam17 and CTL2-19(5').

25 SEQ ID NO: 508 corresponds to the amino acid sequence of CPn0761, which is the CP homologue of CT610, which was identified in clone CTL2-10(5')(3').

SEQ ID NO: 509 corresponds to the amino acid sequence of CPn0760, which is the CP homologue of CT611, which was identified in clone CTL2-10(5').

30 SEQ ID NO: 510 corresponds to the amino acid sequence of CPn0329, which is the CP homologue of CT154, which was identified in clones CTL2gam10 and CTL2gam21.

SEQ ID NO: 511 corresponds to the amino acid sequence of CPn0990, which is the CP homologue of CT833 (infC), which was identified in clone CTL2-12.

5 SEQ ID NO: 512 corresponds to the amino acid sequence of CPn-ORF5, which is the CP homologue of CT ORF3, which was identified in clones CTL2gam15(5'), CTL2-16(5'), CTL2-18(5'), and CTL2-23.

 SEQ ID NO: 513 corresponds to the amino acid sequence of CPn0984, which is the CP homologue of CT827 (nrdA) which was identified in clones CTL2-16(3') and CTL2gam15(3').

10 SEQ ID NO: 514 corresponds to the amino acid sequence of CPn0985, which is the CP homologue of CT828 (nrdB) which was identified in clones CTL2-16(3') CTL2gam15(3').

 SEQ ID NO: 515 corresponds to the amino acid sequence of CPn0349, which is the CP homologue of CT067 (ytgA), which was identified in clone
15 CTL2gam18.

 SEQ ID NO: 516 corresponds to the DNA sequence of CPn-ORF6, which is the CP homologue of CT-ORF4, which was identified in clone CTL2-18(3').

20 SEQ ID NO: 517 corresponds to the DNA sequence of CP-ORF7, which is the CP homologue of CT-ORF5, which was identified in clone CTL2-18(3').

 SEQ ID NO: 518 corresponds to the amino acid sequence of CPn0326, which is the CP homologue of CT087 (malQ), which was identified in clone CTL2-19(5').

25 SEQ ID NO: 519 corresponds to the amino acid sequence of CPn0325, which is the CP homologue of CT088 (sycE), which was identified in clone CTL2-19(5').

 SEQ ID NO: 520 corresponds to the amino acid sequence of CPn0793, which is the CP homologue of CT588 (rbsu), which was identified in clone CTL2gam23.

30 SEQ ID NO: 521 corresponds to the amino acid sequence of CPn0199, which is the CP homologue of CT199 (oppB1), which was identified in clone CTL2gam24.

SEQ ID NO: 522 corresponds to the amino acid sequence of CPn0666, which is the CP homologue of CT545 (dnaE), which was identified in clone CTL2-24.

5 SEQ ID NO: 523 corresponds to the DNA sequence of CPn0065, which is the CP homologue of CT288, which was identified in clone CTL2gam27.

SEQ ID NO: 524 corresponds to the DNA sequence of CPn0444, which is the CP homologue of CT413 (pmpB), which was identified in clone CTL2gam30(5')(3').

10 SEQ ID NO: 525 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT751 (amn) identified from the clones CTL2-1 and CTL2-5.

SEQ ID NO: 526 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT322 (tuff) identified from the clone CTL2-2.

15 SEQ ID NO: 527 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT032 (metG) identified from the clones CTL2gam2, CTL2-3(5') and CTL2-4.

20 SEQ ID NO: 528 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT031 identified from the clone CTL2-3(5')(3').

SEQ ID NO: 529 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT030 (gmK) identified from the clones CTL2-3(3') and CTL2-21.

25 SEQ ID NO: 530 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT064 (lepA) identified from the clone CTL2gam5.

SEQ ID NO: 531 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT265 (accA) identified from the clone CTL2-6.

30 SEQ ID NO: 532 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT624 (msbA) identified from the clones CTL2-6.

SEQ ID NO: 533 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT256 identified from the clones CTL2gam6(5') and CTL2-11(5').

5 SEQ ID NO: 534 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT257 identified from the clones CTL2gam6(5') and CTL2-11(5').

SEQ ID NO: 535 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT384 identified from the clones CTL2gam6(3') and CTL2-11(3').

10 SEQ ID NO: 536 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT473 identified from the clone CTL2-8b.

SEQ ID NO: 537 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT474 identified from the clones CTL2-8b.

15 SEQ ID NO: 538 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT139 (oppA1) identified from the clones CTL2-8b.

20 SEQ ID NO: 539 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT060 (flhA) identified from the clone CTL2-8b.

SEQ ID NO: 540 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT242 identified from the clone CTL2gam8.

25 SEQ ID NO: 541 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT243 (lpxD) identified from the clone CTL2gam8.

30 SEQ ID NO: 542 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT089 identified from the clones CTL2-9, CTL2gam1, CTL2gam17, and CTL2-19(5').

SEQ ID NO: 543 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT610 identified from the clone CTL2-10 (5')(3').

5 SEQ ID NO: 544 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT611 identified from the clone CTL2-10(5').

SEQ ID NO: 545 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT154 identified from the clones CTL2gam10 and CTL2gam21.

10 SEQ ID NO: 546 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT833 (infC) identified from the clone CTL2-12.

SEQ ID NO: 547 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT827 (nrnA) identified from the clones CTL2-16(3') and CTL2gam15(3').

15 SEQ ID NO: 548 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT828 (nrnB) identified from the clones CTL2-16(3') and CTL2gam15(3').

SEQ ID NO: 549 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT067 (yngA) identified from the clone CTL2gam18.

SEQ ID NO: 550 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT088 (sycE) identified from the clones CTL2-19(5').

25 SEQ ID NO: 551 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT087 identified from the clone CTL2-19(5').

SEQ ID NO: 552 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT588 (rsbu) identified from the clone CTL2gam23.

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SEQ ID NO: 553 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT199 (oppB1) identified from the clone CTL2gam24.

5 SEQ ID NO: 554 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT545 (dnaE) identified from the clone CTL2-4.

SEQ ID NO: 555 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT288 identified from the clones CTL2gam27.

10 SEQ ID NO: 556 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT413 (pmpB) identified from the clone CTL2gam30(5')(3').

SEQ ID NO: 557 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT-ORF3 identified from the clones CTL2gam15(5'), CTL2-16(5'), CTL2-18(5') and CTL2-23.

15 SEQ ID NO: 558 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for pCT-ORF4 identified from the clone CTL2-18(3').

20 SEQ ID NO: 559 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT-ORF5 identified from the clones CTL2-18(3').

SEQ ID NO: 560 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT751 (amn) identified from the clones CTL2-1 and CTL2-5.

25 SEQ ID NO: 561 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT322 (tuff) identified from the clone CTL2-2.

30 SEQ ID NO: 562 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT032 (metG) identified from the clones CTL2gam2, CTL2-3(5') and CTL2-4.

SEQ ID NO: 563 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT031 identified from the clone CTL2-3(5')(3').

5 SEQ ID NO: 564 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT030 (gmK) identified from the clones CTL2-3(3') and CTL2-21.

SEQ ID NO: 565 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT064 (lepA) identified from the clone CTL2gam5.

10 SEQ ID NO: 566 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT265 (accA) identified from the clone CTL2-6.

SEQ ID NO: 567 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT624 (msbA) identified from the clones CTL2-6.

15 SEQ ID NO: 568 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT256 identified from the clones CTL2gam6(5') and CTL2-11(5').

20 SEQ ID NO: 569 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT257 identified from the clones CTL2gam6(5') and CTL2-11(5').

SEQ ID NO: 570 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT384 identified from the clones CTL2gam6(3') and CTL2-11(3').

25 SEQ ID NO: 571 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT473 identified from the clone CTL2-8b.

30 SEQ ID NO: 572 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT474 identified from the clones CTL2-8b.

SEQ ID NO: 573 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT139 (oppA1) identified from the clones CTL2-8b.

5 SEQ ID NO: 574 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT060 (flhA) identified from the clone CTL2-8b.

SEQ ID NO: 575 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT242 identified from the clone CTL2gam8.

10 SEQ ID NO: 576 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT243 (lpxD) identified from the clone CTL2gam8.

SEQ ID NO: 577 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT089 identified from the clones CTL2-9, CTL2gam1, CTL2gam17, and CTL2-19(5').

SEQ ID NO: 578 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT610 identified from the clone CTL2-10 (5')(3').

20 SEQ ID NO: 579 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT611 identified from the clone CTL2-10(5').

SEQ ID NO: 580 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT154 identified from the clones CTL2gam10 and CTL2gam21.

25 SEQ ID NO: 581 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT833 (infC) identified from the clone CTL2-12.

30 SEQ ID NO: 582 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT-ORF3 identified from the clones CTL2gam15(5'), CTL2-16(5'), CTL2-18(5') and CTL2-23.

SEQ ID NO: 583 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT827 (nrdA) identified from the clones CTL2-16(3') and CTL2gam15(3').

5 SEQ ID NO: 584 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT828 (nrdB) identified from the clones CTL2-16(3') and CTL2gam15(3').

SEQ ID NO: 585 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT067 (ytgA) identified from the clone CTL2gam18.

10 SEQ ID NO: 586 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for pCT-ORF4 identified from the clone CTL2-18(3').

SEQ ID NO: 587 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT-ORF5 identified from the clones CTL2-18(3').

15 SEQ ID NO: 588 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT087 identified from the clone CTL2-19(5').

SEQ ID NO: 589 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT088 (sycE) identified from the clones CTL2-19(5').

20 SEQ ID NO: 590 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT588 (rsbu) identified from the clone CTL2gam23.

25 SEQ ID NO: 591 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT199 (oppB1) identified from the clone CTL2gam24.

SEQ ID NO: 592 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT545 (dnaE) identified from the clone CTL2-4.

30

SEQ ID NO: 593 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT288 identified from the clones CTL2gam27.

5 SEQ ID NO: 594 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT413 (pmpB) identified from the clone CTL2gam30(5')(3').

SEQ ID NO: 595 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0406, of the Chlamydia trachomatis gene CT102.

10 SEQ ID NO: 596 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0315, of the Chlamydia trachomatis gene CT098.

SEQ ID NO: 597 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0406, of the Chlamydia trachomatis gene CT102.

SEQ ID NO: 598 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0315, of the Chlamydia trachomatis gene CT098.

15 SEQ ID NO: 599 sets forth the amino acid sequence for Chlamydia trachomatis serovar D CT287 protein.

DESCRIPTION OF THE FIGURES

20 Fig. 1 illustrates induction of INF- γ from a *Chlamydia*-specific T cell line activated by target cells expressing clone 4C9-18#2.

Fig. 2 illustrates retroviral vectors pBIB-KS1,2,3 modified to contain a Kosak translation initiation site and stop codons.

Fig. 3 shows specific lysis in a chromium release assay of P815 cells pulsed with *Chlamydia* peptides CtC7.8-12 (SEQ ID NO: 18) and CtC7.8-13 (SEQ ID NO: 19).

25 Fig. 4 shows antibody isotype titers in C57Bl/6 mice immunized with *C. trachomatis* SWIB protein.

Fig. 5 shows *Chlamydia*-specific T-cell proliferative responses in splenocytes from C3H mice immunized with *C. trachomatis* SWIB protein.

30 Fig. 6 illustrates the 5' and 3' primer sequences designed from *C. pneumoniae* which were used to isolate the SWIB and S13 genes from *C. pneumoniae*.

Figs. 7A and 7B show induction of IFN- γ from a human anti-*chlamydia* T-cell line (TCL-8) capable of cross-reacting to *C. trachomatis* and *C. pneumonia* upon activation by monocyte-derived dendritic cells expressing chlamydial proteins.

Fig. 8 shows the identification of T cell epitopes in Chlamydial ribosomal S13 protein with T-cell line TCL 8 EB/DC.

Fig. 9A and B illustrate the proliferative response of CP-21 T-cells generated against *C. pneumoniae*-infected dendritic cells to recombinant *C. pneumonia*-SWIB protein, but not *C. trachomatis* SWIB protein.

Fig. 10 shows the *C. trachomatis*-specific SWIB proliferative responses of a primary T-cell line (TCT-10 EB) from an asymptomatic donor.

Fig. 11 illustrates the identification of T-cell epitope in *C. trachomatis* SWIB with an antigen specific T-cell line (TCL-10 EB).

Fig. 12 shows the *C. trachomatis*-specific proliferative responses of primary T cell lines generated from two patients against the CT specific antigens CT622, CT875 and CT
EB.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the diagnosis and treatment of Chlamydial infection. In one aspect, the compositions of the subject invention include polypeptides that comprise at least one immunogenic portion of a *Chlamydia* antigen, or a variant thereof.

In specific embodiments, the subject invention discloses polypeptides comprising an immunogenic portion of a *Chlamydia* antigen, wherein the *Chlamydia* antigen comprises an amino acid sequence encoded by a polynucleotide molecule disclosed herein, the complements of said nucleotide sequences, and variants of such sequences.

As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins (*i.e.*, antigens), wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising an immunogenic portion of one of the inventive antigens may consist entirely of the immunogenic portion, or may contain additional sequences. The additional sequences

may be derived from the native *Chlamydia* antigen or may be heterologous, and such sequences may (but need not) be immunogenic.

The term "polynucleotide(s)," as used herein, means a single or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases and includes DNA and
5 corresponding RNA molecules, including HnRNA and mRNA molecules, both sense and anti-sense strands, and comprehends cDNA, genomic DNA and recombinant DNA, as well as wholly or partially synthesized polynucleotides. An HnRNA molecule contains introns and corresponds to a DNA molecule in a generally one-to-one manner. An mRNA molecule corresponds to an HnRNA and DNA molecule from which the
10 introns have been excised. A polynucleotide may consist of an entire gene, or any portion thereof. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of "polynucleotide" therefore includes all such operable anti-sense fragments.

An "immunogenic portion" of an antigen is a portion that is capable of
15 reacting with sera obtained from a *Chlamydia*-infected individual (*i.e.*, generates an absorbance reading with sera from infected individuals that is at least three standard deviations above the absorbance obtained with sera from uninfected individuals, in a representative ELISA assay described herein). Such immunogenic portions generally comprise at least about 5 amino acid residues, more preferably at least about 10, and
20 most preferably at least about 20 amino acid residues. Methods for preparing and identifying immunogenic portions of antigens of known sequence are well known in the art and include those summarized in Paul, *Fundamental Immunology*, 3rd ed., Raven Press, 1993, pp. 243-247 and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera
25 and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well known techniques. An immunogenic portion of a native *Chlamydia* protein is a portion
30 that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is

similar to or greater than the reactivity of the full length polypeptide. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A.

Examples of immunogenic portions of antigens contemplated by the present invention include, for example, the T cell stimulating epitopes provided in SEQ ID NO: 9, 10, 18, 19, 31, 39, 93-96, 98, 100-102, 106, 108, 138-140, 158, 167, 168, 246, 247 and 254-256. Polypeptides comprising at least an immunogenic portion of one or more *Chlamydia* antigens as described herein may generally be used, alone or in combination, to detect Chlamydial infection in a patient.

The compositions and methods of the present invention also encompass variants of the above polypeptides and polynucleotide molecules. Such variants include, but are not limited to, naturally occurring allelic variants of the inventive sequences. In particular, variants include other *Chlamydiae* serovars, such as serovars D, E and F, as well as the several LGV serovars which share homology to the inventive polypeptide and polynucleotide molecules described herein. Preferably, the serovar homologues show 95-99% homology to the corresponding polypeptide sequence(s) described herein.

A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the antigenic properties of the polypeptide are retained. In a preferred embodiment, variant polypeptides differ from an identified sequence by substitution, deletion or addition of five amino acids or fewer. Such variants may generally be identified by modifying one of the above polypeptide sequences, and evaluating the antigenic properties of the modified polypeptide using, for example, the representative procedures described herein. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above

polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein. Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants
5 in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and
10 hydropathic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with
15 uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A
20 variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydropathic nature of the
25 polypeptide. Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydropathic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the
30 protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to

enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A polynucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions such that the immunogenicity of the encoded polypeptide is not diminished, relative to the native protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 10 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants as discussed below, or non-naturally occurring variants. The polypeptides provided by the present invention include variants that are encoded by polynucleotide sequences which are substantially homologous to one or more of the polynucleotide sequences specifically recited herein. "Substantial homology," as used herein, refers to polynucleotide sequences that are capable of hybridizing under moderately stringent 15 conditions. Suitable moderately stringent conditions include prewashing in a solution of 5X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5X SSC, overnight or, in the event of cross-species homology, at 45°C with 0.5X SSC; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC 20 containing 0.1% SDS. Such hybridizing polynucleotide sequences are also within the scope of this invention, as are nucleotide sequences that, due to code degeneracy, encode a polypeptide that is the same as a polypeptide of the present invention.

Two nucleotide or polypeptide sequences are said to be "identical" if the sequence of nucleotides or amino acid residues in the two sequences is the same when 25 aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a 30 reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) Fast and sensitive multiple sequence alignments on a microcomputer *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) Optimal alignments in linear space *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) The neighbor joining method. A new method for reconstructing phylogenetic trees *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) Rapid similarity searches of nucleic acid and protein data banks *Proc. Natl. Acad., Sci. USA* 80:726-730.

Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Adv. Appl. Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. (U.S.A.)* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

One illustrative example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nuc. Acids Res.* 25:3389-3402 and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent sequence identity for the polynucleotides and polypeptides of the invention. Software for performing BLAST analyses is publicly available through the National Center for

Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>) In one illustrative example, cumulative scores can be calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix can be used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915) alignments, (B) of 50, expectation (E) of 10, M=5, N=-4 and a comparison of both strands.

Preferably, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or amino acid sequence in the comparison window may comprise additions or deletions (i.e. gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (i.e. the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Therefore, the present invention provides polynucleotide and polypeptide sequences having substantial identity to the sequences disclosed herein, for example those comprising at least 50% or more sequence identity, preferably at least 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or higher, sequence identity compared to a polynucleotide or polypeptide sequence of this invention using the methods described herein, (e.g., BLAST analysis using standard parameters, as described below). One skilled in this art will recognize that these values can be

appropriately adjusted to determine corresponding identity of proteins encoded by two polynucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like.

In additional embodiments, the present invention provides isolated
5 polynucleotides or polypeptides comprising various lengths of contiguous stretches of sequence identical to or complementary to one or more of the sequences disclosed herein. For example, polynucleotides and polypeptides encompassed by this invention may comprise at least about 15, 20, 30, 40, 50, 75, 100, 150, 200, 300, 400, 500 or 1000
10 or more contiguous nucleotides of one or more of the disclosed sequences, as well as all intermediate lengths therebetween. It will be readily understood that "intermediate lengths", in this context, means any length between the quoted values, such as 16, 17, 18, 19, *etc.*; 21, 22, 23, *etc.*; 30, 31, 32, *etc.*; 50, 51, 52, 53, *etc.*; 100, 101, 102, 103, *etc.*; 150, 151, 152, 153, *etc.*; including all integers through the 200-500; 500-1,000, and the like.

15 The polynucleotides of the present invention, or fragments thereof, regardless of the length of the coding sequence itself, may be combined with other DNA sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length may vary considerably. It is therefore contemplated that a nucleic acid fragment
20 of almost any length may be employed, with the total length preferably being limited by the ease of preparation and use in the intended recombinant DNA protocol. For example, illustrative DNA segments with total lengths of about 10,000, about 5000, about 3000, about 2,000, about 1,000, about 500, about 200, about 100, about 50 base pairs in length, and the like, (including all intermediate lengths) are contemplated to be
25 useful in many implementations of this invention.

Also included in the scope of the present invention are alleles of the genes encoding the nucleotide sequences recited in herein. As used herein, an "allele" or "allelic sequence" is an alternative form of the gene which may result from at least one mutation in the nucleic acid sequence. Alleles may result in altered mRNAs or
30 polypeptides whose structure or function may or may not be altered. Any given gene may have none, one, or many allelic forms. Common mutational changes which give rise to alleles are generally ascribed to natural deletions, additions, or substitutions of

nucleotides. Each of these types of changes may occur alone or in combination with the others, one or more times in a given sequence.

In specific embodiments, the subject invention discloses polypeptides comprising at least an immunogenic portion of a *Chlamydia* antigen (or a variant of such an antigen), that comprises one or more of the amino acid sequences encoded by (a) a polynucleotide sequence selected from the group consisting of SEQ ID NO: 358-361, 407-430, 525-559, 582-598; (b) the complements of such DNA sequences or (c) DNA sequences substantially homologous to a sequence in (a) or (b). As discussed in the Examples below, several of the *Chlamydia* antigens disclosed herein recognize a T cell line that recognizes both *Chlamydia trachomatis* and *Chlamydia pneumoniae* infected monocyte-derived dendritic cells, indicating that they may represent an immunoreactive epitope shared by *Chlamydia trachomatis* and *Chlamydia pneumoniae*. The antigens may thus be employed in a vaccine for both *C. trachomatis* genital tract infections and for *C. pneumonia* infections. Further characterization of these *Chlamydia* antigens from *Chlamydia trachomatis* and *Chlamydia pneumonia* to determine the extent of cross-reactivity is provided in Example 6. Additionally, Example 4 describes cDNA fragments (SEQ ID NO: 15, 16 and 33) isolated from *C. trachomatis* which encode proteins (SEQ ID NO: 17-19 and 32) capable of stimulating a *Chlamydia*-specific murine CD8+ T cell line.

In general, *Chlamydia* antigens, and polynucleotide sequences encoding such antigens, may be prepared using any of a variety of procedures. For example, polynucleotide molecules encoding *Chlamydia* antigens may be isolated from a *Chlamydia* genomic or cDNA expression library by screening with a *Chlamydia*-specific T cell line as described below, and sequenced using techniques well known to those of skill in the art. Additionally, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for *Chlamydia*-associated expression (*i.e.*, expression that is at least two fold greater in *Chlamydia*-infected cells than in controls, as determined using a representative assay provided herein). Such screens may be performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polypeptides may be amplified from cDNA

prepared from cells expressing the proteins described herein.. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

5 Antigens may be produced recombinantly, as described below, by inserting a polynucleotide sequence that encodes the antigen into an expression vector and expressing the antigen in an appropriate host. Antigens may be evaluated for a desired property, such as the ability to react with sera obtained from a *Chlamydia*-infected individual as described herein, and may be sequenced using, for example, 10 traditional Edman chemistry. See Edman and Berg, *Eur. J. Biochem.* 80:116-132, 1967.

Polynucleotide sequences encoding antigens may also be obtained by screening an appropriate *Chlamydia* cDNA or genomic DNA library for polynucleotide sequences that hybridize to degenerate oligonucleotides derived from partial amino acid sequences of isolated antigens. Degenerate oligonucleotide sequences for use in such a 15 screen may be designed and synthesized, and the screen may be performed, as described (for example) in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY (and references cited therein). Polymerase chain reaction (PCR) may also be employed, using the above oligonucleotides in methods well known in the art, to isolate a nucleic acid probe from a 20 cDNA or genomic library. The library screen may then be performed using the isolated probe.

An amplified portion may be used to isolate a full length gene from a suitable library (e.g., a *Chlamydia* cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more 25 polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (e.g., by 30 nick-translation or end-labeling with ³²P) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (see

Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using
5 a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into a single contiguous sequence. A full length cDNA molecule can be
10 generated by ligating suitable fragments, using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed
15 using techniques well known in the art (*see*, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.* 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989), and software well known in the art may also be employed. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target sequence at temperatures of about 68°C to 72°C. The amplified region may
20 be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation
25 and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known
30 region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods*

Appl. 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res.* 19:3055-60, 1991). Transcription-Mediated Amplification, or TMA is another method that may be utilized for the amplification of DNA, rRNA, or mRNA, as described in Patent No. PCT/US91/03184. This autocatalytic and isothermic non-PCR based method utilizes two primers and two enzymes: RNA polymerase and reverse transcriptase. One primer contains a promoter sequence for RNA polymerase. In the first amplification, the promoter-primer hybridizes to the target rRNA at a defined site. Reverse transcriptase creates a DNA copy of the target rRNA by extension from the 3' end of the promoter-primer. The RNA in the resulting complex is degraded and a second primer binds to the DNA copy. A new strand of DNA is synthesized from the end of the primer by reverse transcriptase creating double stranded DNA. RNA polymerase recognizes the promoter sequence in the DNA template and initiates transcription. Each of the newly synthesized RNA amplicons re-enters the TMA process and serves as a template for a new round of replication leading to the exponential expansion of the RNA amplicon. Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (e.g., NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length cDNA sequences may also be obtained by analysis of genomic fragments.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (see Adelman et al., *DNA* 2:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding a *Chlamydial* protein, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded

polypeptide is generated *in vivo* (e.g., by transfecting antigen-presenting cells, such as dendritic cells, with a cDNA construct encoding a *Chlamydial* polypeptide, and administering the transfected cells to the patient).

A portion of a sequence complementary to a coding sequence (i.e., an antisense polynucleotide) may also be used as a probe or to modulate gene expression. cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells of tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of a *Chlamydial* protein. Antisense technology can be used to control gene expression through triple-helix formation, which compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (see Gee et al., *In Huber and Carr, Molecular and Immunologic Approaches*, Futura Publishing Co. (Mt. Kisco, NY; 1994)). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (e.g., promoter, enhancer or transcription initiation site), and block transcription of the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

A portion of a coding sequence, or of a complementary sequence, may also be designed as a probe or primer to detect gene expression. Probes may be labeled with a variety of reporter groups, such as radionuclides and enzymes, and are preferably at least 10 nucleotides in length, more preferably at least 20 nucleotides in length and still more preferably at least 30 nucleotides in length. Primers, as noted above, are preferably 22-30 nucleotides in length.

Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl- methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of

particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be
5 apparent to those of ordinary skill in the art.

Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase
10 synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division, Foster City, CA, and may be operated according to the manufacturer's instructions.

As noted above, immunogenic portions of *Chlamydia* antigens may be
15 prepared and identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3d ed., Raven Press, 1993, pp. 243-247 and references cited therein. Such techniques include screening polypeptide portions of the native antigen for immunogenic properties. The representative ELISAs described herein may
20 generally be employed in these screens. An immunogenic portion of a polypeptide is a portion that, within such representative assays, generates a signal in such assays that is substantially similar to that generated by the full length antigen. In other words, an immunogenic portion of a *Chlamydia* antigen generates at least about 20%, and preferably about 100%, of the signal induced by the full length antigen in a model
25 ELISA as described herein.

Portions and other variants of *Chlamydia* antigens may be generated by synthetic or recombinant means. Variants of a native antigen may generally be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis. Sections of the polynucleotide sequence may also be removed using
30 standard techniques to permit preparation of truncated polypeptides.

Recombinant polypeptides containing portions and/or variants of a native antigen may be readily prepared from a polynucleotide sequence encoding the

polypeptide using a variety of techniques well known to those of ordinary skill in the art. For example, supernatants from suitable host/vector systems which secrete recombinant protein into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant protein.

Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides as described herein.

Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a polynucleotide molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as COS or CHO. The DNA sequences expressed in this manner may encode naturally occurring antigens, portions of naturally occurring antigens, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in an isolated, substantially pure, form. Preferably, the polypeptides are at least about 80% pure, more preferably at least about 90% pure and most preferably at least about 99% pure.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known *Chlamydial* protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein. A DNA sequence encoding a fusion protein of the present invention may be constructed using known recombinant

DNA techniques to assemble separate DNA sequences encoding, for example, the first and second polypeptides, into an appropriate expression vector. The 3' end of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8562, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. As an alternative to the use of a peptide linker sequence (when desired), one can utilize non-essential N-terminal amino acid regions (when present) on the first and second polypeptides to separate the functional domains and prevent steric hindrance.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the

immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see*, for example, Stoute et al. *New Engl. J. Med.*, 336:86-91, 1997).

Within preferred embodiments, an immunological fusion partner is
5 derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred
10 embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different
15 fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986).
20 LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA
25 fragment at the amino terminus has been described (*see Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In another embodiment, a *Mycobacterium tuberculosis*-derived Ra12
30 polynucleotide is linked to at least an immunogenic portion of a polynucleotide of this invention. Ra12 compositions and methods for their use in enhancing expression of heterologous polynucleotide sequences is described in U.S. Patent Application

60/158,585, the disclosure of which is incorporated herein by reference in its entirety. Briefly, Ra12 refers to a polynucleotide region that is a subsequence of a *Mycobacterium tuberculosis* MTB32A nucleic acid. MTB32A is a serine protease of 32 KD molecular weight encoded by a gene in virulent and avirulent strains of *M. tuberculosis*. The nucleotide sequence and amino acid sequence of MTB32A have been described (U.S. Patent Application 60/158,585; see also, Skeiky *et al.*, *Infection and Immun.* (1999) 67:3998-4007, incorporated herein by reference. In one embodiment, the Ra12 polypeptide used in the production of fusion polypeptides comprises a C-terminal fragment of the MTB32A coding sequence that is effective for enhancing the expression and/or immunogenicity of heterologous Chlamydial antigenic polypeptides with which it is fused. In another embodiment, the Ra12 polypeptide corresponds to an approximately 14 kD C-terminal fragment of MTB32A comprising some or all of amino acid residues 192 to 323 of MTB32A.

Recombinant nucleic acids, which encode a fusion polypeptide comprising a Ra12 polypeptide and a heterologous Chlamydia polypeptide of interest, can be readily constructed by conventional genetic engineering techniques. Recombinant nucleic acids are constructed so that, preferably, a Ra12 polynucleotide sequence is located 5' to a selected heterologous Chlamydia polynucleotide sequence. It may also be appropriate to place a Ra12 polynucleotide sequence 3' to a selected heterologous polynucleotide sequence or to insert a heterologous polynucleotide sequence into a site within a Ra12 polynucleotide sequence.

In addition, any suitable polynucleotide that encodes a Ra12 or a portion or other variant thereof can be used in constructing recombinant fusion polynucleotides comprising Ra12 and one or more Chlamydia polynucleotides disclosed herein. Preferred Ra12 polynucleotides generally comprise at least about 15 consecutive nucleotides, at least about 30 nucleotides, at least about 60 nucleotides, at least about 100 nucleotides, at least about 200 nucleotides, or at least about 300 nucleotides that encode a portion of a Ra12 polypeptide.

Ra12 polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a Ra12 polypeptide or a portion thereof) or may comprise a variant of such a sequence. Ra12 polynucleotide variants may contain one

or more substitutions, additions, deletions and/or insertions such that the biological activity of the encoded fusion polypeptide is not substantially diminished, relative to a fusion polypeptide comprising a native Ra12 polypeptide. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native Ra12 polypeptide or a portion thereof.

In another aspect, the present invention provides methods for using one or more of the above polypeptides or fusion proteins (or polynucleotides encoding such polypeptides or fusion proteins) to induce protective immunity against Chlamydial infection in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease and/or infection. In other words, protective immunity may be induced to prevent or treat Chlamydial infection.

In this aspect, the polypeptide, fusion protein or polynucleotide molecule is generally present within a pharmaceutical composition or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. Vaccines may comprise one or more of the above polypeptides and an immunostimulant, such as an adjuvant or a liposome (into which the polypeptide is incorporated). Such pharmaceutical compositions and vaccines may also contain other *Chlamydia* antigens, either incorporated into a combination polypeptide or present within a separate polypeptide.

Alternatively, a vaccine may contain polynucleotides encoding one or more polypeptides or fusion proteins as described above, such that the polypeptide is generated *in situ*. In such vaccines, the polynucleotides may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacterial and viral expression systems. Appropriate nucleic acid expression systems contain the necessary polynucleotide sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface. In a

preferred embodiment, the polynucleotides may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective) virus. Techniques for incorporating polynucleotides into such expression systems are well known to those of ordinary skill in the art. The polynucleotides may also be administered as "naked" plasmid vectors as described, for example, in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also be accomplished using an antibody, by methods known to those of ordinary skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (i.e., an artificial membrane vesicle). The uptake of naked polynucleotides may be increased by incorporating the polynucleotides into and/or onto biodegradable beads, which are efficiently transported into the cells. The preparation and use of such systems is well known in the art.

In a related aspect, a polynucleotide vaccine as described above may be administered simultaneously with or sequentially to either a polypeptide of the present invention or a known *Chlamydia* antigen. For example, administration of polynucleotides encoding a polypeptide of the present invention, either "naked" or in a delivery system as described above, may be followed by administration of an antigen in order to enhance the protective immune effect of the vaccine.

Polypeptides and polynucleotides disclosed herein may also be employed in adoptive immunotherapy for the treatment of *Chlamydial* infection. Adoptive immunotherapy may be broadly classified into either active or passive immunotherapy. In active immunotherapy, treatment relies on the *in vivo* stimulation of the endogenous

host immune system with the administration of immune response-modifying agents (for example, vaccines, bacterial adjuvants, and/or cytokines).

In passive immunotherapy, treatment involves the delivery of biologic reagents with established immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate anti-*Chlamydia* effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T lymphocytes (for example, CD8+ cytotoxic T-lymphocyte, CD4+ T-helper), killer cells (such as Natural Killer cells, lymphokine-activated killer cells), B cells, or antigen presenting cells (such as dendritic cells and macrophages) expressing the disclosed antigens. The polypeptides disclosed herein may also be used to generate antibodies or anti-idiotypic antibodies (as in U.S. Patent No. 4,918,164), for passive immunotherapy.

The predominant method of procuring adequate numbers of T-cells for adoptive immunotherapy is to grow immune T-cells *in vitro*. Culture conditions for expanding single antigen-specific T-cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. These *in vitro* culture conditions typically utilize intermittent stimulation with antigen, often in the presence of cytokines, such as IL-2, and non-dividing feeder cells. As noted above, the immunoreactive polypeptides described herein may be used to rapidly expand antigen-specific T cell cultures in order to generate sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast, or B-cells, may be pulsed with immunoreactive polypeptides, or polynucleotide sequence(s) may be introduced into antigen presenting cells, using a variety of standard techniques well known in the art. For example, antigen presenting cells may be transfected or transduced with a polynucleotide sequence, wherein said sequence contains a promoter region appropriate for increasing expression, and can be expressed as part of a recombinant virus or other expression system. Several viral vectors may be used to transduce an antigen presenting cell, including pox virus, vaccinia virus, and adenovirus; also, antigen presenting cells may be transfected with polynucleotide sequences disclosed herein by a variety of means, including gene-gun technology, lipid-mediated delivery, electroporation, osmotic shock, and particulate delivery mechanisms, resulting in efficient and acceptable expression levels as determined by one of ordinary skill in the art. For cultured T-cells to be effective in

therapy, the cultured T-cells must be able to grow and distribute widely and to survive long term *in vivo*. Studies have demonstrated that cultured T-cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (see, for example, Cheever, M., *et al*, "Therapy
5 With Cultured T Cells: Principles Revisited," *Immunological Reviews*, 157:177, 1997).

The polypeptides disclosed herein may also be employed to generate and/or isolate chlamydial-reactive T-cells, which can then be administered to the patient. In one technique, antigen-specific T-cell lines may be generated by *in vivo* immunization with short peptides corresponding to immunogenic portions of the
10 disclosed polypeptides. The resulting antigen specific CD8+ or CD4+ T-cell clones may be isolated from the patient, expanded using standard tissue culture techniques, and returned to the patient.

Alternatively, peptides corresponding to immunogenic portions of the polypeptides may be employed to generate *Chlamydia* reactive T cell subsets by
15 selective *in vitro* stimulation and expansion of autologous T cells to provide antigen-specific T cells which may be subsequently transferred to the patient as described, for example, by Chang *et al*, (*Crit. Rev. Oncol. Hematol.*, 22(3), 213, 1996). Cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as Isolex™ System,
20 available from Nexell Therapeutics, Inc. Irvine, CA. The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

In other embodiments, T-cell and/or antibody receptors specific for the polypeptides disclosed herein can be cloned, expanded, and transferred into other vectors or effector cells for use in adoptive immunotherapy. In particular, T cells may be transfected with the appropriate genes to express the variable domains from
30 chlamydia specific monoclonal antibodies as the extracellular recognition elements and joined to the T cell receptor signaling chains, resulting in T cell activation, specific lysis, and cytokine release. This enables the T cell to redirect its specificity in an MHC-independent manner. See for example, Eshhar, Z., *Cancer Immunol Immunother*, 45(3-

4):131-6, 1997 and Hwu, P., et al, *Cancer Res*, 55(15):3369-73, 1995. Another embodiment may include the transfection of chlamydia antigen specific alpha and beta T cell receptor chains into alternate T cells, as in Cole, DJ, et al, *Cancer Res*, 55(4):748-52, 1995.

5 In a further embodiment, syngeneic or autologous dendritic cells may be pulsed with peptides corresponding to at least an immunogenic portion of a polypeptide disclosed herein. The resulting antigen-specific dendritic cells may either be transferred into a patient, or employed to stimulate T cells to provide antigen-specific T cells which may, in turn, be administered to a patient. The use of peptide-pulsed dendritic cells to
10 generate antigen-specific T cells and the subsequent use of such antigen-specific T cells to eradicate disease in a murine model has been demonstrated by Cheever et al, *Immunological Reviews*, 157:177, 1997). Additionally, vectors expressing the disclosed polynucleotides may be introduced into stem cells taken from the patient and clonally propagated *in vitro* for autologous transplant back into the same patient.

15 Within certain aspects, polypeptides, polynucleotides, T cells and/or binding agents disclosed herein may be incorporated into pharmaceutical compositions or immunogenic compositions (*i.e.*, vaccines). Alternatively, a pharmaceutical composition may comprise an antigen-presenting cell (*e.g.* a dendritic cell) transfected with a *Chlamydial* polynucleotide such that the antigen presenting cell expresses a
20 *Chlamydial* polypeptide. Pharmaceutical compositions comprise one or more such compounds and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds and an immunostimulant. An immunostimulant may be any substance that enhances or potentiates an immune response to an exogenous antigen. Examples of immunostimulants include adjuvants, biodegradable microspheres (*e.g.*,
25 polylactic galactide) and liposomes (into which the compound is incorporated; *see e.g.*, Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds,
30 which may be biologically active or inactive. For example, one or more immunogenic portions of other *Chlamydial* antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid
5 expression systems, bacteria and viral expression systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998, and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial
10 delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope.

In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*, vaccinia or other pox virus, retrovirus, adenovirus, baculovirus,
15 togavirus, bacteriophage, and the like), which often involves the use of a non-pathogenic (defective), replication competent virus.

For example, many viral expression vectors are derived from viruses of the retroviridae family. This family includes the murine leukemia viruses, the mouse mammary tumor viruses, the human foamy viruses, Rous sarcoma virus, and the
20 immunodeficiency viruses, including human, simian, and feline. Considerations when designing retroviral expression vectors are discussed in Comstock *et al.* (1997).

Excellent murine leukemia virus (MLV)-based viral expression vectors have been developed by Kim *et al.* (1998). In creating the MLV vectors, Kim *et al.* found that the entire *gag* sequence, together with the immediate upstream region, could
25 be deleted without significantly affecting viral packaging or gene expression. Further, it was found that nearly the entire U3 region could be replaced with the immediately-early promoter of human cytomegalovirus without deleterious effects. Additionally, MCR and internal ribosome entry sites (IRES) could be added without adverse effects. Based on their observations, Kim *et al.* have designed a series of MLV-based expression
30 vectors comprising one or more of the features described above.

As more has been learned about human foamy virus (HFV), characteristics of HFV that are favorable for its use as an expression vector have been

discovered. These characteristics include the expression of pol by splicing and start of translation at a defined initiation codon. Other aspects of HFV viral expression vectors are reviewed in Bodem *et al.* (1997).

Murakami *et al.* (1997) describe a Rous sarcoma virus (RSV)-based
5 replication-competent avian retrovirus vectors, IR1 and IR2 to express a heterologous gene at a high level. In these vectors, the IRES derived from encephalomyocarditis virus (EMCV) was inserted between the *env* gene and the heterologous gene. The IR1 vector retains the splice-acceptor site that is present downstream of the *env* gene while the IR2 vector lacks it. Murakami *et al.* have shown high level expression of several
10 different heterologous genes by these vectors.

Recently, a number of lentivirus-based retroviral expression vectors have been developed. Kafri *et al.* (1997) have shown sustained expression of genes delivered directly into liver and muscle by a human immunodeficiency virus (HIV)-based expression vector. One benefit of the system is the inherent ability of HIV to transduce
15 non-dividing cells. Because the viruses of Kafri *et al.* are pseudotyped with vesicular stomatitis virus G glycoprotein (VSVG), they can transduce a broad range of tissues and cell types.

A large number of adenovirus-based expression vectors have been developed, primarily due to the advantages offered by these vectors in gene therapy
20 applications. Adenovirus expression vectors and methods of using such vectors are the subject of a number of United States patents, including United States Patent No. 5,698,202, United States Patent No. 5,616,326, United States Patent No. 5,585,362, and United States Patent No. 5,518,913, all incorporated herein by reference.

Additional adenoviral constructs are described in Khatri *et al.* (1997) and
25 Tomanin *et al.* (1997). Khatri *et al.* describe novel ovine adenovirus expression vectors and their ability to infect bovine nasal turbinate and rabbit kidney cells as well as a range of human cell type, including lung and foreskin fibroblasts as well as liver, prostate, breast, colon and retinal lines. Tomanin *et al.* describe adenoviral expression vectors containing the T7 RNA polymerase gene. When introduced into cells
30 containing a heterologous gene operably linked to a T7 promoter, the vectors were able to drive gene expression from the T7 promoter. The authors suggest that this system may be useful for the cloning and expression of genes encoding cytotoxic proteins.

Poxviruses are widely used for the expression of heterologous genes in mammalian cells. Over the years, the vectors have been improved to allow high expression of the heterologous gene and simplify the integration of multiple heterologous genes into a single molecule. In an effort to diminish cytopathic effects and to increase safety, vaccinia virus mutant and other poxviruses that undergo abortive infection in mammalian cells are receiving special attention (Oertli *et al.*, 1997). The use of poxviruses as expression vectors is reviewed in Carroll and Moss (1997).

Togaviral expression vectors, which includes alphaviral expression vectors have been used to study the structure and function of proteins and for protein production purposes. Attractive features of togaviral expression vectors are rapid and efficient gene expression, wide host range, and RNA genomes (Huang, 1996). Also, recombinant vaccines based on alphaviral expression vectors have been shown to induce a strong humoral and cellular immune response with good immunological memory and protective effects (Tubulekas *et al.*, 1997). Alphaviral expression vectors and their use are discussed, for example, in Lundstrom (1997).

In one study, Li and Garoff (1996) used Semliki Forest virus (SFV) expression vectors to express retroviral genes and to produce retroviral particles in BHK-21 cells. The particles produced by this method had protease and reverse transcriptase activity and were infectious. Furthermore, no helper virus could be detected in the virus stocks. Therefore, this system has features that are attractive for its use in gene therapy protocols.

Baculoviral expression vectors have traditionally been used to express heterologous proteins in insect cells. Examples of proteins include mammalian chemokine receptors (Wang *et al.*, 1997), reporter proteins such as green fluorescent protein (Wu *et al.*, 1997), and FLAG fusion proteins (Wu *et al.*, 1997; Koh *et al.*, 1997). Recent advances in baculoviral expression vector technology, including their use in virion display vectors and expression in mammalian cells is reviewed by Possee (1997). Other reviews on baculoviral expression vectors include Jones and Morikawa (1996) and O'Reilly (1997).

Other suitable viral expression systems are disclosed, for example, in Fisher-Hoch *et al.*, *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner *et al.*, *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner *et al.*, *Vaccine* 8:17-21, 1990; U.S. Patent

Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; 5 Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. In other systems, the DNA may be introduced as "naked" DNA, as described, for example, in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The 10 uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

It will be apparent that a vaccine may comprise a polynucleotide and/or a polypeptide component, as desired. It will also be apparent that a vaccine may contain pharmaceutically acceptable salts of the polynucleotides and/or polypeptides provided 15 herein. Such salts may be prepared from pharmaceutically acceptable non-toxic bases, including organic bases (e.g., salts of primary, secondary and tertiary amines and basic amino acids) and inorganic bases (e.g., sodium, potassium, lithium, ammonium, calcium and magnesium salts). While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, 20 the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a 25 wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable 30 microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or

dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, bacteriostats, chelating agents such as EDTA or glutathione, adjuvants (*e.g.*, aluminum hydroxide), solutes that render the formulation isotonic, hypotonic or weakly hypertonic with the blood of a recipient, suspending agents, thickening agents and/or preservatives.

5 Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of immunostimulants may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a

10 substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck

15 and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as

20 GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, under select circumstances, the adjuvant composition may be designed to induce an immune response predominantly of the Th1 type or Th2 type. High levels of Th1-type cytokines (*e.g.*, IFN- γ , TNF α , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an

25 administered antigen. In contrast, high levels of Th2-type cytokines (*e.g.*, IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a

30 greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Corixa Corporation (Seattle, WA; *see* US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555 and WO 99/33488. Immunostimulatory DNA sequences are also described, for example, by Sato et al., *Science* 273:352, 1996. Another preferred adjuvant is a saponin, preferably QS21 (Aquila Biopharmaceuticals Inc., Framingham, MA), which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprise an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210.

Other preferred adjuvants include Montanide ISA 720 (Seppic, France), SAF (Chiron, California, United States), ISCOMS (CSL), MF-59 (Chiron), the SBAS series of adjuvants (*e.g.*, SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart, Belgium), Detox (Corixa Corporation; Seattle, WA), RC-529 (Corixa Corporation; Seattle, WA) and other aminoalkyl glucosaminide 4-phosphates (AGPs), such as those described in pending U.S. Patent Application Serial Nos. 08/853,826 and 09/074,720, the disclosures of which are incorporated herein by reference in their entireties.

Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immunostimulant and a suitable carrier or excipient. The compositions described herein may be administered as part of a sustained release formulation (*i.e.*, a formulation such as a capsule, sponge or gel (composed of polysaccharides, for example) that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology (*see, e.g.*, Coombes et al., *Vaccine* 14:1429-1438, 1996) and

administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane.

5 Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. Such carriers include microparticles of poly(lactide-co-glycolide), as well as polyacrylate, latex, starch, cellulose and dextran. Other delayed-release carriers include supramolecular biovectors, which comprise a non-liquid
10 hydrophilic core (*e.g.*, a cross-linked polysaccharide or oligosaccharide) and, optionally, an external layer comprising an amphiphilic compound, such as a phospholipid (*see e.g.*, U.S. Patent No. 5,151,254 and PCT applications WO 94/20078, WO/94/23701 and WO 96/06638). The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of
15 release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific immune response that targets *Chlamydia*-infected cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells,
20 monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-*Chlamydia* effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety
25 of biological fluids and organs, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to
30 be effective as a physiological adjuvant for eliciting prophylactic or therapeutic immunity (*see* Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with

marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency, and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (see Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide encoding a *Chlamydial* protein (or portion or other variant thereof) such that the *Chlamydial* polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein.

Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the
5 gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the *Chlamydial* polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (e.g., vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide
10 may be covalently conjugated to an immunological partner that provides T cell help (e.g., a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

Routes and frequency of administration of pharmaceutical compositions and vaccines, as well as dosage, will vary from individual to individual. In general, the
15 pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 3 doses may be administered for a 1-36 week period. Preferably, 3 doses are administered, at intervals of 3-4 months, and booster vaccinations may be given periodically thereafter. Alternate protocols may be
20 appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that, when administered as described above, is capable of raising an immune response in an immunized patient sufficient to protect the patient from *Chlamydial* infection for at least 1-2 years. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per
25 kg of host, typically from about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 µg. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier
30 will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier,

such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactic galactide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable
5 microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome in treated patients as compared to non-treated patients. Increases in
10 preexisting immune responses to a *Chlamydial* protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

In another aspect, the present invention provides methods for using the polypeptides described above to diagnose Chlamydial infection. In this aspect, methods
15 are provided for detecting Chlamydial infection in a biological sample, using one or more of the above polypeptides, either alone or in combination. For clarity, the term "polypeptide" will be used when describing specific embodiments of the inventive diagnostic methods. However, it will be clear to one of skill in the art that the fusion
20 proteins of the present invention may also be employed in such methods.

As used herein, a "biological sample" is any antibody-containing sample obtained from a patient. Preferably, the sample is whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid or urine. More preferably, the sample is a blood, serum or plasma sample obtained from a patient. The polypeptides are used in an assay, as
25 described below, to determine the presence or absence of antibodies to the polypeptide(s) in the sample, relative to a predetermined cut-off value. The presence of such antibodies indicates previous sensitization to *Chlamydia* antigens which may be indicative of *Chlamydia*-infection.

In embodiments in which more than one polypeptide is employed, the polypeptides used are preferably complementary (i.e., one component polypeptide will
30 tend to detect infection in samples where the infection would not be detected by another component polypeptide). Complementary polypeptides may generally be identified by

using each polypeptide individually to evaluate serum samples obtained from a series of patients known to be infected with *Chlamydia*. After determining which samples test positive (as described below) with each polypeptide, combinations of two or more polypeptides may be formulated that are capable of detecting infection in most, or all, of the samples tested.

A variety of assay formats are known to those of ordinary skill in the art for using one or more polypeptides to detect antibodies in a sample. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988, which is incorporated herein by reference. In a preferred embodiment, the assay involves the use of polypeptide immobilized on a solid support to bind to and remove the antibody from the sample. The bound antibody may then be detected using a detection reagent that contains a reporter group. Suitable detection reagents include antibodies that bind to the antibody/polypeptide complex and free polypeptide labeled with a reporter group (e.g., in a semi-competitive assay). Alternatively, a competitive assay may be utilized, in which an antibody that binds to the polypeptide is labeled with a reporter group and allowed to bind to the immobilized antigen after incubation of the antigen with the sample. The extent to which components of the sample inhibit the binding of the labeled antibody to the polypeptide is indicative of the reactivity of the sample with the immobilized polypeptide.

The solid support may be any solid material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate, or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681.

The polypeptides may be bound to the solid support using a variety of techniques known to those of ordinary skill in the art. In the context of the present invention, the term "bound" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Binding by adsorption to a well in a microtiter plate or to a membrane is preferred. In

such cases, adsorption may be achieved by contacting the polypeptide, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of polypeptide ranging from about 10 ng to about 1 µg, and preferably about 100 ng, is sufficient to bind an adequate amount of antigen.

Covalent attachment of polypeptide to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the polypeptide. For example, the polypeptide may be bound to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the polypeptide (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is an enzyme linked immunosorbent assay (ELISA). This assay may be performed by first contacting a polypeptide antigen that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that antibodies to the polypeptide within the sample are allowed to bind to the immobilized polypeptide. Unbound sample is then removed from the immobilized polypeptide and a detection reagent capable of binding to the immobilized antibody-polypeptide complex is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific detection reagent.

More specifically, once the polypeptide is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin (BSA) or Tween 20™ (Sigma Chemical Co., St. Louis, MO) may be employed. The immobilized polypeptide is then incubated with the sample, and antibody is allowed to bind to the antigen. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.,* incubation time) is that period of time that is sufficient to detect the presence of antibody within an HGE-infected sample. Preferably, the contact time is sufficient to achieve a level of binding that is at least 95% of that achieved at

equilibrium between bound and unbound antibody. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

5 Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. Detection reagent may then be added to the solid support. An appropriate detection reagent is any compound that binds to the immobilized antibody-polypeptide complex and that can be detected by any of a variety of means known to those in the art. Preferably, the
10 detection reagent contains a binding agent (such as, for example, Protein A, Protein G, immunoglobulin, lectin or free antigen) conjugated to a reporter group. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of binding agent to reporter group may be achieved using standard methods
15 known to those of ordinary skill in the art. Common binding agents may also be purchased conjugated to a variety of reporter groups from many commercial sources (e.g., Zymed Laboratories, San Francisco, CA, and Pierce, Rockford, IL).

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound antibody. An
20 appropriate amount of time may generally be determined from the manufacturer's instructions or by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation
25 counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time),
30 followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of anti-*Chlamydia* antibodies in the sample, the signal detected from the reporter group that remains bound to the solid

support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antigen is incubated with samples from an uninfected patient. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for *Chlamydia*-infection. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, pp. 106-107. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (i.e., sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (i.e., the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for Chlamydial infection.

In a related embodiment, the assay is performed in a rapid flow-through or strip test format, wherein the antigen is immobilized on a membrane, such as nitrocellulose. In the flow-through test, antibodies within the sample bind to the immobilized polypeptide as the sample passes through the membrane. A detection reagent (e.g., protein A-colloidal gold) then binds to the antibody-polypeptide complex as the solution containing the detection reagent flows through the membrane. The detection of bound detection reagent may then be performed as described above. In the strip test format, one end of the membrane to which polypeptide is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing detection reagent and to the area of immobilized polypeptide. Concentration of detection reagent at the polypeptide indicates the presence of anti-*Chlamydia* antibodies in the sample. Typically, the concentration of detection reagent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of polypeptide

immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of antibodies that would be sufficient to generate a positive signal in an ELISA, as discussed above. Preferably, the amount of polypeptide immobilized on the membrane ranges from about 25 ng to about 1 μ g, and
5 more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount (e.g., one drop) of patient serum or blood.

Of course, numerous other assay protocols exist that are suitable for use with the polypeptides of the present invention. The above descriptions are intended to be exemplary only. One example of an alternative assay protocol which may be usefully
10 employed in such methods is a Western blot, wherein the proteins present in a biological sample are separated on a gel, prior to exposure to a binding agent. Such techniques are well known to those of skill in the art.

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to a *Chlamydial* protein. As
15 used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically bind" to a *Chlamydial* protein if it reacts at a detectable level (within, for example, an ELISA) with a *Chlamydial* protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a complex is formed. The ability
20 to bind may be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about 10^3
25 L/mol. The binding constant may be determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients with and without a *Chlamydial* infection using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a *Chlamydial* protein will generate a signal indicating the presence of a *Chlamydial* infection in at
30 least about 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without infection. To determine whether a binding agent satisfies this requirement, biological

samples (*e.g.*, blood, sera, sputum urine and/or tissue biopsies) from patients with and without *Chlamydial* infection (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and
5 without the disease should be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component,
10 an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation
15 of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (*e.g.*, mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen
20 without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically.
25 Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J.*
30 *Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may

be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria

toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitzer), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent
5 may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as
10 albumins (e.g., U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (e.g., U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (e.g., U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating
15 compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating
20 compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in site-specific regions by appropriate methods. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending
25 upon the antibody used, the antigen density, and the rate of clearance of the antibody.

Antibodies may be used in diagnostic tests to detect the presence of *Chlamydia* antigens using assays similar to those detailed above and other techniques well known to those of skill in the art, thereby providing a method for detecting Chlamydial infection in a patient.

30 Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a

polymerase chain reaction (PCR) based assay to amplify *Chlamydia*-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a polypeptide of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a polypeptide of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule encoding one of the polypeptides disclosed herein. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule encoding one of the polypeptides disclosed herein. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis *et al. Ibid*; Ehrlich, *Ibid*). Primers or probes may thus be used to detect *Chlamydia*-specific sequences in biological samples. DNA probes or primers comprising oligonucleotide sequences described above may be used alone or in combination with each other.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

ISOLATION OF DNA SEQUENCES ENCODING *CHLAMYDIA* ANTIGENS

Chlamydia antigens of the present invention were isolated by expression cloning of a genomic DNA library of *Chlamydia trachomatis* LGV II essentially as described by Sanderson *et al. (J. Exp. Med., 1995, 182:1751-1757)* and were shown to induce PBMC proliferation and IFN- γ in an immunoreactive T cell line.

A *Chlamydia*-specific T cell line was generated by stimulating PBMCs from a normal donor with no history of chlamydial genital tract infection with elementary bodies of *Chlamydia trachomatis* LGV II. This T cell line, referred to as TCL-8, was found to recognize both *Chlamydia trachomatis* and *Chlamydia pneumonia* infected monocyte-derived dendritic cells.

A randomly sheared genomic library of *Chlamydia trachomatis* LGV II was constructed in Lambda ZAP (Stratagene, La Jolla, CA) and the amplified library plated out in 96 well microtiter plates at a density of 30 clones/well. Bacteria were induced to express recombinant protein in the presence of 2 mM IPTG for 3 h, then pelleted and resuspended in 200 µl of RPMI 10% FBS. 10 µl of the induced bacterial suspension was transferred to 96 well plates containing autologous monocyte-derived dendritic cells. After a 2 h incubation, dendritic cells were washed to remove free *E. coli* and *Chlamydia*-specific T cells were added. Positive *E. coli* pools were identified by determining IFN-γ production and proliferation of the T cells in response to the pools.

Four positive pools were identified, which were broken down to yield four pure clones (referred to as 1-B1-66, 4-D7-28, 3-G3-10 and 10-C10-31), with insert sizes of 481 bp, 183 bp, 110 bp and 1400 bp, respectively. The determined DNA sequences for 1-B1-66, 4-D7-28, 3-G3-10 and 10-C10-31 are provided in SEQ ID NO: 1-4, respectively. Clone 1-B1-66 is approximately in region 536690 of the *C. trachomatis* genome (NCBI *C. trachomatis* database). Within clone 1-B1-66, an open reading frame (ORF) has been identified (nucleotides 115 - 375) that encodes a previously identified 9 kDa protein (Stephens, et al. Genbank Accession No. AE001320), the sequence of which is provided in SEQ ID NO: 5). Clone 4-D7-28 is a smaller region of the same ORF (amino acids 22-82 of 1-B1-66). Clone 3-G3-10 is approximately in region 74559 of the *C. trachomatis* genome. The insert is cloned in the antisense orientation with respect to its orientation in the genome. The clone 10-C10-31 contains an open reading frame that corresponds to a previously published sequence for S13 ribosomal protein from *Chlamydia trachomatis* (Gu, L. et al. *J. Bacteriology*, 177:2594-2601, 1995). The predicted protein sequences for 4-D7-28 and 10-C10-31 are provided in SEQ ID NO: 6 and 12, respectively. Predicted protein sequences for 3-G3-10 are provided in SEQ ID NO: 7-11.

In a related series of screening studies, an additional T cell line was used to screen the genomic DNA library of *Chlamydia trachomatis* LGV II described above. A *Chlamydia*-specific T cell line (TCT-1) was derived from a patient with a chlamydial genital tract infection by stimulating patient PBMC with autologous monocyte-derived dendritic cells infected with elementary bodies of *Chlamydia trachomatis* LGV II. One clone, 4C9-18 (SEQ ID NO: 21), containing a 1256 bp insert, elicited a specific immune response, as measured by standard proliferation assays, from the *Chlamydia*-specific T cell line TCT-1. Subsequent analysis revealed this clone to contain three known sequences: lipoamide dehydrogenase (Genbank Accession No. AE001326), disclosed in SEQ ID NO: 22; a hypothetical protein CT429 (Genbank Accession No. AE001316), disclosed in SEQ ID NO: 23; and part of an open reading frame of ubiquinone methyltransferase CT428 (Genbank Accession No. AE001316), disclosed in SEQ ID NO: 24.

In further studies involving clone 4C9-18 (SEQ ID NO: 21), the full-length amino acid sequence for lipoamide dehydrogenase (SEQ ID NO: 22) from *C. trachomatis* (LGV II) was expressed in clone CtL2-LPDA-FL, as disclosed in SEQ ID NO: 90.

To further characterize the open reading frame containing the T cell stimulating epitope(s), a cDNA fragment containing nucleotides 1-695 of clone 4C9-18 with a cDNA sequence encoding a 6X-Histidine tag on the amino terminus was subcloned into the NdeI/EcoRI site of the pET17b vector (Novagen, Madison, WI), referred to as clone 4C9-18#2 BL21 pLysS (SEQ ID NO: 25, with the corresponding amino acid sequence provided in SEQ ID NO: 26) and transformed into *E. coli*. Selective induction of the transformed *E. coli* with 2 mM IPTG for three hours resulted in the expression of a 26 kDa protein from clone 4C9-18#2 BL21 pLysS, as evidenced by standard Coomassie-stained SDS-PAGE. To determine the immunogenicity of the protein encoded by clone 4C9-18#2 BL21 pLysS, *E. coli* expressing the 26 kDa protein were titrated onto 1×10^4 monocyte-derived dendritic cells and incubated for two hours. The dendritic cell cultures were washed and 2.5×10^4 T cells (TCT-1) added and allowed to incubate for an additional 72 hours, at which time the level of IFN- γ in the culture supernatant was determined by ELISA. As shown in Fig. 1, the T-cell line TCT-1 was found to respond to induced cultures as measured by IFN- γ , indicating a

Chlamydia-specific T-cell response against the lipoamide dehydrogenase sequence. Similarly, the protein encoded by clone 4C9-18#2 BL21 pLysS was shown to stimulate the TCT-1 T-cell line by standard proliferation assays.

Subsequent studies to identify additional *Chlamydia trachomatis* antigens using the above-described CD4+ T-cell expression cloning technique yielded additional clones. The TCT-1 and TCL-8 *Chlamydia*-specific T-cell lines, as well as the TCP-21 T-cell line were utilized to screen the *Chlamydia trachomatis* LGVII genomic library. The TCP-21 T-cell line was derived from a patient having a humoral immune response to *Chlamydia pneumoniae*. The TCT-1 cell line identified 37 positive pools, the TCT-3 cell line identified 41 positive pools and the TCP-21 cell line identified 2 positive pools. The following clones were derived from 10 of these positive pools. Clone 11-A3-93 (SEQ ID NO: 64), identified by the TCP-21 cell line, is a 1339 bp genomic fragment sharing homology to the HAD superfamily (CT103). The second insert in the same clone shares homology with the fab I gene (CT104) present on the complementary strand. Clone 11-C12-91 (SEQ ID NO: 63), identified using the TCP-21 cell line, has a 269 bp insert that is part of the OMP2 gene (CT443) and shares homology with the 60 kDa cysteine rich outer membrane protein of *C. pneumoniae*.

Clone 11-G10-46, (SEQ ID NO: 62), identified using the TCT-3 cell line, contains a 688 bp insert that shares homology to the hypothetical protein CT610. Clone 11-G1-34, (SEQ ID NO: 61), identified using the TCT-3 cell line, has two partial open reading frames (ORF) with an insert size of 1215 bp. One ORF shares homology to the malate dehydrogenase gene (CT376), and the other ORF shares homology to the glycogen hydrolase gene (CT042). Clone 11-H3-68, (SEQ ID NO: 60), identified using the TCT-3 cell line, has two ORFs with a total insert size of 1180 bp. One partial ORF encodes the plasmid-encoded PGP6-D virulence protein while the second ORF is a complete ORF for the L1 ribosomal gene (CT318). Clone 11-H4-28, (SEQ ID NO: 59), identified using the TCT-3 cell line, has an insert size of 552 bp and is part of the ORF for the dnaK gene (CT396). Clone 12-B3-95, (SEQ ID NO: 58), identified using the TCT-1 cell line, has an insert size of 463 bp and is a part of the ORF for for the lipoamide dehydrogenase gene (CT557). Clones 15-G1-89 and 12-B3-95 are identical, (SEQ ID NO: 55 and 58, respectively), identified using the TCT-1 cell line, has an insert size of 463 bp and is part of the ORF for the lipoamide dehydrogenase gene

(CT557). Clone 12-G3-83, (SEQ ID NO: 57), identified using the TCT-1 cell line, has an insert size of 1537 bp and has part of the ORF for the hypothetical protein CT622.

Clone 23-G7-68, (SEQ ID NO: 79), identified using the TCT-3 cell line, contains a 950 bp insert and contains a small part of the L11 ribosomal ORF, the entire
5 ORF for L1 ribosomal protein and a part of the ORF for L10 ribosomal protein. In addition, this clone also identified the patient lines CT4, CT5, CT11, CT12, and CHH037. Clone 22-F8-91, (SEQ ID NO: 80), identified using the TCT-1 cell line, contains a 395 bp insert that contains a part of the pmpC ORF on the complementary strand of the clone. Clone 21-E8-95, (SEQ ID NO: 81), identified using the TCT-3 cell
10 line, contains a 2,085 bp insert which contains part of CT613 ORF, the complete ORF for CT612, the complete ORF for CT611 and part of the ORF for CT610. Clone 19-F12-57, (SEQ ID NO: 82), identified using the TCT-3 cell line, contains a 405 bp insert which contains part of the CT 858 ORF and a small part of the recA ORF. Clone 19-F12-53, (SEQ ID NO: 83), identified using the TCT-3 cell line, contains a 379 bp insert
15 that is part of the ORF for CT455 encoding glutamyl tRNA synthetase. Clone 19-A5-54, (SEQ ID NO: 84), identified using the TCT-3 cell line, contains a 715 bp insert that is part of the ORF3 (complementary strand of the clone) of the cryptic plasmid. Clone 17-E11-72, (SEQ ID NO: 85), identified using the TCT-1 cell line, contains a 476 bp insert that is part of the ORF for Opp_2 and pmpD. The pmpD region of this clone is
20 covered by the pmpD region of clone 15-H2-76. Clone 17-C1-77, (SEQ ID NO: 86), identified using the the patient cell lines CT3, CT1, CT4, and CT12, contains a 1551 bp insert that is part of the CT857 ORF, as well as part of the CT858 ORF. Clone 15-H2-76, (SEQ ID NO: 87), identified using the TCT-1 cell line, contains a 3,031 bp insert that contains a large part of the pmpD ORF, part of the CT089 ORF, as well as part of
25 the ORF for SycE. Clone 15-A3-26, (SEQ ID NO: 88), contains a 976 bp insert that contains part of the ORF for CT858. Clone 17-G4-36, (SEQ ID NO: 267), identified using the patient lines CL8, TCT-10, CT1, CT5, CT13, and CHH037, contains a 680 bp insert that is in frame with beta-gal in the plasmid and shares homology to part of the ORF for DNA-directed RNA polymerase beta subunit (CT315 in SerD).

30 Several of the clones described above share homology to various polymorphic membrane proteins. The genomic sequence of *Chlamydia trachomatis* contains a family of nine polymorphic membrane protein genes, referred to as pmp.

These genes are designated pmpA, pmpB, pmpC, pmpD, pmpE, pmpF, pmpG, pmpH and pmpI. Proteins expressed from these genes are believed to be of biological relevance in generating a protective immune response to a *Chlamydial* infection. In particular, pmpC, pmpD, pmpE and pmpI contain predictable signal peptides, suggesting they are outer membrane proteins, and therefore, potential immunological targets.

Based on the *Chlamydia trachomatis* LGVII serovar sequence, primer pairs were designed to PCR amplify the full-length fragments of pmpC, pmpD, pmpE, pmpG, pmpH and pmpI. The resulting fragments were subcloned into the DNA vaccine vector JA4304 or JAL, which is JA4304 with a modified linker (SmithKline Beecham, London, England). Specifically, PmpC was subcloned into the JAL vector using the 5' oligo GAT AGG CGC GCC GCA ATC ATG AAA TTT ATG TCA GCT ACT GCT G and the 3' oligo CAG AAC GCG TTT AGA ATG TCA TAC GAG CAC CGC A, as provided in SEQ ID NO: 197 and 198, respectively. PCR amplification of the gene under conditions well known in the art and ligation into the 5' ASCI/3' MluI sites of the JAL vector was completed after inserting the short nucleotide sequence GCAATC (SEQ ID NO: 199) upstream of the ATG to create a Kozak-like sequence. The resulting expression vector contained the full-length pmpC gene comprising 5325 nucleotides (SEQ ID NO: 173) containing the hypothetical signal sequence, which encodes a 187 kD protein (SEQ ID NO: 179). The pmpD gene was subcloned into the JA4304 vaccine vector following PCR amplification of the gene using the following oligos: 5' oligo-TGC AAT CAT GAG TTC GCA GAA AGA TAT AAA AAG C (SEQ ID NO: 200) and 3' oligo- CAG AGC TAG CTT AAA AGA TCA ATC GCA ATC CAG TAT TC (SEQ ID NO: 201). The gene was ligated into the a 5' blunted HIII/3' MluI site of the JA4304 vaccine vector using standard techniques well known in the art. The CAATC (SEQ ID NO: 202) was inserted upstream of the ATG to create a Kozak-like sequence. This clone is unique in that the last threonine of the HindIII site is missing due to the blunting procedure, as is the last glycine of the Kozak-like sequence. The insert, a 4593 nucleotide fragment (SEQ ID NO: 172) is the full-length gene for pmpD containing the hypothetical signal sequence, which encodes a 161 kD protein (SEQ ID NO: 178). PmpE was subcloned into the JA4304 vector using the 5' oligo- TGC AAT CAT GAA AAA AGC GTT TTT CTT TTT C (SEQ ID NO: 203), and the 3' oligo- CAG AAC

GCG TCT AGA ATC GCA GAG CAA TTT C (SEQ ID NO: 204). Following PCR amplification, the gene was ligated into the 5' blunted *HindIII*/3' *MluI* site of JA4304. To facilitate this, a short nucleotide sequence, TGCAATC (SEQ ID NO: 293), was added upstream of the initiation codon for creating a Kozak-like sequence and reconstituting the *HindIII* site. The insert is the full-length *pmpE* gene (SEQ ID NO: 171) containing the hypothetical signal sequence. The *pmpE* gene encodes a 105 kD protein (SEQ ID NO: 177). The *pmpG* gene was PCR amplified using the 5' oligo- GTG CAA TCA TGA TTC CTC AAG GAA TTT ACG (SEQ ID NO: 205), and the 3' oligo- CAG AAC GCG TTT AGA ACC GGA CTT TAC TTC C (SEQ ID NO: 206) and subcloned into the JA4304 vector. Similar cloning strategies were followed for the *pmpI* and *pmpK* genes. In addition, primer pairs were designed to PCR amplify the full-length or overlapping fragments of the *pmp* genes, which were then subcloned for protein expression in the pET17b vector (Novagen, Madison, WI) and transfected into *E. coli* BL21 pLysS for expression and subsequent purification utilizing the histidine-nickel chromatographic methodology provided by Novagen. Several of the genes encoding the recombinant proteins, as described below, lack the native signal sequence to facilitate expression of the protein. Full-length protein expression of *pmpC* was accomplished through expression of two overlapping fragments, representing the amino and carboxy termini. Subcloning of the *pmpC*-amino terminal portion, which lacks the signal sequence, (SEQ ID NO: 187, with the corresponding amino acid sequence provided in SEQ ID NO: 195) used the 5' oligo- CAG ACA TAT GCA TCA CCA TCA CCA TCA CGA GGC GAG CTC GAT CCA AGA TC (SEQ ID NO: 207), and the 3' oligo- CAG AGG TAC CTC AGA TAG CAC TCT CTC CTA TTA AAG TAG G (SEQ ID NO: 208) into the 5' *NdeI*/3' *KpnI* cloning site of the vector. The carboxy terminus portion of the gene, *pmpC*-carboxy terminal fragment (SEQ ID NO: 186, with the corresponding amino acid sequence provided in SEQ ID NO: 194), was subcloned into the 5' *NheI*/3' *KpnI* cloning site of the expression vector using the following primers: 5' oligo- CAG AGC TAG CAT GCA TCA CCA TCA CCA TCA CGT TAA GAT TGA GAA CTT CTC TGG C (SEQ ID NO: 209), and 3' oligo- CAG AGG TAC CTT AGA ATG TCA TAC GAG CAC CGC AG (SEQ ID NO: 210). *PmpD* was also expressed as two overlapping proteins. The *pmpD*-amino terminal portion, which lacks the signal sequence, (SEQ ID NO: 185, with the corresponding amino acid sequence provided in

SEQ ID NO: 193) contains the initiating codon of the pET17b and is expressed as a 80 kD protein. For protein expression and purification purposes, a six-histidine tag follows the initiation codon and is fused at the 28th amino acid (nucleotide 84) of the gene. The following primers were used, 5' oligo, CAG ACA TAT GCA TCA CCA TCA CCA
5 TCA CGG GTT AGC (SEQ ID NO: 211), and the 3' oligo- CAG AGG TAC CTC AGC TCC TCC AGC ACA CTC TCT TC (SEQ ID NO: 212), to splice into the 5' Ndel/3' KPN cloning site of the vector. The pmpD-carboxy terminus portion (SEQ ID NO: 184) was expressed as a 92 kD protein (SEQ ID NO: 192). For expression and subsequent purification, an additional methionine, alanine and serine was included,
10 which represent the initiation codon and the first two amino acids from the pET17b vector. A six-histidine tag downstream of the methionine, alanine and serine is fused at the 691st amino acid (nucleotide 2073) of the gene. The 5' oligo- CAG AGC TAG CCA TCA CCA TCA CCA TCA CGG TGC TAT TTC TTG CTT ACG TGG (SEQ ID NO: 213) and the 3' oligo- CAG AGG TAC TTn AAA AGA TCA ATC GCA ATC
15 CAG TAT TCG (SEQ ID NO: 214) were used to subclone the insert into the 5' NheI/3' KPN cloning site of the expression vector. PmpE was expressed as a 106kD protein (SEQ ID NO: 183 with the corresponding amino acid sequence provided in SEQ ID NO: 191). The pmpE insert also lacks the native signal sequence. PCR amplification of the gene under conditions well known in the art was performed using the following
20 oligo primers: 5' oligo- CAG AGG ATC CAC ATC ACC ATC ACC ATC ACG GAC TAG CTA GAG AGG TTC (SEQ ID NO: 215), and the 3' oligo- CAG AGA ATT CCT AGA ATC GCA GAG CAA TTT C (SEQ ID NO: 216), and the amplified insert was ligated into a 5' BamHI/3' EcoRI site of JA4304. The short nucleotide sequence, as provided in SEQ ID NO: 217, was inserted upstream of the initiation codon for creating
25 the Kozak-like sequence and reconstituting the HindIII site. The expressed protein contains the initiation codon and the downstream 21 amino acids from the pET17b expression vector, i.e., MASMTGGQQMGRDSSLVPSSDP (SEQ ID NO: 218). In addition, a six-histidine tag is included upstream of the sequence described above and is fused at the 28th amino acid (nucleotide 84) of the gene, which eliminates the
30 hypothetical signal peptide. The sequences provided in SEQ ID NO: 183 with the corresponding amino acid sequence provided in SEQ ID NO: 191 do not include these additional sequences. The pmpG gene (SEQ ID NO: 182, with the corresponding

amino acid sequence provided in SEQ ID No; 190) was PCR amplified under conditions well known in the art using the following oligo primers: 5' oligo- CAG AGG TAC CGC ATC ACC ATC ACC ATC ACA TGA TTC CTC AAG GAA TTT ACG (SEQ ID NO: 219), and the 3' oligo- CAG AGC GGC CGC TTA GAA CCG GAC TTT ACT TCC (SEQ ID NO: 220), and ligated into the 5' KPN/3' NotI cloning site of the expression vector. The expressed protein contains an additional amino acid sequence at the amino end, namely, MASMTGGQNGRDSSLVPHHHHHH (SEQ ID NO: 221), which comprises the initiation codon and additional sequence from the pET17b expression vector. The pmpI gene (SEQ ID NO: 181, with the corresponding amino acid sequence provided in SEQ ID No; 189) was PCR amplified under conditions well known in the art using the following oligo primers: 5' oligo- CAG AGC TAG CCA TCA CCA TCA CCA TCA CCT CTT TGG CCA GGA TCC C (SEQ ID NO: 222), and the 3' oligo- CAG AAC TAG TCT AGA ACC TGT AAG TGG TCC (SEQ ID NO: 223), and ligated into the expression vector at the 5' NheI/3' SpeI cloning site. The 95 kD expressed protein contains the initiation codon plus an additional alanine and serine from the pET17b vector at the amino end of the protein. In addition, a six-histidine tag is fused at the 21st amino acid of the gene, which eliminates the hypothetical signal peptide.

Clone 14H1-4, (SEQ ID NO: 56), identified using the TCT-3 cell line, contains a complete ORF for the TSA gene, thiol specific antioxidant – CT603 (the CT603 ORF is a homolog of CPn0778 from *C. pneumoniae*). The TSA open reading frame in clone 14-H1-4 was amplified such that the expressed protein possess an additional methionine and a 6x histidine tag (amino terminal end). This amplified insert was sub-cloned into the Nde/EcoRI sites of the pET17b vector. Upon induction of this clone with IPTG, a 22.6 kDa protein was purified by Ni-NTA agarose affinity chromatography. The determined amino acid sequence for the 195 amino acid ORF of clone 14-H1-4 encoding the TSA gene is provided in SEQ ID NO: 65. Further analysis yielded a full-length clone for the TSA gene, referred to as CTL2-TSA-FL, with the full-length amino acid sequence provided in SEQ ID NO: 92.

Further studies yielded 10 additional clones identified by the TCT-1 and TCT-3 T-cell lines, as described above. The clones identified by the TCT-1 line are: 16-D4-22, 17-C5-19, 18-C5-2, 20-G3-45 and 21-C7-66; clones identified by the TCT-3

cell line are: 17-C10-31, 17-E2-9, 22-A1-49 and 22-B3-53. Clone 21-G12-60 was recognized by both the TCT-1 and TCT-3 T cell lines. In addition, clone 20-G3-45, which contained sequence specific for pmpB, was identified against the patient lines CT1 and CT4. Clone 16-D4-22 (SEQ ID NO: 119), identified using the TCT-1 cell line
5 contains a 953 bp insert that contains two genes, parts of open reading frame 3 (ORF3) and ORF4 of the *C. trachomatis* plasmid for growth within mammalian cells. Clone 17-C5-19 (SEQ ID NO: 118), contains a 951 bp insert that contains part of the ORF for DT431, encoding for clpP_1 protease and part of the ORF for CT430 (diaminopimelate epimerase). Clone 18-C5-2 (SEQ ID NO: 117) is part of the ORF for S1 ribosomal
10 protein with a 446 bp insert that was identified using the TCT-1 cell line. Clone 20-G3-45 (SEQ ID NO: 116), identified by the TCT-1 cell line, contains a 437 bp insert that is part of the pmpB gene (CT413). Clone 21-C7-8 (SEQ ID NO: 115), identified by the TCT-1 line, contains a 995bp insert that encodes part of the dnaK like protein. The insert of this clone does not overlap with the insert of the TCT-3 clone 11-H4-28 (SEQ
15 ID NO: 59), which was shown to be part of the dnaK gene CT396. Clone 17-C10-31 (SEQ ID NO: 114), identified by the TCT-3 cell line, contains a 976 bp insert. This clone contains part of the ORF for CT858, a protease containing IRBP and DHR domains. Clone 17-E2-9 (SEQ ID NO: 113) contains part of ORFs for two genes, CT611 and CT610, that span a 1142 bp insert. Clone 22-A1-49 (SEQ ID NO: 112),
20 identified using the TCT-3 line, also contains two genes in a 698 bp insert. Part of the ORF for CT660 (DNA gyrase{gyrA_2}) is present on the top strand where as the complete ORF for a hypothetical protein CT659 is present on the complementary strand. Clone 22-B3-53 (SEQ ID NO: 111), identified by the TCT-1 line, has a 267 bp insert that encodes part of the ORF for GroEL (CT110). Clone 21-G12-60 (SEQ ID
25 NO: 110), identified by both the TCT-1 and TCT-3 cell lines contains a 1461 bp insert that contains partial ORFs for hypothetical proteins CT875, CT229 and CT228.

Additional *Chlamydia* antigens were obtained by screening a genomic expression library of *Chlamydia trachomatis* (LGV II serovar) in Lambda Screen-1 vector (Novagen, Madison, WI) with sera pooled from several *Chlamydia*-infected
30 individuals using techniques well known in the art. The following immuno-reactive clones were identified and the inserts containing *Chlamydia* genes sequenced: CTL2#1 (SEQ ID NO: 71); CTL2#2 (SEQ ID NO: 70); CTL2#3-5' (SEQ ID NO: 72, a first

determined genomic sequence representing the 5' end); CTL2#3-3' (SEQ ID NO: 73, a second determined genomic sequence representing the 3' end); CTL2#4 (SEQ ID NO: 53); CTL2#5 (SEQ ID NO: 69); CTL2#6 (SEQ ID NO: 68); CTL2#7 (SEQ ID NO: 67); CTL2#8b (SEQ ID NO: 54); CTL2#9 (SEQ ID NO: 66); CTL2#10-5' (SEQ ID NO: 74, a first determined genomic sequence representing the 5' end); CTL2#10-3' (SEQ ID NO: 75, a second determined genomic sequence representing the 3' end); CTL2#11-5' (SEQ ID NO: 45, a first determined genomic sequence representing the 5' end); CTL2#11-3' (SEQ ID NO: 44, a second determined genomic sequence representing the 3' end); CTL2#12 (SEQ ID NO: 46); CTL2#16-5' (SEQ ID NO: 47); CTL2#18-5' (SEQ ID NO: 49, a first determined genomic sequence representing the 5' end); CTL2#18-3' (SEQ ID NO: 48, a second determined genomic sequence representing the 3' end); CTL2#19-5' (SEQ ID NO: 76, the determined genomic sequence representing the 5' end); CTL2#21 (SEQ ID NO: 50); CTL2#23 (SEQ ID NO: 51; and CTL2#24 (SEQ ID NO: 52).

Additional *Chlamydia trachomatis* antigens were identified by serological expression cloning. These studies used sera pooled from several *Chlamydia*-infected individuals, as described above, but, IgA, and IgM antibodies were used in addition to IgG as a secondary antibody. Clones screened by this method enhance detection of antigens recognized by an early immune response to a *Chlamydia* infection, that is a mucosal humoral immune response. The following immunoreactive clones were characterized and the inserts containing *Chlamydia* genes sequenced: CTL2gam-1 (SEQ ID NO: 290), CTL2gam-2 (SEQ ID NO: 289), CTL2gam-5 (SEQ ID NO: 288), CTL2gam-6-3' (SEQ ID NO: 287, a second determined genomic sequence representing the 3' end), CTL2gam-6-5' (SEQ ID NO: 286, a first determined genomic sequence representing the 5' end), CTL2gam-8 (SEQ ID NO: 285), CTL2gam-10 (SEQ ID NO: 284), CTL2gam-13 (SEQ ID NO: 283), CTL2gam-15-3' (SEQ ID NO: 282, a second determined genomic sequence representing the 3' end), CTL2gam-15-5' (SEQ ID NO: 281, a first determined genomic sequence representing the 5' end), CTL2gam-17 (SEQ ID NO: 280), CTL2gam-18 (SEQ ID NO: 279), CTL2gam-21 (SEQ ID NO: 278), CTL2gam-23 (SEQ ID NO: 277), CTL2gam-24 (SEQ ID NO: 276), CTL2gam-26 (SEQ ID NO: 275), CTL2gam-27 (SEQ ID NO: 274), CTL2gam-28 (SEQ ID NO: 273), CTL2gam-30-3' (SEQ ID NO: 272, a second determined genomic sequence

representing the 3' end) and CTL2gam-30-5' (SEQ ID NO: 271, a first determined genomic sequence representing the 5' end).

EXAMPLE 2

5 INDUCTION OF T CELL PROLIFERATION AND INTERFERON- γ PRODUCTION BY *CHLAMYDIA TRACHOMATIS* ANTIGENS

The ability of recombinant *Chlamydia trachomatis* antigens to induce T cell proliferation and interferon- γ production is determined as follows.

10 Proteins are induced by IPTG and purified by Ni-NTA agarose affinity chromatograph (Webb et al., *J. Immunology* 157:5034-5041, 1996). The purified polypeptides are then screened for the ability to induce T-cell proliferation in PBMC preparations. PBMCs from *C. trachomatis* patients as well as from normal donors whose T-cells are known to proliferate in response to *Chlamydia* antigens, are cultured
15 in medium comprising RPMI 1640 supplemented with 10% pooled human serum and 50 μ g/ml gentamicin. Purified polypeptides are added in duplicate at concentrations of 0.5 to 10 μ g/mL. After six days of culture in 96-well round-bottom plates in a volume of 200 μ L, 50 μ L of medium is removed from each well for determination of IFN- γ levels, as described below. The plates are then pulsed with 1 μ Ci/well of tritiated
20 thymidine for a further 18 hours, harvested and tritium uptake determined using a gas scintillation counter. Fractions that result in proliferation in both replicates three fold greater than the proliferation observed in cells cultured in medium alone are considered positive.

IFN- γ is measured using an enzyme-linked immunosorbent assay
25 (ELISA). ELISA plates are coated with a mouse monoclonal antibody directed to human IFN- γ (PharMingen, San Diego, CA) in PBS for four hours at room temperature. Wells are then blocked with PBS containing 5% (W/V) non-fat dried milk for 1 hour at room temperature. The plates are washed six times in PBS/0.2% TWEEN-20 and samples diluted 1:2 in culture medium in the ELISA plates are incubated overnight at
30 room temperature. The plates are again washed and a polyclonal rabbit anti-human IFN- γ serum diluted 1:3000 in PBS/10% normal goat serum is added to each well. The

plates are then incubated for two hours at room temperature, washed and horseradish peroxidase-coupled anti-rabbit IgG (Sigma Chemical So., St. Louis, MO) is added at a 1:2000 dilution in PBS/5% non-fat dried milk. After a further two hour incubation at room temperature, the plates are washed and TMB substrate added. The reaction is
5 stopped after 20 min with 1 N sulfuric acid. Optical density is determined at 450 nm using 570 nm as a reference wavelength. Fractions that result in both replicates giving an OD two fold greater than the mean OD from cells cultured in medium alone, plus 3 standard deviations, are considered positive.

Using the above methodology, recombinant 1B1-66 protein (SEQ ID
10 NO: 5) as well as two synthetic peptides corresponding to amino acid residues 48-67 (SEQ ID NO: 13; referred to as 1-B1-66/48-67) and 58-77 (SEQ ID NO: 14, referred to as 1B1-66/58-77), respectively, of SEQ ID NO: 5, were found to induce a proliferative response and IFN- γ production in a Chlamydia-specific T cell line used to screen a genomic library of *C. trachomatis* LGV II.

Further studies have identified a *C. trachomatis*-specific T-cell epitope in
15 the ribosomal S13 protein. Employing standard epitope mapping techniques well known in the art, two T-cell epitopes in the ribosomal S13 protein (rS13) were identified with a *Chlamydia*-specific T-cell line from donor CL-8 (T-cell line TCL-8 EB/DC). Fig. 8 illustrates that the first peptide, rS13 1-20 (SEQ ID NO: 106), is 100%
20 identical with the corresponding *C. pneumoniae* sequence, explaining the cross-reactivity of the T-cell line to recombinant *C. trachomatis*- and *C. pneumoniae*-rS13. The response to the second peptide rS13 56-75 (SEQ ID NO: 108) is *C. trachomatis*-specific, indicating that the rS13 response in this healthy asymptomatic donor was elicited by exposure to *C. trachomatis* and not to *C. pneumoniae*, or any other microbial
25 infection.

As described in Example 1, Clone 11-C12-91 (SEQ ID NO: 63), identified using the TCP-21 cell line, has a 269 bp insert that is part of the OMP2 gene (CT443) and shares homology with the 60 kDa cysteine rich outer membrane protein of *C. pneumoniae*, referred to as OMCB. To further define the reactive epitope(s), epitope
30 mapping was performed using a series of overlapping peptides and the immunoassay previously described. Briefly, proliferative responses were determined by stimulating 2.5×10^4 TCP-21 T-cells in the presence of 1×10^4 monocyte-derived dendritic cells

with either non-infectious elementary bodies derived from *C. trachomatis* and *C. pneumoniae*, or peptides derived from the protein sequence of *C. trachomatis* or *C. pneumoniae* OMCB protein (0.1 µg/ml). The TCP-21 T-cells responded to epitopes CT-OMCB #167-186, CT-OMCB #171-190, CT-OMCB #171-186, and to a lesser
5 extent, CT-OMCB #175-186 (SEQ ID NO: 249-252, respectively). Notably, the TCP-21 T-cell line also gave a proliferative response to the homologous *C. pneumoniae* peptide CP-OMCB #171-186 (SEQ ID NO: 253), which was equal to or greater than the response to the *C. trachomatis* peptides. The amino acid substitutions in position two (i.e., Asp for Glu) and position four (i.e., Cys for Ser) did not alter the proliferative
10 response of the T-cells and therefore demonstrating this epitope to be a cross-reactive epitope between *C. trachomatis* and *C. pneumoniae*.

To further define the epitope described above, an additional T-cell line, TCT-3, was used in epitope mapping experiments. The immunoassays were performed as described above, except that only peptides from *C. trachomatis* were tested. The T-
15 cells gave a proliferative response to two peptides, CT-OMCB #152-171 and CT-OMCB #157-176 (SEQ ID NO: 246 and 247, respectively), thereby defining an additional immunogenic epitope in the cysteine rich outer membrane protein of *C. trachomatis*.

Clone 14H1-4, (SEQ ID NO: 56, with the corresponding full-length
20 amino acid sequence provided in SEQ ID NO: 92), was identified using the TCT-3 cell line in the CD4 T-cell expression cloning system previously described, and was shown to contain a complete ORF for the, thiol specific antioxidant gene (CT603), referred to as TSA. Epitope mapping immunoassays were performed, as described above, to further define the epitope. The TCT-3 T-cells line exhibited a strong proliferative
25 response to the overlapping peptides CT-TSA #96-115, CT-TSA #101-120 and CT-TSA #106-125 (SEQ ID NO: 254-256, respectively) demonstrating an immunoreactive epitope in the thiol specific antioxidant gene of *C. trachomatis* serovar LGVII.

EXAMPLE 3

PREPARATION OF SYNTHETIC POLYPEPTIDES

5 Polypeptides may be synthesized on a Millipore 9050 peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N',N'',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugating or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the
10 following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0-60% acetonitrile (containing 0.1% TFA) in water
15 (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray mass spectrometry and by amino acid analysis.

EXAMPLE 4

20 ISOLATION AND CHARACTERIZATION OF DNA SEQUENCES ENCODING
CHLAMYDIA ANTIGENS USING RETROVIRAL EXPRESSION VECTOR
SYSTEMS AND SUBSEQUENT IMMUNOLOGICAL ANALYSIS

A genomic library of *Chlamydia trachomatis* LGV II was constructed by
25 limited digests using BamHI, BglII, BstYI and MboI restriction enzymes. The restriction digest fragments were subsequently ligated into the BamHI site of the retroviral vectors pBIB-KS1,2,3. This vector set was modified to contain a Kosak translation initiation site and stop codons in order to allow expression of proteins from short DNA genomic fragments, as shown in Fig. 2. DNA pools of 80 clones were
30 prepared and transfected into the retroviral packaging line Phoenix-Ampho, as described in Pear, W.S., Scott, M.L. and Nolan, G.P., Generation of High Titre, Helper-free Retroviruses by Transient Transfection. Methods in Molecular Medicine: Gene

Therapy Protocols, Humana Press, Totowa, NJ, pp. 41-57. The *Chlamydia* library in retroviral form was then transduced into H2-Ld expressing P815 cells, which were then used as target cells to stimulate an antigen specific T-cell line.

A *Chlamydia*-specific, murine H2^d restricted CD8⁺ T-cell line was expanded in culture by repeated rounds of stimulation with irradiated *C. trachomatis*-infected J774 cells and irradiated syngeneic spleen cells, as described by Starnbach, M., in *J. Immunol.*, 153:5183, 1994. This *Chlamydia*-specific T-cell line was used to screen the above *Chlamydia* genomic library expressed by the retrovirally-transduced P815 cells. Positive DNA pools were identified by detection of IFN- γ production using 5
10
Elispot analysis (SEE Lavani et al., *J. Experimental Medicine* 186:859-865, 1997).

Two positive pools, referred to as 2C7 and 2E10, were identified by IFN- γ 5
10
Elispot assays. Stable transductants of P815 cells from pool 2C7 were cloned by limiting dilution and individual clones were selected based upon their capacity to elicit IFN- γ production from the *Chlamydia*-specific CTL line. From this screening process, 15
four positive clones were selected, referred to as 2C7-8, 2C7-9, 2C7-19 and 2C7-21. Similarly, the positive pool 2E10 was further screened, resulting in an additional positive clone, which contains three inserts. The three inserts are fragments of the CT016, tRNA synthase and clpX genes (SEQ ID NO: 268-270, respectively).

Transgenic DNA from these four positive 2C7 clones were PCR 20
amplified using pBIB-KS specific primers to selectively amplify the *Chlamydia* DNA insert. Amplified inserts were gel purified and sequenced. One immunoreactive clone, 2C7-8 (SEQ ID NO: 15, with the predicted amino acid sequence provided in SEQ ID NO: 32), is a 160 bp fragment with homology to nucleotides 597304-597145 of *Chlamydia trachomatis*, serovar D (NCBI, BLASTN search; SEQ ID NO: 33, with the 25
predicted amino acid sequence provided in SEQ ID NO: 34). The sequence of clone 2C7-8 maps within two putative open reading frames from the region of high homology described immediately above, and in particular, one of these putative open reading frames, consisting of a 298 amino acid fragment (SEQ ID NO: 16, with the predicted amino acid sequence provided in SEQ ID NO: 17), was demonstrated to exhibit 30
immunological activity.

Full-length cloning of the 298 amino acid fragment (referred to as CT529 and/or the Cap1 gene) from serovar L2 was obtained by PCR amplification using 5'-

ttttgaagcaggttaggtgaatatg (forward) (SEQ ID NO: 159) and 5'-ttaagaaatttaaaatccctta (reverse) (SEQ ID NO: 160) primers, using purified *C. trachomatis* L2 genomic DNA as template. This PCR product was gel-purified, cloned into pCRBlunt (Invitrogen, Carlsbad, CA) for sequencing, and then subcloned into the *EcoRI* site of pBIB-KMS, a derivative of pBIB-KS for expression. The *Chlamydia pneumoniae* homologue of CT529 is provided in SEQ ID NO: 291, with the corresponding amino acid sequence provided in SEQ ID NO: 292.

Full-length DNA encoding various CT529 serovars were amplified by PCR from bacterial lysates containing 10^5 IFU, essentially as described (Denamur, E., C. Sayada, A. Souriau, J. Orfila, A. Rodolakis and J. Elion. 1991. J. Gen. Microbiol. 137: 2525). The following serovars were amplified as described: Ba (SEQ ID NO: 134, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 135); E (BOUR) and E (MTW447) (SEQ ID NO: 122, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 123); F (N11) (SEQ ID NO: 128, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 129); G; (SEQ ID NO: 126, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 127); Ia (SEQ ID NO: 124, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 125); L1 (SEQ ID NO: 130, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 131); L3 (SEQ ID NO: 132, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 133); I (SEQ ID NO: 263, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 264); K (SEQ ID NO: 265, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 266); and MoPn (SEQ ID NO: 136, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 137). PCR reactions were performed with Advantage Genomic PCR Kit (Clontech, Palo Alto, CA) using primers specific for serovar L2 DNA (external to the ORF). Primers sequences were 5'-ggtataatactctctaaatttg (forward-SEQ ID NO: 161) and 5'-agataaaaaaggctgttgc' (reverse-SEQ ID NO: 162) except for MoPn which required 5'-ttttgaagcaggttaggtgaatatg (forward-SEQ ID NO: 163) and 5'-ttacaataagaaaagctaagcactttgt (reverse-SEQ ID NO: 164). PCR amplified DNA was purified with QIAquick PCR purification kit (Qiagen, Valencia, CA) and cloned in pCR2.1 (Invitrogen, Carlsbad, CA) for sequencing.

Sequencing of DNA derived from PCR amplified inserts of immunoreactive clones was done on an automated sequencer (ABI 377) using both a pBIB-KS specific forward primer 5'-ccttacagctcctctgac (SEQ ID NO: 165) and a reverse primer 3'-gtttccggccctcacattg (SEQ ID NO: 166). PCRBlunt cloned DNA coding for CT529 serovar L2 and pCR2.1 cloned DNA coding for CT529 serovar Ba, E (BOUR), E (MTW447), F (NI1), G, Ia, K, L1, L3 and MoPn were sequenced using T7 promoter primer and universal M13 forward and M13 reverse primers.

To determine if these two putative open reading frames (SEQ ID NO: 16 and 20) encoded a protein with an associated immunological function, overlapping peptides (17-20 amino acid lengths) spanning the lengths of the two open reading frames were synthesized, as described in Example 3. A standard chromium release assay was utilized to determine the percent specific lysis of peptide-pulsed H2^d restricted target cells. In this assay, aliquots of P815 cells (H2^d) were labeled at 37° C for one hour with 100 µCi of ⁵¹Cr in the presence or absence of 1 µg/ml of the indicated peptides. Following this incubation, labeled P815 cells were washed to remove excess ⁵¹Cr and peptide, and subsequently plated in duplicate in microculture plates at a concentration of 1,000 cells/well. Effector CTL (*Chlamydia*-specific CD8 T cells) were added at the indicated effector:target ratios. Following a 4 hour incubation, supernatants were harvested and measured by gamma-counter for release of ⁵¹Cr into the supernatant. Two overlapping peptides from the 298 amino acid open reading frame did specifically stimulate the CTL line. The peptides represented in SEQ ID NO: 138-156 were synthesized, representing the translation of the L2 homologue of the serovar D open reading frame for CT529 (Cap1 gene) and 216 amino acid open reading frame. As shown in Fig. 3, peptides CtC7.8-12 (SEQ ID NO: 18, also referred to as Cap1#132-147, SEQ ID NO: 139) and CtC7.8-13 (SEQ ID NO: 19, also referred to as Cap1#138-155, SEQ ID NO: 140) were able to elicit 38 to 52% specific lysis, respectively, at an effector to target ratio of 10:1. Notably, the overlap between these two peptides contained a predicted H2^d (K^d and L^d) binding peptide. A 10 amino acid peptide was synthesized to correspond to this overlapping sequence (SEQ ID NO: 31) and was found to generate a strong immune response from the anti-*Chlamydia* CTL line by elispot assay. Significantly, a search of the most recent Genbank database revealed no proteins have previously been described for this gene. Therefore, the putative open

reading frame encoding clone 2C7-8 (SEQ ID NO: 15) defines a gene which encompasses an antigen from *Chlamydia* capable of stimulating antigen-specific CD8+ T-cells in a MHC-I restricted manner, demonstrating this antigen could be used to develop a vaccine against *Chlamydia*.

5 To confirm these results and to further map the epitope, truncated peptides (SEQ ID NO: 138-156) were made and tested for recognition by the T-cells in an IFN- γ ELISPOT assay. Truncations of either Ser139 (Cap1#140-147, SEQ ID NO: 146) or Leu147 (Cap1#138-146, SEQ ID NO: 147) abrogate T-cell recognition. These results indicate that the 9-mer peptide Cap1#139-147 (SFIGGITYL, SEQ ID NO: 145)
10 is the minimal epitope recognized by the *Chlamydia*-specific T-cells.

Sequence alignments of Cap1 (CT529) from selected serovars of *C. trachomatis* (SEQ ID NO: 121, 123, 125, 127, 129, 131, 133, 135, 137 and 139) shows one of the amino acid differences is found in position 2 of the proposed epitope. The homologous serovar D peptide is SIIGGITYL (SEQ ID NO: 168). The ability of
15 SFIGGITYL and SIIGGITYL to target cells for recognition by the *Chlamydia* specific T-cells was compared. Serial dilutions of each peptide were incubated with P815 cells and tested for recognition by the T-cells in a ^{51}Cr release assay, as described above. The *Chlamydia*-specific T-cells recognize the serovar L2 peptide at a minimum concentration of 1 nM and the serovar D peptide at a minimum concentration of 10 nM.

20 Further studies have shown that a Cap1#139-147-specific T-cell clone recognizes *C. trachomatis* infected cells. To confirm that Cap1₁₃₉₋₁₄₇ is presented on the surface of *Chlamydia* infected cells, Balb-3T3 (H-2^d) cells were infected with *C. trachomatis* serovar L2 and tested to determine whether these cells are recognized by a CD8+ T-cell clone specific for Cap1#139-147 epitope (SEQ ID NO: 145). The T-cell
25 clone specific for Cap1#139-147 epitope was obtained by limiting dilution of the line 69 T-cells. The T-cell clone specifically recognized the *Chlamydia* infected cells. In these experiments, target cells were *C. trachomatis* infected (positive control) or uninfected Balb/3T3 cells, showing 45%, 36% and 30% specific lysis at 30:1, 10:1 and 3:1 effector to target ratios, respectively; or Cap1#139-147 epitope (SEQ ID NO: 145)
30 coated, or untreated P815 cells, showing 83%, 75% and 58% specific lysis at 30:1, 10:1 and 3:1 effector to target ratios, respectively (negative controls having less than 5% lysis in all cases). This data suggests that the epitope is presented during infection.

In vivo studies show Cap1#139-147 epitope-specific T-cells are primed during murine infection with *C. trachomatis*. To determine if infection with *C. trachomatis* primes a Cap1#139-147 epitope-specific T-cell response, mice were infected i.p. with 10^8 IFU of *C. trachomatis* serovar L2. Two weeks after infection, the mice were sacrificed and spleen cells were stimulated on irradiated syngeneic spleen cells pulsed with Cap1#139-147 epitope peptide. After 5 days of stimulation, the cultures were used in a standard ^{51}Cr release assay to determine if there were Cap1#139-147 epitope-specific T-cells present in the culture. Specifically, spleen cells from a *C. trachomatis* serovar L2 immunized mouse or a control mouse injected with PBS after a 5 days culture with Cap1#139-147 peptide-coated syngeneic spleen cells and CD8+ T-cells able to specifically recognize Cap1#139-147 epitope gave 73%, 60% and 32% specific lysis at a30:1, 10:1 and 3:1 effector to target ratios, respectively. The control mice had a percent lysis of approximately 10% at a 30:1 effector to target ratio, and steadily declining with lowering E:T ratios. Target cells were Cap1#139-147 peptide-coated, or untreated P815 cells. These data suggest that Cap1#139-147 peptide-specific T-cells are primed during murine infection with *C. trachomatis*.

Ct529 Localization

Studies were performed demonstrating that Ct529 (referred to herein as Cap-1) localizes to the inclusion membrane of *C. trachomatis*-infected cells and is not associated with elementary bodies or reticulate bodies. As described above, Cap-1 was identified as a product from *Chlamydia* that stimulates CD8+ CTL. These CTL are protective in a murine model of infection, thus making Cap-1 a good vaccine candidate. Further, since these CTL are MHC-I restricted, the Cap-1 gene must have access to the cytosol of infected cells, which may be a unique characteristic of specific *Chlamydial* gene products. Therefore, determination of the cellular localization of the gene products would be useful in characterizing Cap-1 as a vaccine candidate. To detect the intracellular localization of Cap-1, rabbit polyclonal antibodies directed against a recombinant polypeptide encompassing the N-terminal 125 amino acids of Cap-1 (SEQ ID NO: 305, with the amino acid sequence including the N-terminal 6-His tag provided in SEQ ID NO: 304) were used to stain McCoy cells infected with *Chlamydiae*.

Rabbit-anti-Cap-1 polyclonal antibodies were obtained by hyper-immunization of rabbits with a recombinant polypeptide, rCt529c1-125 (SEQ ID NO: 305) encompassing the N-terminal portion of Cap-1. Recombinant rCt529c1-125 protein was obtained from *E. coli* transformed with a pET expression plasmid (as described above) encoding the nucleotides 1-375 encoding the N-terminal 1-125 amino acids of Cap-1. Recombinant protein was purified by Ni-NTA using techniques well known in the art. For a positive control antiserum, polyclonal antisera directed against elementary bodies were made by immunization of rabbits with purified *C. trachomatis* elementary bodies (Biodesign, Sacco, Maine). Pre-immune sera derived from rabbits prior to immunization with the Cap-1 polypeptide was used as a negative control.

Immunocytochemistry was performed on McCoy cell monolayers grown on glass coverslips inoculated with either *C. trachomatis* serovar L2 or *C. psittaci*, strain 6BC, at a concentration of 10^6 IFU (Inclusion Forming Units) per ml. After 2 hours, medium was aspirated and replaced with fresh RP-10 medium supplemented with cycloheximide (1.0 μ g/ml). Infected cells were incubated at in 7% CO₂ for 24 hours and fixed by aspirating medium, rinsing cells once with PBS and methanol fixation for 5 minutes. For antigen staining, fixed cell monolayers were washed with PBS and incubated at 37°C for 2 hours with 1:100 dilutions of specific or control antisera. Cells were rinsed with PBS and incubated for 1 hour with fluorescein isothiocyanate (FITC)-labeled, anti-rabbit IgG (KPL, Gaithersburg) and stained with Evans blue (0.05%) in PBS. Fluorescence was observed with a 100X objective (Zeiss epifluorescence microscope), and photographed (Nikon UFX-11A camera).

Results from this study show Cap-1 localizes to the inclusion membrane of *C. trachomatis*-infected cells. Cap-1 specific antibody labeled the inclusion membranes of *C. trachomatis*-infected cells, but not *Chlamydial* elementary bodies contained in these inclusions or released by the fixation process. Conversely, the anti-elementary body antibody clearly labeled the bacterial bodies, not only within the inclusions, but those released by the fixation process. Specificity of the anti-Cap-1 antibody is demonstrated by the fact that it does not stain *C. psittaci*-infected cells. Specificity of the Cap-1 labeling is also shown by the absence of reactivity in pre-immune sera. These results suggest that Cap-1 is released from the bacteria and becomes associated with the *Chlamydial* inclusion membrane. Therefore, Cap-1 is a

gene product which may be useful for stimulating CD8+ T cells in the development of a vaccine against infections caused by *Chlamydia*.

The relevance of the Cap-1 gene as a potential CTL antigen in a vaccine against *Chlamydia* infection is further illustrated by two additional series of studies.

- 5 First, CTL specific for the MHC-I epitope of Cap-1 CT529 #138-147 peptide of *C. trachomatis* (SEQ ID NO: 144) have been shown to be primed to a high frequency during natural infection. Specifically, Balb/C mice were inoculated with 10^6 I.F.U. of *C. trachomatis*, serova L2. After 2 weeks, spleens were harvested and quantified by
- 10 Elispot analysis for the number of IFN- γ secreting cells in response to Cap-1 #138-147 peptide-pulsed antigen presenting cells. In two experiments, the number of IFN- γ -secreting cells in 10^5 splenocytes was about 1% of all CD8+ T-cells. This high frequency of responding CD8+ CTL to the MHC-1 epitope (Cap-1 CT529 #138-147 peptide) suggest that Cap-1 is highly immunogenic in infections.

- Results from a second series of studies have shown that the Cap-1
- 15 protein is almost immediately accessible to the cytosol of the host cell upon infection. This is shown in a time-course of Cap-1 CT529 #138-147 peptide presentation. Briefly, 3T3 cells were infected with *C. trachomatis* serovar L2 for various lengths of time, and then tested for recognition by Cap-1 CT529 #138-147 peptide-specific CTL. The results show that *C. trachomatis*-infected 3T3 cells are targeted for recognition by the
- 20 antigen-specific CTL after only 2 hours of infection. These results suggest that Cap-1 is an early protein synthesized in the development of *C. trachomatis* elementary bodies to reticulate bodies. A CD8+ CTL immune response directed against a gene product expressed early in infection may be particularly efficacious in a vaccine against *Chlamydia* infection.

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EXAMPLE 5

GENERATION OF ANTIBODY AND T-CELL RESPONSES IN MICE IMMUNIZED WITH *CHLAMYDIA* ANTIGENS

- 30 Immunogenicity studies were conducted to determine the antibody and CD4+ T cell responses in mice immunized with either purified SWIB or S13 proteins formulated with Montanide adjuvant, or DNA-based immunizations with pcDNA-3 expression

vectors containing the DNA sequences for SWIB or S13. SWIB is also referred to as clone 1-B1-66 (SEQ ID NO: 1, with the corresponding amino acid sequence provided in SEQ ID NO: 5), and S13 ribosomal protein is also referred to as clone 10-C10-31 (SEQ ID NO: 4, with the corresponding amino acid sequence provided in SEQ ID NO: 12).

5 In the first experiment, groups of three C57BL/6 mice were immunized twice and monitored for antibody and CD4+ T-cell responses. DNA immunizations were intradermal at the base of the tail and polypeptide immunizations were administered by subcutaneous route. Results from standard ³H-incorporation assays of spleen cells from immunized mice shows a strong proliferative response from the group immunized with

10 purified recombinant SWIB polypeptide (SEQ ID NO: 5). Further analysis by cytokine induction assays, as previously described, demonstrated that the group immunized with SWIB polypeptide produced a measurable IFN- γ and IL-4 response. Subsequent ELISA-based assays to determine the predominant antibody isotype response in the experimental group immunized with the SWIB polypeptide were performed. Fig. 4

15 illustrates the SWIB-immunized group gave a humoral response that was predominantly IgG1.

In a second experiment, C3H mice were immunized three times with 10 μ g purified SWIB protein (also referred to as clone 1-B1-66, SEQ ID NO: 5) formulated in either PBS or Montanide at three week intervals and harvested two weeks after the

20 third immunization. Antibody titers directed against the SWIB protein were determined by standard ELISA-based techniques well known in the art, demonstrating the SWIB protein formulated with Montanide adjuvant induced a strong humoral immune response. T-cell proliferative responses were determined by a XTT-based assay (Scudiero, et al, *Cancer Research*, 1988, 48:4827). As shown in Fig. 5, splenocytes

25 from mice immunized with the SWIB polypeptide plus Montanide elicited an antigen specific proliferative response. In addition, the capacity of splenocytes from immunized animals to secrete IFN- γ in response to soluble recombinant SWIB polypeptide was determined using the cytokine induction assay previously described. The splenocytes from all animals in the group immunized with SWIB polypeptide formulated with

30 montanide adjuvant secreted IFN- γ in response to exposure to the SWIB Chlamydia antigen, demonstrating an *Chlamydia*-specific immune response.

In a further experiment, C3H mice were immunized at three separate time points at the base of the tail with 10 µg of purified SWIB or S13 protein (*C. trachomatis*, SWIB protein, clone 1-B1-66, SEQ ID NO: 5, and S13 protein, clone 10-C10-31, SEQ ID NO: 4) formulated with the SBAS2 adjuvant (SmithKline Beecham, London, England). Antigen-specific antibody titers were measured by ELISA, showing both polypeptides induced a strong IgG response, ranging in titers from 1×10^{-4} to 1×10^{-5} . The IgG1 and IgG2a components of this response were present in fairly equal amounts. Antigen-specific T-cell proliferative responses, determined by standard ^3H -incorporation assays on spleen cells isolated from immunized mice, were quite strong for SWIB (50,000 cpm above the negative control) and even stronger for s13 (100,000 cpm above the negative control). The IFN γ production was assayed by standard ELISA techniques from supernatant from the proliferating culture. *In vitro* restimulation of the culture with S13 protein induced high levels of IFN γ production, approximately 25 ng/ml versus 2 ng/ml for the negative control. Restimulation with the SWIB protein also induced IFN γ , although to a lesser extent.

In a related experiment, C3H mice were immunized at three separate time points with 10 µg of purified SWIB or S13 protein (*C. trachomatis*, SWIB protein, clone 1-B1-66, SEQ ID NO: 5, and S13 protein, clone 10-C10-31, SEQ ID NO: 4) mixed with 10 µg of Cholera Toxin. Mucosal immunization was through intranasal inoculation. Antigen-specific antibody responses were determined by standard ELISA techniques. Antigen-specific IgG antibodies were present in the blood of SWIB-immunized mice, with titers ranging from 1×10^{-3} to 1×10^{-4} , but non-detectable in the S13-immunized animals. Antigen-specific T-cell responses from isolated splenocytes, as measured by IFN γ production, gave similar results to those described immediately above for systemic immunization.

An animal study was conducted to determine the immunogenicity of the CT529 serovar LGVII CTL epitope, defined by the CT529 10mer consensus peptide (CSFIGGITYL – SEQ ID NO: 31), which was identified as an H2-Kd restricted CTL epitope. BALB/c mice (3 mice per group) were immunized three times with 25 µg of peptide combined with various adjuvants. The peptide was administered systemically at the base of the tail in either SKB Adjuvant System SBAS-2", SBAS-7 (SmithKline

Beecham, London, England) or Montanide. The peptide was also administered intranasally mixed with 10ug of Cholera Toxin (CT). Naive mice were used as a control. Four weeks after the 3rd immunization, spleen cells were restimulated with LPS-blasts pulsed with 10ug/ml CT529 10mer consensus peptide at three different effector to LPS-blasts ratios : 6, 1.5 and 0.4 at 1×10^6 cell/ml. After 2 restimulations, effector cells were tested for their ability to lyse peptide pulsed P815 cells using a standard chromium release assay. A non-relevant peptide from chicken egg ovalbumin was used as a negative control. The results demonstrate that a significant immune response was elicited towards the CT529 10mer consensus peptide and that antigen-specific T-cells capable of lysing peptide-pulsed targets were elicited in response to immunization with the peptide. Specifically, antigen-specific lytic activities were found in the SBAS-7 and CT adjuvanted group while Montanide and SBAS-2" failed to adjuvant the CTL epitope immunization.

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EXAMPLE 6

EXPRESSION AND CHARACTERIZATION OF *CHLAMYDIA PNEUMONIAE* GENES

The human T-cell line, TCL-8, described in Example 1, recognizes *Chlamydia trachomatis* as well as *Chlamydia pneumonia* infected monocyte-derived dendritic cells, suggesting *Chlamydia trachomatis* and *pneumonia* may encode cross-reactive T-cell epitopes. To isolate the *Chlamydia pneumonia* genes homologous to *Chlamydia trachomatis* LGV II clones 1B1-66, also referred to as SWIB (SEQ ID NO: 1) and clone 10C10-31, also referred to as S13 ribosomal protein (SEQ ID NO: 4), HeLa 229 cells were infected with *C. pneumonia* strain TWAR (CDC/CWL-029). After three days incubation, the *C. pneumonia*-infected HeLa cells were harvested, washed and resuspended in 200 μ l water and heated in a boiling water bath for 20 minutes. Ten microliters of the disrupted cell suspension was used as the PCR template.

C. pneumonia specific primers were designed for clones 1B1-66 and 10C10-31 such that the 5' end had a 6X-Histidine tag and a Nde I site inserted, and the 3' end had a stop codon and a BamHI site included (Fig. 6). The PCR products were amplified and sequenced by standard techniques well known in the art. The *C.*

pneumonia-specific PCR products were cloned into expression vector pET17B (Novagen, Madison, WI) and transfected into *E. coli* BL21 pLysS for expression and subsequent purification utilizing the histidine-nickel chromatographic methodology provided by Novagen. Two proteins from *C. pneumonia* were thus generated, a 10-11 kDa protein referred to as CpSWIB (SEQ ID NO: 27, and SEQ ID NO: 78 having a 6X His tag, with the corresponding amino acid sequence provided in SEQ ID NO: 28, respectively), a 15 kDa protein referred to as CpS13 (SEQ ID NO: 29, and SEQ ID NO: 77, having a 6X His tag, with the corresponding amino acid sequence provided in SEQ ID NO: 30 and 91, respectively).

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EXAMPLE 7

INDUCTION OF T CELL PROLIFERATION AND INTERFERON- γ
PRODUCTION BY *CHLAMYDIA PNEUMONIAE* ANTIGENS

The ability of recombinant *Chlamydia pneumoniae* antigens to induce T cell proliferation and interferon- γ production is determined as follows.

Proteins are induced by IPTG and purified by Ni-NTA agarose affinity chromatography (Webb et al., *J. Immunology* 157:5034-5041, 1996). The purified polypeptides are then screened for the ability to induce T-cell proliferation in PBMC preparations. PBMCs from *C. pneumoniae* patients as well as from normal donors whose T-cells are known to proliferate in response to *Chlamydia* antigens, are cultured in medium comprising RPMI 1640 supplemented with 10% pooled human serum and 50 μ g/ml gentamicin. Purified polypeptides are added in duplicate at concentrations of 0.5 to 10 μ g/mL. After six days of culture in 96-well round-bottom plates in a volume of 200 μ l, 50 μ l of medium is removed from each well for determination of IFN- γ levels, as described below. The plates are then pulsed with 1 μ Ci/well of tritiated thymidine for a further 18 hours, harvested and tritium uptake determined using a gas scintillation counter. Fractions that result in proliferation in both replicates three fold greater than the proliferation observed in cells cultured in medium alone are considered positive.

30

IFN- γ was measured using an enzyme-linked immunosorbent assay (ELISA). ELISA plates are coated with a mouse monoclonal antibody directed to human IFN- γ (PharMingen, San Diego, CA) in PBS for four hours at room temperature. Wells are then blocked with PBS containing 5% (W/V) non-fat dried milk for 1 hour at room temperature. The plates are washed six times in PBS/0.2% TWEEN-20 and samples diluted 1:2 in culture medium in the ELISA plates are incubated overnight at room temperature. The plates are again washed and a polyclonal rabbit anti-human IFN- γ serum diluted 1:3000 in PBS/10% normal goat serum is added to each well. The plates are then incubated for two hours at room temperature, washed and horseradish peroxidase-coupled anti-rabbit IgG (Sigma Chemical Co., St. Louis, MO) is added at a 1:2000 dilution in PBS/5% non-fat dried milk. After a further two hour incubation at room temperature, the plates are washed and TMB substrate added. The reaction is stopped after 20 min with 1 N sulfuric acid. Optical density is determined at 450 nm using 570 nm as a reference wavelength. Fractions that result in both replicates giving an OD two fold greater than the mean OD from cells cultured in medium alone, plus 3 standard deviations, are considered positive.

A human anti-*Chlamydia* T-cell line (TCL-8) capable of cross-reacting to *C. trachomatis* and *C. pneumonia* was used to determine whether the expressed proteins described in the example above, (i.e., CpSWIB, SEQ ID NO: 27, and SEQ ID NO: 78 having a 6X His tag, with the corresponding amino acid sequence provided in SEQ ID NO: 28, respectively, and the 15 kDa protein referred to as CpS13 SEQ ID NO: 29, and SEQ ID NO: 77, having a 6X His tag, with the corresponding amino acid sequence provided in SEQ ID NO: 30 and 91, respectively), possessed T-cell epitopes common to both *C. trachomatis* and *C. pneumonia*. Briefly, *E. coli* expressing *Chlamydial* proteins were titred on 1×10^4 monocyte-derived dendritic cells. After two hours, the dendritic cells cultures were washed and 2.5×10^4 T cells (TCL-8) added and allowed to incubate for an additional 72 hours. The amount of IFN- γ in the culture supernatant was then determined by ELISA. As shown in Figs. 7A and 7B, the TCL-8 T-cell line specifically recognized the S13 ribosomal protein from both *C. trachomatis* and *C. pneumonia* as demonstrated by the antigen-specific induction of IFN- γ , whereas only the SWIB protein from *C. trachomatis* was recognized by the T-cell line. To

validate these results, the T cell epitope of *C. trachomatis* SWIB was identified by epitope mapping using target cells pulsed with a series of overlapping peptides and the T-cell line TCL-8. 3H-thymidine incorporation assays demonstrated that the peptide, referred to as C.t.SWIB 52-67, of SEQ ID NO: 39 gave the strongest proliferation of the
5 TCL-8 line. The homologous peptides corresponding to the SWIB of *C. pneumoniae* sequence (SEQ ID NO: 40), the topoisomerase-SWIB fusion of *C. pneumoniae* (SEQ ID NO: 43) and *C. trachomatis* (SEQ ID NO: 42) as well as the human SWI domain (SEQ ID NO: 41) were synthesized and tested in the above assay. The T-cell line TCL-8 only recognized the *C. trachomatis* peptide of SEQ ID NO: 39 and not the
10 corresponding *C. pneumoniae* peptide (SEQ ID NO: 40), or the other corresponding peptides described above (SEQ ID NO: 41-43).

Chlamydia-specific T cell lines were generated from donor CP-21 with a positive serum titer against *C. pneumoniae* by stimulating donor PBMC with either *C. trachomatis* or *C. pneumoniae*-infected monocyte-derived dendritic cells, respectively.
15 T-cells generated against *C. pneumoniae* responded to recombinant *C. pneumoniae*-SWIB but not *C. trachomatis*-SWIB, whereas the T-cell line generated against *C. trachomatis* did not respond to either *C. trachomatis*- or *C. pneumoniae*-SWIB (see Fig. 9). The *C. pneumoniae*-SWIB specific immune response of donor CP-21 confirms the *C. pneumoniae* infection and indicates the elicitation of *C. pneumoniae*-SWIB specific
20 T-cells during *in vivo* *C. pneumoniae* infection.

Epitope mapping of the T-cell response to *C. pneumoniae*-SWIB has shown that Cp-SWIB-specific T-cells responded to the overlapping peptides Cp-SWIB 32-51 (SEQ ID NO: 101) and Cp-SWIB 37-56 (SEQ ID NO: 102), indicating a *C. pneumoniae*-SWIB-specific T-cell epitope Cp-SWIB 37-51 (SEQ ID NO: 100).

25 In additional experiments, T-cell lines were generated from donor CP1, also a *C. pneumoniae* seropositive donor, by stimulating PBMC with non-infectious elementary bodies from *C. trachomatis* and *C. pneumoniae*, respectively. In particular, proliferative responses were determined by stimulating 2.5×10^4 T-cells in the presence of 1×10^4 monocyte-derived dendritic cells and non-infectious elementary bodies
30 derived from *C. trachomatis* and *C. pneumoniae*, or either recombinant *C. trachomatis* or *C. pneumoniae* SWIB protein. The T-cell response against SWIB resembled the data obtained with T-cell lines from CP-21 in that *C. pneumoniae*-SWIB, but not *C.*

trachomatis-SWIB elicited a response by the *C. pneumoniae* T-cell line. In addition, the *C. trachomatis* T-cell line did not proliferate in response to either *C. trachomatis* or *C. pneumoniae* SWIB, though it did proliferate in response to both CT and CP elementary bodies. As described in Example 1, Clone 11-C12-91 (SEQ ID NO: 63), identified using the TCP-21 cell line, has a 269 bp insert that is part of the OMP2 gene (CT443) and shares homology with the 60 kDa cysteine rich outer membrane protein of *C. pneumoniae*, referred to as OMCB. To further define the reactive epitope(s), epitope mapping was performed using a series of overlapping peptides and the immunoassay previously described. Briefly, proliferative responses were determined by stimulating 2.5×10^4 TCP-21 T-cells in the presence of 1×10^4 monocyte-derived dendritic cells with either non-infectious elementary bodies derived from *C. trachomatis* and *C. pneumoniae*, or peptides derived from the protein sequence of *C. trachomatis* or *C. pneumoniae* OMCB protein (0.1 µg/ml). The TCP-21 T-cells responded to epitopes CT-OMCB #167-186, CT-OMCB #171-190, CT-OMCB #171-186, and to a lesser extent, CT-OMCB #175-186 (SEQ ID NO: 249-252, respectively). Notably, the TCP-21 T-cell line also gave a proliferative response to the homologous *C. pneumoniae* peptide CP-OMCB #171-186 (SEQ ID NO: 253), which was equal to or greater than the response to the *C. trachomatis* peptides. The amino acid substitutions in position two (i.e., Asp for Glu) and position four (i.e., Cys for Ser) did not alter the proliferative response of the T-cells and therefore demonstrating this epitope to be a cross-reactive epitope between *C. trachomatis* and *C. pneumoniae*.

EXAMPLE 8

IMMUNE RESPONSES OF HUMAN PBMC AND T-CELL LINES AGAINST CHLAMYDIA ANTIGENS

The examples provided herein suggest that there is a population of healthy donors among the general population that have been infected with *C. trachomatis* and generated a protective immune response controlling the *C. trachomatis* infection. These donors remained clinically asymptomatic and seronegative for *C. trachomatis*. To characterize the immune responses of normal donors against chlamydial antigens which had been identified by CD4 expression cloning, PBMC

- obtained from 12 healthy donors were tested against a panel of recombinant *chlamydial* antigens including *C. trachomatis*-, *C. pneumoniae*-SWIB and *C. trachomatis*-, *C. pneumoniae*-S13. The data are summarized in Table I below. All donors were seronegative for *C. trachomatis*, whereas 6/12 had a positive *C. pneumoniae* titer.
- 5 Using a stimulation index of >4 as a positive response, 11/12 of the subjects responded to *C. trachomatis* elementary bodies and 12/12 responded to *C. pneumoniae* elementary bodies. One donor, AD104, responded to recombinant *C. pneumoniae*-S13 protein, but not to recombinant *C. trachomatis*-S13 protein, indicating a *C. pneumoniae*-specific response. Three out of 12 donors had a *C. trachomatis*-SWIB, but not a *C.*
- 10 *pneumoniae*-SWIB specific response, confirming a *C. trachomatis* infection. *C. trachomatis* and *C. pneumoniae*- S13 elicited a response in 8/12 donors suggesting a chlamydial infection. These data demonstrate the ability of SWIB and S13 to elicit a T-cell response in PBMC of normal study subjects.

Table I.

Immune response of normal study subjects against <i>Chlamydia</i>										
Donor	Sex	<i>Chlamydia</i> IgG titer	CT EB	CP EB	CT Swib	CP Swib	CT S13	CP S13	CT IpdA	CT TSA
AD100	male	negative	++	+++	+	-	++	++	-	nt
AD104	female	negative	+++	++	-	-	-	++	-	nt
AD108	male	CP 1:256	++	++	+	+/-	+	+	+	nt
AD112	female	negative	++	++	+	-	+	-	+/-	nt
AD120	male	negative	-	+	-	-	-	-	-	nt
AD124	female	CP 1:128	++	++	-	-	-	-	-	nt
AD128	male	CP 1:512	+	++	-	-	++	+	++	-
AD132	female	negative	++	++	-	-	+	+	-	-
AD136	female	CP 1:128	+	++	-	-	+/-	-	-	-
AD140	male	CP 1:256	++	++	-	-	+	+	-	-
AD142	female	CP 1:512	++	++	-	-	+	+	+	-
AD146	female	negative	++	++	-	-	++	+	+	-

- CT= *Chlamydia trachomatis*; CP= *Chlamydia pneumoniae*; EB= *Chlamydia* elementary bodies; Swib= recombinant *Chlamydia* Swib protein; S13= recombinant *Chlamydia* S13 protein; IpdA= recombinant *Chlamydia* IpdA protein; TSA= recombinant *Chlamydia* TSA protein. Values represent results from standard proliferation assays. Proliferative responses were determined by stimulating 3×10^5 PBMC with 1×10^4 monocyte-derived dendritic cells pre-incubated with the respective recombinant antigens or elementary bodies (EB). Assays were harvested after 6 days with a ^3H -thymidine pulse for the last 18h.

SI: Stimulation index

- +/-: SI ~ 4
 +: SI > 4
 ++: SI 10-30
 +++: SI > 30

In a first series of experiments, T-cell lines were generated from a healthy female individual (CT-10) with a history of genital exposure to *C. trachomatis* by stimulating T-cells with *C. trachomatis* LGV II elementary bodies as previously described. Although the study subject was exposed to *C. trachomatis*, she did not seroconvert and did not develop clinical symptoms, suggesting donor CT-10 may have developed a protective immune response against *C. trachomatis*. As shown in Fig. 10, a primary *Chlamydia*-specific T-cell line derived from donor CT-10 responded to *C. trachomatis*-SWIB, but not *C. pneumoniae*-SWIB recombinant proteins, confirming the exposure of CT-10 to *C. trachomatis*. Epitope mapping of the T-cell response to *C. trachomatis*-SWIB showed that this donor responded to the same epitope Ct-SWIB 52-67 (SEQ ID NO: 39) as T-cell line TCL-8, as shown in Fig. 11.

Additional T-cell lines were generated as described above for various *C. trachomatis* patients. A summary of the patients' clinical profile and proliferative responses to various *C. trachomatis* and *C. pneumoniae* elementary bodies and recombinant proteins are summarized in Table II as follows:

Proliferative response of <i>C. trachomatis</i> patients											
Patients	Clinical manifestation	IgG titer	CT EB	CP EB	CT Swib	CP Swib	CT S13	CP S13	CT lpdA	CT TSA	
CT-1	NGU	negative	+	+	-	-	++	++	++	+	
CT-2	NGU	negative	++	++	-	-	+	+/-	-	-	
CT-3	asymptomatic shed Eb Dx was HPV	Ct 1:512 Cp 1:1024 Cps 1:256	+	+	-	-	+	-	+	-	
CT-4	asymptomatic shed Eb	Ct 1:1024	+	+	-	-	-	-	-	-	
CT-5	BV	Ct 1:256 Cp 1:256	++	++	-	-	+	-	-	-	
CT-6	perinial rash discharge	Cp 1:1024	+	+	-	-	-	-	-	-	
CT-7	BV genital ulcer	Ct 1:512 Cp 1:1024	+	+	-	-	+	+	+	-	
CT-8	Not known	Not tested	++	++	-	-	-	-	-	-	
CT-9	asymptomatic	Ct 1:128 Cp 1:128	+++	++	-	-	++	+	+	-	
CT-10	Itch mild vulvar	negative	++	++	-	-	-	-	-	-	
CT-11	BV, abnormal pap	Ct 1: 512	+++	+++	-	-	+++	+/-	++	+	
CT-12	asymptomatic	Cp 1: 512	++	++	-	-	++	+	+	-	

NGU= Non-Gonococcal Urethritis; BV= Bacterial Vaginosis; CT= *Chlamydia trachomatis*; CP= *Chlamydia pneumoniae*; EB= *Chlamydia* elementary bodies; Swib= recombinant *Chlamydia* Swib protein; S13= recombinant *Chlamydia* S13 protein; lpdA= recombinant *Chlamydia* lpdA protein; TSA= recombinant *Chlamydia* TSA protein

Values represent results from standard proliferation assays. Proliferative responses were determined by stimulating 3×10^5 PBMC with the respective recombinant antigens or elementary bodies (EB). Assays were harvested after 6 days with a ^3H -thymidine pulse for the last 18 hours.

SI: Stimulation index

+/-: SI ~ 4

+: SI > 4

++: SI 10-30

+++ : SI > 30

Using the panel of asymptomatic (as defined above) study subjects and *C. trachomatis* patients, as summarized in Tables I and II, a comprehensive study of the immune responses of PBMC derived from the two groups was conducted. Briefly, PBMCs from *C. pneumoniae* patients as well as from normal donors are cultured in medium comprising RPMI 1640 supplemented with 10% pooled human serum and 50 μ g/ml gentamicin. Purified polypeptides, a panel of recombinant *chlamydial* antigens including *C. trachomatis*-, *C. pneumoniae*-SWIB and S13, as well as *C. trachomatis* lpdA and TSA are added in duplicate at concentrations of 0.5 to 10 μ g/mL. After six days of culture in 96-well round-bottom plates in a volume of 200 μ l, 50 μ l of medium is removed from each well for determination of IFN- γ levels, as described below. The plates are then pulsed with 1 μ Ci/well of tritiated thymidine for a further 18 hours, harvested and tritium uptake determined using a gas scintillation counter. Fractions that result in proliferation in both replicates three fold greater than the proliferation observed in cells cultured in medium alone are considered positive.

Proliferative responses to the recombinant *Chlamydiae* antigens demonstrated that the majority of asymptomatic donors and *C. trachomatis* patients recognized the *C. trachomatis* S13 antigen (8/12) and a majority of the *C. trachomatis* patients recognized the *C. pneumoniae* S13 antigen (8/12), with 4/12 asymptomatic donors also recognizing the *C. pneumoniae* S13 antigen. Also, six out of twelve of the *C. trachomatis* patients and four out of twelve of the asymptomatic donors gave a proliferative response to the lpdA antigen of *C. trachomatis*. These results demonstrate that the *C. trachomatis* and *C. pneumoniae* S13 antigen, *C. trachomatis* Swib antigen and the *C. trachomatis* lpdA antigen are recognized by the asymptomatic donors, indicating these antigens were recognized during exposure to *Chlamydia* and an immune response elicited against them. This implies these antigens may play a role in conferring protective immunity in a human host. In addition, the *C. trachomatis* and *C. pneumoniae* S13 antigen is recognized equally well among the *C. trachomatis* patients, therefore indicating there may be epitopes shared between *C. trachomatis* and *C. pneumoniae* in the S13 protein. Table III summarizes the results of these studies.

Table III.

Antigen	Normal Donors	C.t. Patients
C.t.-Swib	3/12	0/12
C.p.-Swib	0/12	0/12
C.t.-S13	8/12	8/12
C.p.-S13	4/12	8/12
lpdA	4/12	6/12
TSA	0/12	2/12

A series of studies were initiated to determine the cellular immune response to short-term T-cell lines generated from asymptomatic donors and *C. trachomatis* patients. Cellular immune responses were measured by standard proliferation assays and IFN- γ , as described in Example 7. Specifically, the majority of the antigens were in the form of single *E. coli* clones expressing Chlamydial antigens, although some recombinant proteins were also used in the assays. The single *E. coli* clones were titrated on 1×10^4 monocyte-derived dendritic cells and after two hours, the culture was washed and 2.5×10^4 T-cells were added. The assay using the recombinant proteins were performed as previously described. Proliferation was determined after four days with a standard ^3H -thymidine pulse for the last 18 hours. Induction of IFN- γ was determined from culture supernatants harvested after four days using standard ELISA assays, as described above. The results show that all the *C. trachomatis* antigens tested, except for C.T. Swib, elicited a proliferative response from one or more different T-cell lines derived from *C. trachomatis* patients. In addition, proliferative responses were elicited from both the *C. trachomatis* patients and asymptomatic donors for the following *Chlamydia* genes, CT622, groEL, pmpD, CT610 and rS13.

The 12G3-83 clone also contains sequences to CT734 and CT764 in addition to CT622, and therefore these gene sequence may also have immunoreactive epitopes. Similarly, clone 21G12-60 contains sequences to the hypothetical protein genes CT229 and CT228 in addition to CT875; and 15H2-76 also contains sequences

from CT812 and CT088, as well as sharing homology to the *sysE* gene. Clone 11H3-61 also contains sequences sharing homology to the PGP6-D virulence protein.

Table IV.

Clone	C. t. Antigen (putative*)	TCL from Asymp. Donors	TCL from C. t. Patients	SEQ ID NO:
1B1-66 (E. coli)	Swib	2/2	0/4	5
1B1-66 (protein)	Swib	2/2	0/4	5
12G3-83 (E. coli)	CT622*	2/2	4/4	57
22B3-53 (E. coli)	groEL	1/2	4/4	111
22B3-53 (protein)	groEL	1/2	4/4	111
15H2-76 (E. coli)	PmpD*	1/2	3/4	87
11H3-61 (E. coli)	rL1*	0/2	3/4	60
14H1-4 (E. coli)	TSA	0/2	3/4	56
14H1-4 (protein)	TSA	0/2	3/4	56
11G10-46 (E. coli)	CT610	1/2	1/4	62
10C10-17 (E. coli)	rS13	1/2	1/4	62
10C10-17 (protein)	rS13	1/2	1/4	62
21G12-60 (E. coli)	CT875*	0/2	2/4	110
11H4-32 (E. coli)	dnaK	0/2	2/4	59
21C7-8 (E. coli)	dnaK	0/2	2/4	115
17C10-31 (E. coli)	CT858	0/2	2/4	114

5

EXAMPLE 9

PROTECTION STUDIES USING *CHLAMYDIA* ANTIGENS1. SWIB

10

Protection studies were conducted in mice to determine whether immunization with chlamydial antigens can impact on the genital tract disease resulting from chlamydial inoculation. Two models were utilized; a model of intravaginal inoculation

that uses a human isolate containing a strain of *Chlamydia psittaci* (MTW447), and a model of intrauterine inoculation that involves a human isolate identified as *Chlamydia trachomatis*, serovar F (strain NII). Both strains induce inflammation in the upper genital tract, which resemble endometritis and salpingitis caused by *Chlamydia trachomatis* in women. In the first experiment, C3H mice (4 mice per group) were immunized three times with 100 µg of pcDNA-3 expression vector containing *C. trachomatis* SWIB DNA (SEQ ID NO: 1, with the corresponding amino acid sequence provided in SEQ ID NO: 5). Inoculations were at the base of the tail for systemic immunization. Two weeks after the last immunization, animals were progesterone treated and infected, either thru the vagina or by injection of the inoculum in the uterus. Two weeks after infection, the mice were sacrificed and genital tracts sectioned, stained and examined for histopathology. Inflammation level was scored (from + for very mild, to +++++ for very severe). Scores attributed to each single oviduct/ovary were summed and divided by the number of organs examined to get a mean score of inflammation for the group. In the model of uterine inoculation, negative control-immunized animals receiving empty vector showed consistent inflammation with an ovary /oviduct mean inflammation score of 6.12, in contrast to 2.62 for the DNA-immunized group. In the model of vaginal inoculation and ascending infection, negative control-immunized mice had an ovary /oviduct mean inflammation score of 8.37, versus 5.00 for the DNA-immunized group. Also, in the later model, vaccinated mice showed no signs of tubal occlusion while negative control vaccinated groups had inflammatory cells in the lumen of the oviduct

In a second experiment, C3H mice (4 mice per group) were immunized three times with 50 µg of pcDNA-3 expression vector containing *C. trachomatis* SWIB DNA (SEQ ID NO: 1, with the corresponding amino acid sequence provided in SEQ ID NO: 5) encapsulated in Poly Lactide co-Glycolide microspheres (PLG); immunizations were made intra-peritoneally. Two weeks after the last immunization, animal were progesterone treated and infected by inoculation of *C. psittaci* in the vagina. Two weeks after infection, mice were sacrificed and genital tracts sectioned, stained and examined for histopathology. Inflammation level was scored as previously described. Scores attributed to each single oviduct /ovary were summed and divided by the number of examined organs to get a mean of inflammation for the group. Negative control-

immunized animals receiving PLG-encapsulated empty vector showed consistent inflammation with an ovary /oviduct mean inflammation score of 7.28, versus 5.71 for the PLG-encapsulated DNA immunized group. Inflammation in the peritoneum was 1.75 for the vaccinated group versus 3.75 for the control.

5 In a third experiment, C3H mice (4 per group) were immunized three times with 10 µg of purified recombinant protein, either SWIB (SEQ ID NO: 1, with the corresponding amino acid sequence provided in SEQ ID NO: 5, or S13 (SEQ ID NO: 4, with the corresponding amino acid sequence provided in SEQ ID NO: 12) mixed with Cholera Toxin (CT); the preparation was administered intranasally upon anaesthesia in a
10 20 µL volume. Two weeks after the last immunization, animals were progesterone treated and infected, either by vaginal inoculation of *C. psittaci* or by injection of *C. trachomatis* serovar F in the uterus. Two weeks after infection, the mice were sacrificed and genital tracts sectioned, stained and examined for histopathology. The degree of inflammation was scored as described above. Scores attributed to each single
15 oviduct /ovary were summed and divided by the number of examined organs to get a mean score of inflammation for the group. In the model of uterine inoculation, negative control- immunized animals receiving cholera toxin alone showed an ovary /oviduct mean inflammation score of 4.25 (only 2 mice analyzed ; 2 other died) versus 5.00 for the S13 plus cholera toxin-immunized group, and 1.00 for the SWIB plus cholera toxin.
20 Untreated infected animals had an ovary /oviduct mean inflammation score of 7. In the model of vaginal inoculation and ascending infection, negative control-immunized mice had an ovary /oviduct mean inflammation score of 7.37 versus 6.75 for the S13 plus cholera toxin-immunized group and 5.37 for the SWIB plus cholera toxin-immunized group. Untreated infected animals had an ovary /oviduct mean inflammation score of 8.

25 The three experiments described above suggest that SWIB-specific protection is obtainable. This protective effect is more marked in the model of homologous infection but is still present when in a heterologous challenge infection with *C. psittaci*.

2. CT529/Cap1

CT529/Cap1 was identified earlier as a product from Chlamydia that stimulates CD8+ CTL. In this example, we sought to confirm that immunization with Cap1 would be protective in an animal model of chlamydia infection.

5 To generate recombinant vaccinia virus for delivery of a Cap1 immunogenic fragment, a DNA fragment containing a modified Kozak sequence and base pairs 319-530 of the cap1 gene (CT529) was amplified from *C. trachomatis* L2 genomic DNA using PCR™ and ligated into pSC11ss (Earl PL, Koenig S, Moss B (1991) Biological and immunological properties of human immunodeficiency virus type 1 envelope
10 glycoprotein: analysis of proteins with truncations and deletions expressed by recombinant vaccinia viruses. *J Virol.* 65:31-41). DNA digested with SalI and StuI. The portion of the cap1 gene ligated into pSC11ss encodes amino acids 107-176 of Cap1 protein, containing the previously identified CTL epitope of amino acids 139-147. The resulting plasmid was used to transfect CV-1 cells (ATCC# CCL-70; Jensen FC et
15 al. (1964) Infection of human and simian tissue cultures with Rous Sarcoma Virus. *Proc. Natl. Acad. Sci. USA* 52: 53-59.) which were subsequently infected with wild-type vaccinia virus. Homologous recombination between the wild-type virus and plasmid DNA generated recombinant vaccinia viruses which were selected on the basis of both beta-galactosidase expression and the inactivation of thymidine kinase, as
20 described previously (Chakrabarti et al, *Mol Cell Biol.* 1985, 5(12):3403-9). Recombinant virus was plaque purified three times and titered after growth in human TK-143B cells. Virus preparations were treated with equal volume of 0.25 mg/ml trypsin for 30 mins. at 37°C and diluted in PBS prior to immunization of mice. Groups of 5 mice were used for all experimental and control groups. The data presented below
25 are representative of three independent experiments.

A group of mice was immunized with 10^6 of the recombinant vaccinia i.p. and was allowed to recover for 3 weeks. Negative control groups were immunized with either buffer alone or wild-type vaccinia. As a positive control, a group of mice was infected i.v. with 10^6 i.f.u. of *C. trachomatis*. The number of organisms given to the
30 positive control group has been previously shown to be cleared within 2 weeks. After 3 weeks, animals in each of the groups were challenged i.v. with 10^6 i.f.u. of *C.*

trachomatis. Three days after challenge the mice were sacrificed and the number of i.f.u. per spleen was determined.

The mean number of organisms found in the spleens of animals immunized with the vaccinia virus expressing Cap1 (7.1×10^4) was 2.6-fold fewer ($p < 0.01$; Wilcoxon's-Rank Sum analysis) than animals in the control groups immunized with either buffer (1.8×10^5) or wild-type vaccinia (1.9×10^5). Animals in the positive group had 77-fold fewer organisms (2.4×10^3) per spleen than animals in the negative control groups ($p < 0.01$; Wilcoxon's-Rank Sum analysis). These data demonstrate that immunization with an immunogenic fragment of Cap1 can afford a statistically significant level of protection against *C. trachomatis* infection.

EXAMPLE 10

Pmp/Ra12 FUSION PROTEINS

Various Pmp/Ra12 fusion constructs were generated by first synthesizing PCR fragments of a Pmp gene using primers containing a Not I restriction site. Each PCR fragment was then ligated into the NotI restriction site of pCRX1. The pCRX1 vector contains the 6HisRa12 portion of the fusion. The Ra12 portion of the fusion construct encodes a polypeptide corresponding to amino acid residues 192-323 of *Mycobacterium tuberculosis* MTB32A, as described in U.S. Patent Application 60/158,585, the disclosure of which is incorporated herein by reference. The correct orientation of each insert was determined by its restriction enzyme pattern and its sequence was verified. Multiple fusion constructs were made for PmpA, PmpB, PmpC, PmpF and PmpH, as described further below:

PmpA Fusion Proteins

PmpA is 107 kD protein containing 982 aa and was cloned from serovar E. The PmpA protein was divided into 2 overlapping fragments, the PmpA(N-terminal) and (C-terminal) portions.

PmpA(N-term) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCATGTTTATAACAAAGGAAC TTATG (SEQ ID NO: 306)

GAGAGCGGCCGCTTACTTAGGTGAGAAGAAGGGAGTTTC (SEQ ID NO: 307) respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 308, encoding a 66 kD protein (619aa) expressing the segment 1-473 aa of PmpA. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 309.

5 PmpA(C-term) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCCATTCTATTCATTTCTTTGATCCTG (SEQ ID NO: 310)

GAGAGCGGCCGCTTAGAAGCCAACATAGCCTCC (SEQ ID NO: 311)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 312, encoding a 74 kD protein (691aa) expressing the segment 438-982 aa of PmpA. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 313.

PmpF Fusion Proteins

PmpF is 112 kD protein containing 1034 aa and was cloned from the serovar E. PmpF protein was divided into 2 overlapping fragments, the PmpF(N-term) and (C-term) portions.

15 PmpF(N-term) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCATGATTAAGAAGAACTTCTCTATCC (SEQ ID NO: 314)

GAGAGCGGCCGCTTATAATTCTGCATCATCTTCTATGGC (SEQ ID NO: 315)

respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 316, encoding a 69 kD protein (646aa) expressing the segment 1-499 aa of PmpF. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 317.

20 PmpF(C-term) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGACATACGAAGCTTGATGGG (SEQ ID NO: 318)

GAGAGCGGCCGCTTAAAGACCAGAGCTCCTCC (SEQ ID NO: 319)

respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 320, encoding a 77 kD protein (715aa) expressing the segment 466-1034aa of PmpF. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 321.

PmpH Fusion Proteins

PmpH is 108 kD protein containing 1016 aa and was cloned from the serovar E. PmpH protein was divided into 2 overlapping fragments, the PmpH(N-term) and (C-term) portions.

- 5 PmpH(N-term) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCATGCCCTTTTCITTGAGATCTAC (SEQ ID NO: 322)

GAGAGCGGCCGCTTACACAGATCCATTACCGACTG (SEQ ID NO: 323)

- respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 324, encoding a 64 kD protein (631aa) expressing the segment 1-484 aa of PmpH. The
10 amino acid sequence of the fusion protein is set forth in SEQ ID NO: 325. The donor line CHH037 was found to be reactive against this protein.

PmpH(C-term) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGATCCTGTAGTACAAAATAATTCAGC (SEQ ID NO: 326)

GAGAGCGGCCGCTTAAAAGATTCTATTCAAGCC (SEQ ID NO: 327)

- 15 respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 328, encoding a 77 kD protein (715aa) expressing the segment 449-1016aa of PmpH. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 329. The patient line CT12 was found to be reactive in response to this protein.

PmpB Fusion Proteins

- 20 PmpB is 183 kD protein containing 1750 aa and was cloned from the serovar E. PmpB protein was divided into 4 overlapping fragments, PmpB(1), (2), (3) and (4).

PmpB(1) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCATGAAATGGCTGTCAGCTACTGCG (SEQ ID NO: 330)

- 25 GAGAGCGGCCGCTTACTTAATGCGAATTTCTTCAAG (SEQ ID NO: 331)

respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 332, and encodes a 53 kD protein (518aa) expressing the segment 1-372 aa of PmpB. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 333.

PmpB(2) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGGTGACCTCTCAATTCAATCTTC (SEQ ID NO: 334)

GAGAGCGGCCGCTTAGTTCTCTGTGTACAGATAAGGAGAC (SEQ ID NO: 335)

- respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 336 and
5 encodes a 60 kD protein (585aa) expressing the segment 330-767 aa of PmpB. The
amino acid sequence of the fusion protein is set forth in SEQ ID NO: 337. Cell lines
derived from patient lines CT1, CT3, CT4 responded to this recombinant pmpB protein.

PmpB(3) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGACCAACTGAATATCTCTGAGAAC (SEQ ID NO: 338)

- 10 GAGCGGCCGCTTAAGAGACTACGTGGAGTTCTG (SEQ ID NO: 339)

respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 340
encodes a 67 kD protein (654aa) expressing the segment 732-1236 aa of PmpB. The
amino acid sequence of the fusion protein is set forth in SEQ ID NO: 341

PmpB(4) was amplified by the sense and antisense primers:

- 15 GAGAGCGGCCGCTCGGAACCTATTGTGTTCTCTTCTG (SEQ ID NO: 342)

GAGAGCGGCCGCTTAGAAGATCATGCGAGCACCGC (SEQ ID NO: 343)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID
NO: 344 encodes a 76 kD protein (700aa) expressing the segment 1160-1750 of PmpB.
The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 345.

- 20 PmpC Fusion Proteins

PmpC is 187 kD protein containing 1774 aa and was cloned from the
serovar E/1.2. PmpC protein was divided into 3 overlapping fragments, PmpC(1), (2)
and (3).

PmpC(1) was amplified by the sense and antisense primers:

- 25 GAGAGCGGCCGCTCATGAAATTTATGTCAGCTACTGC (SEQ ID NO: 346)

GAGAGCGGCCGCTTACCCTGTAATTCAGTGATGGTC (SEQ ID NO: 347)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 348 and encodes a 51 kD protein (487aa) expressing the segment 1-340 aa of PmpC. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 349.

PmpC(2) was amplified by the sense and antisense primers:

5 GAGAGCGGCCGCTCGATACACAAGTATCAGAATCACC (SEQ ID NO: 350)

GAGAGCGGCCGCTTAAGAGGACGATGAGACACTCTCG (SEQ ID NO: 351)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 352 and encodes a 60 kD protein (583aa) expressing the segment 305-741 aa of PmpC. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 353.

10 PmpC(3) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGATCAATCTAACGAAAACACAGACG (SEQ ID NO: 354)

GAGAGCGGCCGCTTAGACCAAAGCTCCATCAGCAAC (SEQ ID NO: 355)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 356 and encodes a 70 kD protein (683aa) expressing the segment 714-1250 aa of

15 PmpC. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 357.

EXAMPE 11

IMMUNOGENICITY OF CT622

Chlamydia-specific T cells lines were generated from two patients with

20 Chlamydia infections and the lines were designated CT1 and CT13. The T cell lines were either generated against monocyte-derived dendritic cells infected *C. trachomatis* serovar E for 72 hours (CT1-ERB) or against killed serovar E elementary bodies (EB) (CT13-EEB). Once generated, the lines were tested against the recombinant Chlamydia-specific protein, CT622 in a proliferation assay. Proliferation assays were

25 performed by stimulating 2.5×10^4 T cells in the presence of 1×10^4 monocyte-derived dendritic cells with either recombinant CT antigens (2 μ g/ml) or Chlamydia EBs (1 μ g/ml). The assay was incubated for 4 days with a ^3H -thymidine pulse for the last 18 hours.

The cell line CT1-ERB demonstrated proliferative responses significantly above the media controls when stimulated with CT622, CT875, and CT EB. The cell line CT13-EEB demonstrated a proliferative response significantly above media controls when stimulated with CT622, CT875, and CT EB (see Figure 12).

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EXAMPLE 12

CLONING AND EXPRESSION OF FULL LENGTH CHLAMYDIATRACHOMATIS GENES CT611, ORF3 AND OppA1

Recombinant protein expression of the full-length open reading frames was performed for clones containing genes CT611, ORF-3, and oppA1. The clones that contained the genes of interest were CtL2-8 (SEQ ID NO:285) which encoded 4 ORFs (CT474, CT473, CT060, and CT139), CtL2-10 (SEQ ID NO:284) which encoded the ORFs of CT610 and CT611, and clones 16CtL2-16 (SEQ ID NO:47), 16-D4-22 (SEQ ID NO:119) and 19-A5-54 (SEQ ID NO:84) which all contained sequences related to ORF-3. Sequences within CtL2-10 (Ct-610) and CtL2-16 (ORF-3) were also independently identified by the T-cell expression cloning approach. The clone CtL2-8 was further investigated as this clone had stimulated the proliferative responses and IFN-gamma production by two T cell lines generated against serovar E.

15

Cloning and expression of clone sequences:

CtL2-10 was found to encode two open reading frames (ORFs), CT610 and CT611, and these were found organized adjacent to each other within the genomic clone. The full length ORF of CT610 (containing a PQQ synthesis domain) was previously expressed and demonstrated to stimulate the proliferative responses of T cell lines generated against Chlamydia. To determine whether the second ORF, CT611, was also recognized by T cells, the full-length sequence of CT611 was PCR amplified and engineered for protein expression. The nucleotide sequence is disclosed in SEQ ID NO:361 with the corresponding amino acid sequence disclosed in SEQ ID NO:365.

20

25

The second serological clone, CtL2-8, was found to contain 4 ORFs (CT474, CT473, CT060, and CT139). Overlapping peptides to the three smallest predicted ORFs (CT474, CT473, and CT060) did not stimulate the proliferative responses of T

30

cell lines. This suggested that the immunostimulatory antigen resides in the fourth ORF, CT139. The ORF of CT139 is approximately 450 nucleotides. The full-length nucleotide sequence is disclosed in SEQ ID NO:359 and the full-length amino acid sequence is disclosed in SEQ ID NO:363. Amino acid sequence comparison from Genbank revealed that it is an oligo-peptide binding protein (oppA1) as well as belonging to the peptide ABC transporter family. This protein is 462 amino acids long with a predicted size of 48.3kDa and appears to contain 2 trans-membrane regions.

To express the full-length sequence of oppA1, oligonucleotides were designed which specifically amplified sequences starting from amino acid residue 22 (devoid of the first transmembrane domain), the nucleotide sequence for which is disclosed in SEQ ID NO:358 and, the amino acid sequence of which is disclosed in SEQ ID NO:362. This was shown to express the protein in *E. coli*.

The full-length cloning and recombinant protein expression of ORF-3 was also achieved. The nucleotide and amino acid sequences are disclosed in SEQ ID NOs:360 and 364, respectively.

EXAMPLE 13

RECOMBINANT CHLAMYDIAL ANTIGENS RECOGNIZED BY T CELL LINES

Patient T cell lines were generated from the following donors: CT1, CT2, CT3, CT4, CT5, CT6, CT7, CT8, CT9, CT10, CT11, CT12, CT13, CT14, CT15, and CT16, some of which were discussed above. A summary of their details is included in Table V.

Table V: <i>C. trachomatis</i> patients						
Patients	Gender	Age	Clinical Manifestation	Serovar	IgG titer	Multiple Infections
CT1	M	27	NGU	LCR	Negative	No
CT2	M	24	NGU	D	Negative	E
CT3	M	43	Asymptomatic	J	Ct 1:512	No

			Shed Eb Dx was HPV		Cp 1:1024 Cps 1:256	
CT4	F	25	Asymptomatic Shed Eb	J	Ct 1:1024	Y
CT5	F	27	BV	LCR	Ct 1:256 Cp 1:256	F/F
CT6	M	26	Perinial rash Discharge, dysuria	G	Cp 1:1024	N
CT7	F	29	BV Genital ulcer	E	Ct 1:512 Cp 1:1024	N
CT8	F	24	Not Known	LCR	Not tested	NA
CT9	M	24	asymptomatic	LCR	Ct 1:128 Cp 1:128	N
CT10	F	20	Mild itch vulvar	negative	negative	12/1/98
CT11	F	21	BV Abnormal pap smear	J	Ct 1:512	F/F3/E/E/ PID 6/96
CT12	M	20	asymptomatic	LCR	Cp 1:512	N
CT13	F	18	BV, gonorrhea, Ct vaginal discharge, dysuria	G	Ct 1:1024	N
CT14	M	24	NGU	LCR	Ct 1:256	N

					Cp 1:256	
CT15	F	21	Muco-purulent cervicitis Vaginal discharge	culture	Ct 1:256 Ct IgM 1:320 Cp 1:64	N
CT16	M	26	Asymptomatic/ contact	LCR	NA	N
CL8	M	38	No clinical history of disease	negative	negative	N

NGU=Non-Gonococcal Urethritis; BV=Bacterial Vaginosis; CT=Chlamydia trachomatis; Cp=Chlamydia pneumoniae; Eb=Chlamydia elementary bodies; HPV=human papilloma virus; Dx=diagnosis; PID=pelvic inflammatory disease;

5 LCR=Ligase chain reaction.

PBMC were collected from a second series of donors and T cell lines have been generated from a sub-set of these. A summary of the details for three such T cell lines is listed in the table below.

10

Table III: Normal Donors				
Donor	Gender	Age	CT IgG Titer	CP IgG Titer
CHH011	F	49	1:64	1:16
CHH037	F	22	0	0
CHH042	F	25	0	1:16

Donor CHH011 is a healthy 49 year old female donor sero-negative for *C. trachomatis*. PBMC produced higher quantities of IFN-gamma in response to *C. trachomatis* elementary bodies as compared to *C. pneumoniae* elementary bodies, indicating a *C. trachomatis*-specific response. Donor CHH037 is a 22 year old healthy

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- female donor sero-negative for *C. trachomatis*. PBMC produced higher quantities of IFN-gamma in response to *C. trachomatis* elementary bodies as compared to *C. pneumoniae* elementary bodies, indicating a *C. trachomatis*-specific response. CHH042 is a 25 year old healthy female donor with an IgG titer of 1:16 to *C. pneumoniae*.
- 5 PBMC produced higher quantities of IFN-gamma in response to *C. trachomatis* elementary bodies as compared to *C. pneumoniae* elementary bodies, indicating a *C. trachomatis*-specific response.

- Recombinant proteins for several *Chlamydia trachomatis* genes were generated as described above. Sequences for MOMP was derived from serovar F. The
- 10 genes CT1875, CT622, pmp-B-2, pmpA, and CT529 were derived from serovar E and sequences for the genes gro-EL, Swib, pmpD, pmpG, TSA, CT610, pmpC, pmpE, S13, lpdA, pmpI, and pmpH-C were derived from LII.

- Several of the patient and donor lines described above were tested against the recombinant Chlamydia proteins. Table IV summarizes the results of the T
- 15 cell responses to these recombinant Chlamydia proteins.

Table VII: Recombinant Chlamydia Antigens Recognized By T Cell Lines

Antigen	Sero-var	#of hits	C L8 L2	CT 10 E	CT1 E	CT3 E	CT4 L2	CT5 E	CT 11 E	CT 12 E	CT 13 E	CH H-011 E	CH H-037 E
gro-EL (CT110)	L2	10	-	+	+	+	+	+	+	+	+	+	+
MompF (CT681)	F	10	-	+	+	+	+	+	+	+	+	+	+
CT875	E	8	-	+	+	-	+	+	+	+	+	-	+
SWIB (CT460)	L2	8	+	+	-	+	-	+	-	+	+	+	+
pmpD (CT812)	L2	5	-	+	+	+	+	-	-	+	+	-	-

pmpG (CT871)	L2	6	-	+	+	-	+	+	nt	-	+	+	-
TSA (CT603)	L2	6	-	-	+	+	+	+	-	-	+	-	+
CT622	E	3	-	-	+	-	+	-	-	-	+	-	-
CT610	L2	3	-	+	-	+	-	-	-	+	-	-	-
pmpB-2 (CT413)	E	3	-	-	+	+	+	-	-	-	-	-	-
pmpC (CT414)	L2	4	-	-	-	+	-	+	-	+	-	-	+
pmpE (CT869)	L2	3	-	+	+	-	-	-	-	-	+	-	-
S13 (CT509)	L2	2	+	-	-	-	+	-	-	-	-	-	-
lpdA (CT557)	L2	3	-	-	+	+	-	-	-	-	-	+	-
pmpI (CT874)	L2	2	-	-	+	-	-	-	-	-	-	+	-
pmpH-C (CT872)	L2	1	-	-	-	-	-	-	-	+	-	-	-
pmpA (CT412)	E	0	-	-	-	-	-	-	-	-	-	-	-
CT529	E	0	-	-	-	-	-	-	-	-	-	-	-

Although the present invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, changes and modifications can be carried out without departing from the scope of the invention

5 which is intended to be limited only by the scope of the appended claims.

Claims

What is Claimed:

1. A composition for eliciting an immune response comprising a Chlamydia Cap1 protein or an immunogenic fragment thereof and an immunostimulant.
2. The composition of claim 1, wherein the immunogenic fragment comprises at least a CTL epitope consisting essentially of amino acids 139-147 of a Cap1 protein.
3. The composition of claim 1, wherein the Cap 1 protein comprises an amino acid sequence set forth in SEQ ID NO: 121 or a sequence having at least about 90% identity to the sequence set forth in SEQ ID NO: 121.
4. The composition of claim 1, wherein the Cap1 protein or immunogenic fragment thereof comprises a sequence set forth in any one of SEQ ID NOs: 121, 123, 125, 127, 129, 131, 133, 135, 137 and 139.
5. The composition of claim 1, wherein the immunogenic fragment comprises amino acids 107-176 of a Cap1 protein.
6. The composition of claim 5, wherein the immunogenic fragment comprises amino acids 107-176 of a Cap1 protein having an amino acid sequence set forth in any one of SEQ ID NOs: 121, 123, 125, 127, 129, 131, 133, 135, 137 and 139.
7. The composition of claim 1, wherein the immunogenic fragment is

immunologically reactive with a CD8+ T-cell of a Chlamydia-infected animal.

8. A method for stimulating a Chlamydia-specific T-cell response in an animal comprising administering to an animal an effective amount of a composition according to claim 1.

9. A method for inhibiting the development of a Chlamydia infection in an animal, comprising administering to an animal an effective amount of a composition according to claim 1.

10. A composition for eliciting an immune response comprising an isolated polynucleotide that encodes a Chlamydia Cap1 protein or an immunogenic fragment thereof and an immunostimulant.

11. The composition of claim 10, wherein the immunogenic fragment comprises at least the CTL epitope sequence consisting essentially of amino acids 139-147 of a Cap1 protein.

12. The composition of claim 10, wherein the Cap 1 protein comprises an amino acid sequence set forth in SEQ ID NO: 121 or a sequence having at least about 90% identity to the sequence set forth in SEQ ID NO: 121.

13. The composition of claim 10, wherein the Cap1 protein or immunogenic fragment thereof comprises a sequence set forth in any one of SEQ ID NOs: 121, 123, 125, 127, 129, 131, 133, 135, 137 and 139.

14. The composition of claim 10, wherein the immunogenic fragment comprises amino acids 107-176 of a Cap1 protein.

15. The composition of claim 14, wherein the immunogenic fragment comprises amino acids 107-176 of a Cap1 protein having an amino acid sequence set forth in any one of SEQ ID NOs: 121, 123, 125, 127, 129, 131, 133, 135, 137 and 139.

16. The composition of claim 10, wherein the immunogenic fragment is immunologically reactive with a CD8+ T-cell of a Chlamydia-infected animal.

17. The composition of claim 10, wherein the isolated polynucleotide is operably linked within a viral delivery vector.

18. The composition of claim 17, wherein the viral delivery vector is a vaccinia virus delivery vector.

19. A method for stimulating a Chlamydia-specific T-cell response in an animal comprising administering to said animal an effective amount of a composition according to claim 10.

20. A method for inhibiting the development of a Chlamydia infection in an animal, comprising administering to an animal said effective amount of a composition according to claim 10.

21. A method for inhibiting the development of a Chlamydia infection in an animal, comprising administering to said animal an effective amount of a composition according to claim 18.

22. An isolated polynucleotide comprising a sequence selected from the group consisting of:

- (a) sequences provided in SEQ ID NO:358-361;
- (b) complements of the sequences provided in SEQ ID NO:358-361;
- (c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NO:358-361;
- (d) sequences that hybridize to a sequence provided in SEQ ID NO:358-361, under highly stringent conditions;
- (e) sequences having at least 95% identity to a sequence of SEQ ID NO:358-361;
- (f) sequences having at least 99% identity to a sequence of SEQ ID NO:358-361; and
- (g) degenerate variants of a sequence provided in SEQ ID NO:358-361.

23. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

- (a) sequences encoded by a polynucleotide of claim 22;
- (b) sequences having at least 95% identity to a sequence encoded by a polynucleotide of claim 22; and
- (c) sequences having at least 99% identity to a sequence encoded by a polynucleotide of claim 22.

24. An isolated polypeptide comprising at least an immunogenic fragment of a polypeptide sequence selected from the group consisting of:

- (a) a polypeptide sequence set forth in SEQ ID NO:362-365,
- (b) a polypeptide sequence having at least 95% identity with a sequence set forth in SEQ ID NO:362-365, and

(c) a polypeptide sequence having at least 99% identity with a sequence set forth in SEQ ID NO:362-365.

25. An expression vector comprising a polynucleotide of claim 22 operably linked to an expression control sequence.

26. A host cell transformed or transfected with an expression vector according to claim 25.

27. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a polypeptide of any one of claims 23 and 24.

28. A method for detecting the presence of Chlamydia in a patient, comprising the steps of:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with a binding agent that binds to a polypeptide of any one of claims 23 and 24;
- (c) detecting in the sample an amount of polypeptide that binds to the binding agent; and
- (d) comparing the amount of polypeptide to a predetermined cut-off value and therefrom determining the presence of Chlamydia in the patient.

29. A fusion protein comprising at least one polypeptide according to claim 23 or claim 24.

30. An oligonucleotide that hybridizes to a sequence recited in SEQ ID NO: 358-361 under highly stringent conditions.

31. A method for stimulating and/or expanding T cells specific for a Chlamydia protein, comprising contacting T cells with at least one component selected from the group consisting of:

- (a) a polypeptide according to claim 23 or claim 24;
- (b) a polynucleotide according to claim 22; and

(c) an antigen-presenting cell that expresses a polynucleotide according to claim 22,

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

32. An isolated T cell population, comprising T cells prepared according to the method of claim 31.

33. A composition comprising a first component selected from the group consisting of physiologically acceptable carriers and immunostimulants, and a second component selected from the group consisting of:

- (a) a polypeptide according to claim 23 or claim 24;
- (b) a polynucleotide according to claim 27;
- (c) an antibody according to claim 27;
- (d) a fusion protein according to claim 29;
- (e) a T cell population according to claim 32; and
- (f) an antigen presenting cell that expresses a polypeptide according to claim 23 or claim 24.

34. A method for stimulating an immune response in a patient, comprising administering to the patient a composition selected from the group consisting of;

- (a) a composition of claim 33;
- (b) a polynucleotide sequence of any one of SEQ ID NO:407-430, 525-559, and 582-598; and
- (c) a polypeptide sequence of any one of SEQ ID NO:431-454 and 560-581.

35. A method for the treatment of Chlamydia infection in a patient, comprising administering to the patient a composition selected from the group consisting of;

- (a) a composition of claim 33;

- (b) a polynucleotide sequence of any one of SEQ ID NO: 407-430, 525-559, and 582-598; and
- (d) a polypeptide sequence of any one of SEQ ID NO: 431-454 and 560-581.

36. A method for determining the presence of Chlamydia in a patient, comprising the steps of:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with an oligonucleotide according to claim 30;
- (c) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and
- (d) comparing the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefore determining the presence of the cancer in the patient.

37. A diagnostic kit comprising at least one oligonucleotide according to claim 30.

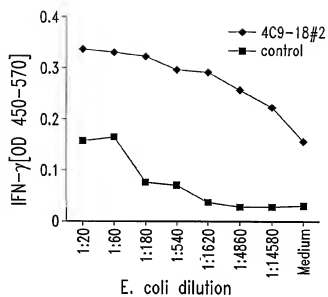
38. A diagnostic kit comprising at least one antibody according to claim 27 and a detection reagent, wherein the detection reagent comprises a reporter group.

39. A method for the treatment of Chlamydia in a patient, comprising the steps of:

- (a) incubating CD4+ and/or CD8+ T cells isolated from a patient with at least one component selected from the group consisting of:
 - (i) a polypeptide according to any one of claims 23 and 24;
 - (ii) a polypeptide sequence of any one of SEQ ID NO: 431-454 and 560-581;
 - (iii) a polynucleotide according to claim 22;
 - (iv) a polynucleotide sequence of any one of SEQ ID NO: 407-430, 525-559 and 582-598;

- (v) an antigen presenting cell that expresses a polypeptide sequence set forth in any one of claims 23 and 24;
- (vi) an antigen presenting cell that expresses a polypeptide sequence of any one of SEQ ID NO: 431-454 and 560-581, such that the T cells proliferate; and
 - (b) administering to the patient an effective amount of the proliferated T cells.

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*Fig. 1*

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Retroviral vector
pBIB-KS



Kozak-Start

GA TCT	GCC GCC ACC	ATG	GAA TTC GAT ATC GGA TCC CTG CAG
A	CGG CGG TGG	TAC	CTT AAG CTA TAG CCT AGG GAC GTC

(BglII) EcoRI BamHI PstI

ReadingFrame 1

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TTC GAA	CTC GAG CTC	GCG CCG GCG	ATT	AAT GGA CTC AGC T

HindIII XhoI NotI Stop Stop Stop (SalI) KS1+

Kozak-Start

GA TCT	GCC GCC ACC	ATG	GGA ATT CGA TAT CGG ATC CCT GCA G
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(BglII) EcoRI BamHI PstI

ReadingFrame 1

AA GCT TGA	GCT CGA GCG CGG CGG	CTA ATT AGC	TGA G
TT CGA ACT	CGA GCT CGC GCC GGC	GAT TAA TGG	ACT CAG CT

HindIII XhoI NotI Stop Stop Stop (SalI) KS2+

Kozak-Start

GA TCT	GCC GCC ACC	ATG	GGG AAT TCG ATA TCG GAT CCC TGC AG
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(BglII) EcoRI BamHI PstI

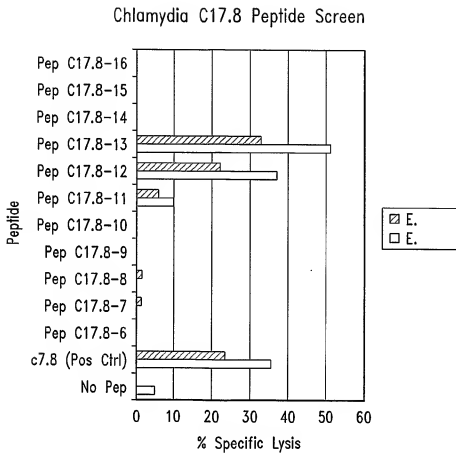
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Fig. 2

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*Fig. 3*

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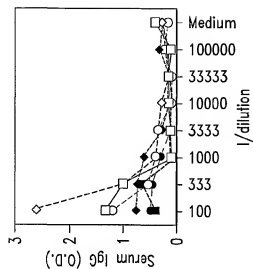


Fig. 4C

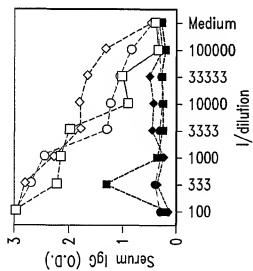


Fig. 4B

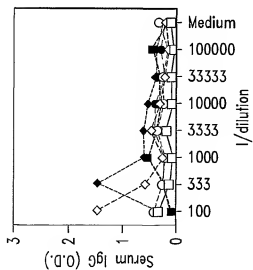


Fig. 4A

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 Mouse B/IgG1
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 Mouse B/IgG2a
 Mouse C/IgG2a

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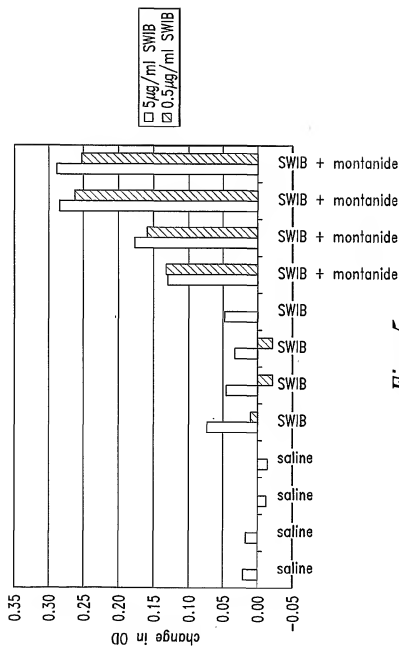


Fig. 5

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CP SWIB Nde (5' primer)

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CP SWIB EcoRI (3' primer)

5' CTCGAGGAATTCTTATTTACAATATGTTTGA

CP S13 Nde (5' primer)

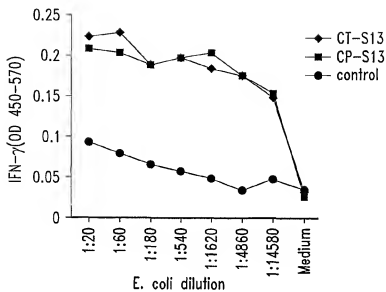
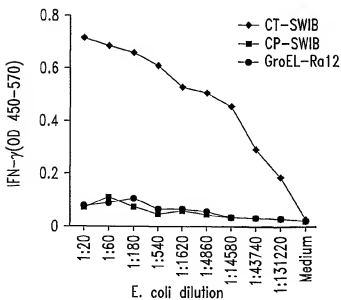
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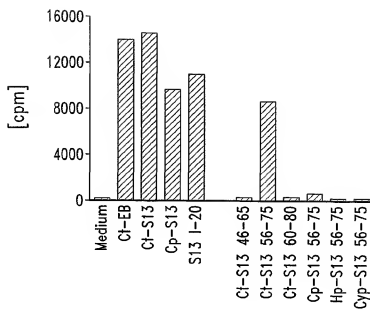
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Fig. 6

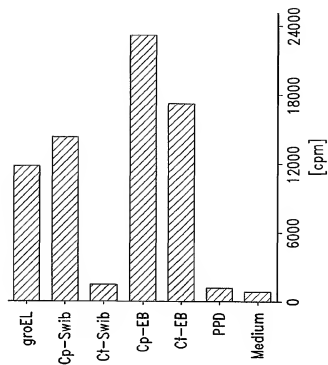
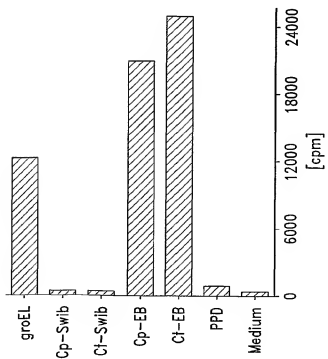
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*Fig. 7A**Fig. 7B*

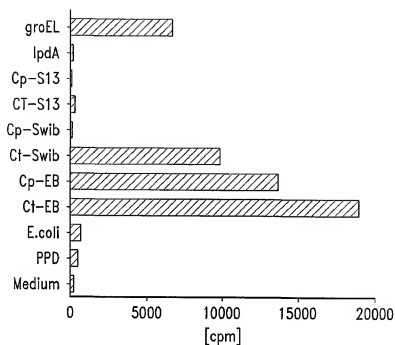
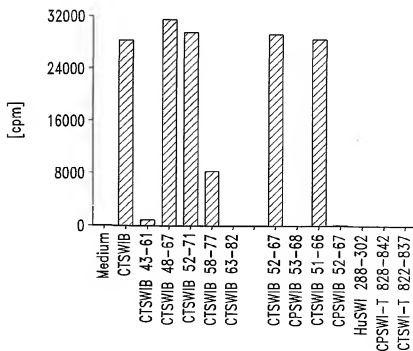
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*Fig. 8*

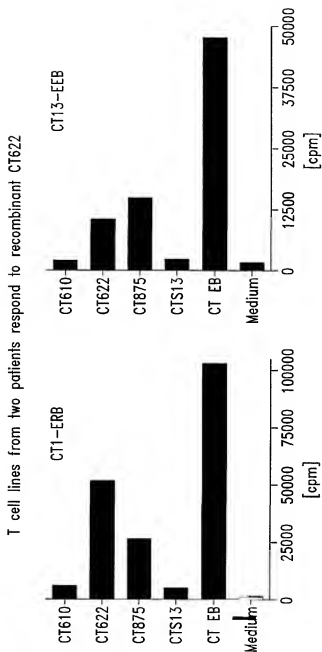
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*Fig. 9B**Fig. 9A*

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*Fig. 10**Fig. 11*

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*Fig. 12*

SEQUENCE LISTING

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 Fling, Steven P.
 Skeiky, Yasir A. W.
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gagatcgcggt tcggtttaat atcaatggga atgtcgaaag atacgattac gtctctgatt 300
ctataggagcg ccggtttgaat acagaaaaata ttggcttgga taaagctggt gttatttgtg 360
atgaacgcgg agtcatccct accgatggcca caatgcccac aaacgtacct aacatttatg 420
ctattggaga tatcacagga aaatggcaac ttgcccatgt agcttctcat caaggaatca 480
ttgcagcagca gaatataggt gcccataaag aggaaatcga ttactctgct gtcccttctg 540
tgatctttac ctcccttgaa gtccgttcag taggcctctc cccaacagca gctcaacaac 600
atctctctct tcgcttacct ttctgaaaaa atttgataca gaagaagaat tctctgcaca 660
cttgcgaggga ggaggcgctc tggaaagacca gttgaattta gctaagtttt ctgagcggtt 720
tgattctcttg cgagaattat ccgctaagct tggttacgat agcgatggag agactgggga 780
tttcttcaac gaggagtacg acgacgaaga agagaaaac aaaccgaaga aaactacgaa 840
actgtgagct aagaagagcg gttcataagc cttgcttita aggtttggta gtttacttc 900
tctaaaaatcc aaatgggtgc tgtgccaaaa agtagtttgc gtttccgcat agggcgtaaa 960

tgcgtgcgat	gaaagattgc	ttcgagagcg	gcacgcgcgt	ggagatcccg	gatactttct	1020
ttcagatacg	aataagcata	gctgttccca	gaataaaaac	ggcgacgcgt	aggaacaaca	1080
agatttagat	agagcttggt	tagcaggttaa	actgggttat	atgttgctgg	gcgtgttagt	1140
tctagaatac	ccaagtgtcc	ttccagttgt	aatactcgat	acacttccct	aagagcctct	1200
aatggatagg	ataagttccg	taatccatag	gccatagaag	ctaaacgaaa	cgtatt	1256

<210> 22
 <211> 601
 <212> DNA
 <213> *Chlamydia trachomatis*

<400> 22						
ctcgtgccgg	cacgagcaaa	gaaatccctc	aaaaaatggc	cattattggc	ggtggtgtga	60
tccgttgcca	attcgtttcc	ttattccata	cgttaggtcc	cgaaagttct	gtgatcgaa	120
caagctctca	aatccttgct	ttgaataatc	cagatatctc	aaaaaccatg	ttcgataaat	180
tcacccgaca	aggactccgt	ttcgtactag	aagcctctgt	atcaaatatt	gaggatata	240
gagatccggt	tcggtttaa	atcaatggga	atgtcgaa	atcagattac	gttctcgtat	300
ctataggcgc	ccgtttgaat	acagaaaata	ttgcttgga	taaagctggg	gttattttgt	360
atgaacgcgg	gtcatccct	acogatgcca	caatgcgcac	aaacgtacct	aacatttatg	420
ctattggaga	tatcacagga	aaatggcaac	ttgccactgt	agcttctcat	caaggaaatc	480
ttgcagcgcg	gaatataggt	ggccataaag	aggaaatcga	ttactctgct	gtccctctct	540
tgatctttac	cttccctgaa	gtcgcttcag	taggcctctc	cccaacagca	gtcacaacac	600
a						601

<210> 23
 <211> 270
 <212> DNA
 <213> *Chlamydia trachomatis*

<400> 23						
acatctcctt	cttcgcttac	ttttctgaa	aaatttgata	cagaagaaga	attctcgcga	60
cactctgcag	gaggagggcg	tctggaagac	cagttgaatt	tagctaagtt	ttctgagcgt	120
tttgattctt	tcgcgagaatt	atccgcgaag	cttggttacg	atagcgatgg	agagactggg	180
gatttcttca	cgaggagga	cgacgacgaa	gaagaggaaa	tcaaacccgaa	gaaaactacg	240
aaacgtggac	gtaagaagag	ccgttccata				270

<210> 24
 <211> 363
 <212> DNA
 <213> *Chlamydia trachomatis*

<400> 24						
ttacttctct	aaaatccaaa	tggttgctgt	gccccaaagt	agtttgctgt	tcoggatagg	60
gcgttaatgc	gctgcgatgaa	agattgcttc	gagagcggca	tcgcgtggga	gatcccgat	120
actttctctc	agatcacgaat	aagcatagct	gttcccgaaa	taaaaacggc	cgaagctagg	180
acacaaacga	tttagtagat	gcttggttag	caggtaaaat	gggttatatg	ttgctggggc	240
tggttagttc	agaataccaca	agtgctctcc	aggttgtaat	actcgatata	cttccctaa	300
agcctcta	ggaataggata	agttccgtaa	tcctagggcc	atagaagcta	aacgaaacgt	360
att						363

<210> 25
 <211> 696
 <212> DNA
 <213> *Chlamydia trachomatis*

<400> 25						
gctcgtgcgc	gcacgagcaa	agaaaatccct	caaaaaatgg	ccattattgg	cgggtggtgtg	60
atcggttggtg	aattcgtctc	cttattccat	acgttaggct	ccgaagtctc	tgtgatcgaa	120
gcaagctctc	aaatccttgc	tttgaataat	ccagatatct	caaaaaccat	gttcgatata	180
ttcacccgac	aaggactccg	tttcgtaata	gaagcctctg	tatcaaatat	tgaggatata	240
ggagatcgcg	ttcgtttaac	tatcaatggg	aatgtcgaag	aatacgatta	cgttctcgtg	300

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tctataggac gcgctttgaa tacagaaaat attggcttgg ataaagctgg tgttatttgg 360
gatgaacggc gactcatccc tacogatgcc acaatgcgca caaacgtacc taacatttat 420
gctattggag atatcacagg aaaatggcaa cttgcccatg tagcttctca tcaaggaatc 480
attgcagcac ggaatatagg tggccataaa gaggaatcgc attactctgc tgtcccttct 540
gtgatcttta ccttccttga agtcgcttca gtaggcctct cccaacagc agctcaacaa 600
catctccttc ttcgcttact ttttctgaaa aatttgatac agaagaagaa ttccctgcac 660
acttgcgagg aggaggcgct ctggaagacc agttga 696

```

<210> 26
 <211> 231
 <212> PRT
 <213> Chlamydia trachomatis

```

<400> 26
Ala Arg Ala Gly Thr Ser Lys Glu Ile Pro Gln Lys Met Ala Ile Ile
1      5      10      15
Gly Gly Gly Val Ile Gly Cys Glu Phe Ala Ser Leu Phe His Thr Leu
20      25      30
Gly Ser Glu Val Ser Val Ile Glu Ala Ser Ser Gln Ile Leu Ala Leu
35      40      45
Asn Asn Pro Asp Ile Ser Lys Thr Met Phe Asp Lys Phe Thr Arg Gln
50      55      60
Gly Leu Arg Phe Val Leu Glu Ala Ser Val Ser Asn Ile Glu Asp Ile
65      70      75      80
Gly Asp Arg Val Arg Leu Thr Ile Asn Gly Asn Val Glu Glu Tyr Asp
85      90      95
Tyr Val Leu Val Ser Ile Gly Arg Arg Leu Asn Thr Glu Asn Ile Gly
100      105      110
Leu Asp Lys Ala Gly Val Ile Cys Asp Glu Arg Gly Val Ile Pro Thr
115      120      125
Asp Ala Thr Met Arg Thr Asn Val Pro Asn Ile Tyr Ala Ile Gly Asp
130      135      140
Ile Thr Gly Lys Trp Gln Leu Ala His Val Ala Ser His Gln Gly Ile
145      150      155      160
Ile Ala Ala Arg Asn Ile Gly Gly His Lys Glu Glu Ile Asp Tyr Ser
165      170      175
Ala Val Pro Ser Val Ile Phe Thr Phe Pro Glu Val Ala Ser Val Gly
180      185      190
Leu Ser Pro Thr Ala Ala Gln Gln His Leu Leu Leu Arg Leu Leu Phe
195      200      205
Leu Lys Asn Leu Ile Gln Lys Lys Asn Ser Ser His Thr Cys Glu Glu
210      215      220
Glu Gly Val Trp Lys Thr Ser
225      230

```

<210> 27
 <211> 264
 <212> DNA
 <213> Chlamydia pneumoniae

```

<400> 27
atgagtcaaa aaaataaaaa ctctgctttt atgcatcccg tgaatatttc cacagattta 60
gcagttatag ttggcaaggg acctatgccc agaaccgaaa ttgtaaaagaa agtttgggaa 120
tacattaaaa aacacaactg tcaggatcaa aaaaaataaac gtaatatcct tcccgatgcg 180
aatcttgcca aagtcttttg ctctagtgat cctatcgaca tgttccaaat gaccaaaagcc 240
ctttcaaac atattgtaaa ataa 264

```

<210> 28
 <211> 87
 <212> PRT
 <213> Chlamydia pneumoniae

<400> 28
 Met Ser Gln Lys Asn Lys Ser Ala Phe Met His Pro Val Asn Ile
 1 5 10 15
 Ser Thr Asp Leu Ala Val Ile Val Gly Lys Gly Pro Met Pro Arg Thr
 20 25 30
 Glu Ile Val Lys Lys Val Trp Glu Tyr Ile Lys Lys His Asn Cys Gln
 35 40 45
 Asp Gln Lys Asn Lys Arg Asn Ile Leu Pro Asp Ala Asn Leu Ala Lys
 50 55 60
 Val Phe Gly Ser Ser Asp Pro Ile Asp Met Phe Gln Met Thr Lys Ala
 65 70 75 80
 Leu Ser Lys His Ile Val Lys
 85

<210> 29
 <211> 369
 <212> DNA
 <213> Chlamydia pneumoniae

<400> 29
 atgccacgca tcattggaat tgatattcct gcaagaaaa agttaaaaaat aagctcgaca 60
 tatatttatg gaataggatc agctcgttct gatgaaatca ttaaaaaagtt gaagtttagat 120
 ccctgaggcaa gagcctctga attaaactgaa gaagaagtag gacgactgaa ctctctgcta 180
 caatcagaat ataccctaga aggggatttg cgacgtcggt ttcaatcgga tatcaaaaga 240
 ttgatcgcca tcattcttta tcgaggtcag agacatagac tttctttacc agtaagagga 300
 caacgtacaa aaactaattc tcgtactcga aaaggtaaaa gaaaaacagt cgcaggtaag 360
 aagaataaa 369

<210> 30
 <211> 122
 <212> PRT
 <213> Chlamydia pneumoniae

<400> 30
 Met Pro Arg Ile Ile Gly Ile Asp Ile Pro Ala Lys Lys Lys Leu Lys
 1 5 10 15
 Ile Ser Leu Thr Tyr Ile Tyr Gly Ile Gly Ser Ala Arg Ser Asp Glu
 20 25 30
 Ile Ile Lys Lys Leu Lys Leu Asp Pro Glu Ala Arg Ala Ser Glu Leu
 35 40 45
 Thr Glu Glu Glu Val Gly Arg Leu Asn Ser Leu Leu Gln Ser Glu Tyr
 50 55 60
 Thr Val Glu Gly Asp Leu Arg Arg Arg Val Gln Ser Asp Ile Lys Arg
 65 70 75 80
 Leu Ile Ala Ile His Ser Tyr Arg Gly Gln Arg His Arg Leu Ser Leu
 85 90 95
 Pro Val Arg Gly Gln Arg Thr Lys Thr Asn Ser Arg Thr Arg Lys Gly
 100 105 110
 Lys Arg Lys Thr Val Ala Gly Lys Lys Lys
 115 120

<210> 31
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in the lab

<400> 31

Cys Ser Phe Ile Gly Gly Ile Thr Tyr Leu
1 5 10

<210> 32
<211> 53
<212> PRT
<213> Chlamydia trachomatis

<400> 32
Leu Cys Val Ser His Lys Arg Arg Ala Ala Ala Val Cys Ser Phe
1 5 10 15
Ile Gly Gly Ile Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile
20 25 30
Leu Phe Val Asn Lys Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Thr
35 40 45
Lys Ala Asn Met Gly
50

<210> 33
<211> 161
<212> DNA
<213> Chlamydia trachomatis

<400> 33
atctttgtgt gtctcataag cgcagagcgg ctgctggctgt ctgtagcatc atcggaggaa 60
ttacctacct cgcgacattc ggagctatcc gtccgattct gttgtcaac aaaatgctgg 120
caaaaccggt tctttcttcc caaactaaag caaatatggg a 161

<210> 34
<211> 53
<212> PRT
<213> Chlamydia trachomatis

<400> 34
Leu Cys Val Ser His Lys Arg Arg Ala Ala Ala Val Cys Ser Ile
1 5 10 15
Ile Gly Gly Ile Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile
20 25 30
Leu Phe Val Asn Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr
35 40 45
Lys Ala Asn Met Gly
50

<210> 35
<211> 55
<212> DNA
<213> Chlamydia pneumoniae

<400> 35
gatatacata tgcataacca tcaccatcac atgagtcasa aaaaataaaa actct 55

<210> 36
<211> 33
<212> DNA
<213> Chlamydia pneumoniae

<400> 36
ctcgaggaaat tcttatttta caatatgttt gga 33

<210> 37
<211> 53

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<212> DNA
<213> Chlamydia pneumoniae

<400> 37
gatatacata tgcataacca tcaccatcac atgccacgca tcattggaat gat      53

<210> 38
<211> 30
<212> DNA
<213> Chlamydia pneumoniae

<400> 38
ctcagggaat tcttatttct tcttacctgc      30

<210> 39
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 39
Lys Arg Asn Ile Asn Pro Asp Asp Lys Leu Ala Lys Val Phe Gly Thr
1           5           10           15

<210> 40
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> made in the lab

<400> 40
Lys Arg Asn Ile Leu Pro Asp Ala Asn Leu Ala Lys Val Phe Gly Ser
1           5           10           15

<210> 41
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> made in the lab

<400> 41
Lys Glu Tyr Ile Asn Gly Asp Lys Tyr Phe Gln Gln Ile Phe Asp
1           5           10           15

<210> 42
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> made in the lab

<400> 42
Lys Lys Ile Ile Ile Pro Asp Ser Lys Leu Gln Gly Val Ile Gly Ala

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1 5 10 15

<210> 43
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> made in the lab

<400> 43
 Lys Lys Leu Leu Val Pro Asp Asn Asn Leu Ala Thr Ile Ile Gly
 1 5 10 15

<210> 44
 <211> 509
 <212> DNA
 <213> Chlamydia

<400> 44
 ggagctcgaa ttcggcagca gagtgcctat tgttttgcag gctttgtctg atgatagcga 60
 taccgtacgt gagattgctg tacaagtagc tgttatgtat ggttctagtt gcttactgcg 120
 cgccgtgggc gatttagcga aaaatgattc ttctattcaa gtaacgcatca ctgcttatcg 180
 tgctgcagcc gtgttgagaga tacaagatct tgtgcctcat ttaacgagttg tagtccaaaa 240
 tacacaatta gatggaacgg aaagaagaga agcttggaga tctttatgtg ttcttactcg 300
 gcctcatagt ggtgtattaa ctggcataga tcaagcttta atgacctgtg agatgtttaa 360
 ggaatatcct gaaagagtga cggaaagaaca gattcgtaca ttattggctg cagataatcc 420
 agaagtgcag gtagctactt tacagatcat tctgagagga ggtagagtat tccgggtcatc 480
 ttctataatg gaatcggttc tcgtgcgcg 509

<210> 45
 <211> 481
 <212> DNA
 <213> Chlamydia

<220>
 <221> misc_feature
 <222> 23
 <223> n=A,T,C or G

<400> 45
 gatccgaatt cggcacgagg cantatttac tcccaacatt acggttccaa ataagcgata 60
 aggttctcta ataaggaagt taatgtaaga ggctttttta ttgcttttgc taaggttagta 120
 ttgcaaacgc acgcgattga atgatacgca agccatttcc atcatggaaa agaacccttg 180
 gacaaaaata caaaggaggt tcaactcctaa ccagaaaaag ggagagttag ttccatggg 240
 ttttccctat atacaccggt ttcacacaat taggagccgc gtctagtatt tggaatacaa 300
 attgtcccca agcgaatttt gttcctgttt cagggatttc tcttaattgt tctgtcagcc 360
 atccgcctat ggttaacgcaa ttagctgtag taggaagatc aactccaaac aggtcataga 420
 aatcagaaag ctcataggtg cctgcagcaa taacaacatt cttgtctgag tgagcgaatt 480
 g 481

<210> 46
 <211> 427
 <212> DNA
 <213> Chlamydia

<220>
 <221> misc_feature
 <222> 20
 <223> n=A,T,C or G

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<400> 46
gatccgaatt cggcacgagn tttttcctgt tttttcttag ttttttagtg tcccggagca 60
ataacacaga tcaaaagaagc gccattcagt ttaggctctg actcaacaaa acctatgtcc 120
tctaagccct gacacattct ttgaacaacc ttatgccctg gtccgggata agccaactct 180
cgcccccgaa acatacaaga aacctttact ttatttccct tctcaataaa ggctctagct 240
tgctttgctt tcgtaagaaa gtctgttatca tcatatttag gcttaagctt aacctcttgg 300
atacgacctt ggtgctgtgc tttcttacta tcttttctct ttttagttat gtctgaacga 360
tacttccctg agtccatgat ttgtcacaca ggaggtctct agtttgaagc aacctctgtc 420
cgaattcc

```

```

<210> 47
<211> 600
<212> DNA
<213> Chlamydia

```

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<220>
<221> misc_feature
<222> 522
<223> n=A,T,C or G

```

```

<400> 47
gatccgaatt cggcacgaga tgcttctatt acaattgggt tggatgcgga aaaagcttac 60
cagcttattc tagaaaagtt gggagatcaa attcttgggt gaattgctga tactatttgt 120
gatagtacag tccaagatat tttagacaaa atcacacaag acccttctct aggtttgttg 180
aaagctttta acaactttcc aatcactaat aaaattcaat gcaacgggtt attcaactcc 240
aggaacattg aaactttatt aggaggaact gaaataggaa aattcacagt cacaaccaaa 300
agctctggga gcatgttctt agtctcagca gatattatlg catcaagaat ggaagggcgc 360
gtttgttagt ctttggtacg agaaggtgat tctaagccct agcgatttag ttatggatag 420
tcactagggc ttccataatt atgtagtcta agaacagaaa ttattaatac aggattgact 480
ccgacaacgt attcattacg ttaggcgggt tttagaaagc gngtggtagt ggttaatgcc 540
ctttctaatt gcaatgatat tttaggaata acaaatcttc taatgtatct tttttggagg 600

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<210> 48
<211> 600
<212> DNA
<213> Chlamydia

```

```

<400> 48
ggagctcgaa ttgggcacga gctctatgaa tatccaattc tctaaaactg tcggataaaa 60
atgatgcagg aattaggctc acactatctt tttttgtttc gcaaatgatt gatttttaaa 120
cttttgatgt gtatactatg tctgttaagc cttttgtgtt acttctgaca ctgagcccca 180
atccagaaga taatttggat tgcgggtcta ggtcagcaag taacactttt ttccctaaaa 240
attgggcccc gttgcstccc acgttttaga aaagtgttgt ttttccagtl cctcccttaa 300
aagagcaaaa asctaaggtg tgcaaatcaa ctccaacgtt agagtaagtt atctattcag 360
ccttgaaaaa catgtctctt ctgacaagaa taagcataat caaagccttt tttagcttta 420
aactgttatc cctcaatttt tcaagaacag gagagctctg gaataatcct aaagagtttt 480
ctatttgttg aagcagtcct agaattagtg agacactttt atggttagag tctaaggagg 540
aatttaagaa agttaacttt tccctgttta ctgattttt taggtctaat tcggggaaat 600

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```

<210> 49
<211> 600
<212> DNA
<213> Chlamydia

```

```

<400> 49
gatccgaatt cggcacgaga tgcttctatt acaattgggt tggatgcgga aaaagcttac 60
cagcttattc tagaaaagtt gggagatcaa attcttgggt gaattgctga tactatttgt 120
gatagtacag tccaagatat tttagacaaa atcacacaag acccttctct aggtttgttg 180
aaagctttta acaactttcc aatcactaat aaaattcaat gcaacgggtt attcaactcc 240
aggaacattg aaactttatt aggaggaact gaaataggaa aattcacagt cacaaccaaa 300
agctctggga gcatgttctt agtctcagca gatattatlg catcaagaat ggaagggcgc 360

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gttggtcttag ctttggtacg agaaggtgat tctaagccct acgcgattag ttaaggatac 420
tcatcaggcg ttcttaattt atgtagtcta agaacccagaa ttattaatac aggtattgact 480
ccgacaacgt attcatatag tgtaggcggt ttagaagcgc gtgtggtatg gggttaatgcc 540
ctttctaatg gcaatgatat tttagggaata acaaatactt ctaatgtatc ttttttgagg 600

```

```

<210> 50
<211> 406
<212> DNA
<213> Chlamydia

```

```

<400> 50
gatcogaatt cggcagcaggt tcttagcttg ctaattacg taattaacca aactaaaggg 60
gctatcaaat agcttattca gtctttcatt agttaaacga tcttttctag ccatgactca 120
tctatgttct ttacagtata aaaatacttc ttaaaacttg atatgtctga atcaaatcat 180
cattaaaccac aacataatca aattcgctag cggcagcaat ttgcacagcg ctatgtctca 240
atctttcttt ctctctggaa tctttctctg aatcccgagc attcaaacgg cgctcaagtt 300
cttcttgaga gggagcttga ataaaaatgt gactgcgcgc atttgccttc tcagagccaa 360
agctccttgt acatcaatca cggctatgca gtctcgtgcc gaattc 406

```

```

<210> 51
<211> 602
<212> DNA
<213> Chlamydia

```

```

<400> 51
gatcogaatt cggcagcaga tattttagac aaaatcacaa cagacccttc tctaggtttg 60
ttgaaagctt ttaacaactt tccaatcact aataaaattc aatgcacggg gttattcact 120
cccaggaaac ttgaaacttt attaggagga actgaaatag gaaaattcac agtccacccc 180
aaaagctctg ggagcgtgtt cttagtctca gcagatatta ttgcacaaag aatggaagcg 240
ggcgttgttg tagcttttgt acgagaaggt gatttotaag cctacgcgat tagttatgga 300
tactatcag gcgttcttaa ttatgtagt ctaagaacca gaattattaa tacagagttg 360
acctcgacaa cgtattcatt acgtgtaggg ggttttagaa cgggtgttgt atgggttaat 420
gccttttcta atggcaatga tatttttaga ataacaataa ctctaatgt atcttttttg 480
gaggtaatat ctaacaacaa cgccttaaca attttttatt gatttttctt ataggtttta 540
tatttagaga aaaaagttcg aattacgggg ttgttatgc aaaataaact cgtgcgcgat 600
tc 602

```

```

<210> 52
<211> 145
<212> DNA
<213> Chlamydia

```

```

<400> 52
gatcogaatt cggcagcagc togtgccgat gtgttcaaca gcatccatag gatgggcagt 60
caaatatact ccaagttaatt cttttttctt ttccaacaac tctctaggag agcgttgatg 120
aacattttca gctcgtgcgc aattc 145

```

```

<210> 53
<211> 450
<212> DNA
<213> Chlamydia

```

```

<400> 53
gatcogaatt cggcagcagg taatcggcac cgcactgctg acactcatct cctcgagctc 60
gatcaaaccc acacttgagg caagtaccta caacataacg gtccgctaaa aacttccctt 120
cttcttcaga atacagctgt tcggtaacct gattctctac cagtccgcgt tctcgcaagt 180
ttcgatagaa atcttgacca atagcaggat gataagcggt cgtagtctcg gaaaagaaat 240
ctacagaaat ttccaatttc ttgaaggtat ctttatgaag cttatgatac atgtcgacat 300
attcttgata ccccatgcct gccaaactctg cattaaaggt aattgcgatt ccgtattcat 360
cagaaccaca aatatacaaa acctctttgc cttgtagtct ctgaaaacgc gcataaacat 420
ctgcaggcaa ataagccctg tgccgaattc 450

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<210> 54
 <211> 716
 <212> DNA
 <213> Chlamydia

<400> 54
 gatcgaaatt cggcagcagc ggcacgagtt ttctgatagc gatttacaat cctttattca 60
 acttttgccct agagaggcac actatactaa gaagtttctt ggggtgtgtg cacagtcctg 120
 tcgtcagggg attctctgct aggggttaggg gaaaaaaccc ttattactat gaccatgcgc 180
 atgtggaaatt acattccata gactttcgca tcattcccaa catttacaca gctctacacc 240
 tcttaagaag aggtgacgtg gattgggtgg ggcagccttg gccaccaagg attccttttg 300
 agcttcggac tacctctgct ctctacacc attaccctgt agatggcaca ttctggctta 360
 ttcttaattcc caaagatcct gtaacttctt ctctatctaa tcgtcagcga ttgattgctg 420
 ccatccaaaa ggaaaaactg gtgaagcaag ctttaggaac acaatatoga gtatogtga 480
 gctctccatc tcacagagga atcatagctc atcaagaagc ttctactcct ttctcctgga 540
 aaattacttt gatatactcc aataatatta cgcgtgttca cgcgttggcc gaggtatcca 600
 aaaaatgatc gacaaggagc acgctaaatt tgtacatacc ccaaaatcaa tcagccatct 660
 aggcaaatgg aatatcaagg taacacgtat acaactgggg atctcgtgcc gaaltc 716

<210> 55
 <211> 463
 <212> DNA
 <213> Chlamydia trachomatis

<400> 55
 tctcaaatcc ttgctttgaa taatccagat atttcaaaaa ccatgttcga taaattcacc 60
 cgacaagctc tccgtttcgt actagaagcc tctgtatcaa atattgagga tataggagat 120
 cgcgttcggc taactatcaa tgggaatgtc gaagaatacg attacgttct cgtatctata 180
 ggacgcgctt tgaatacaga aaattattgc ttggataaag ctggtgttat ttgtgatgaa 240
 cgcggagtcg tccctaccga tgccacaatg gcacacaaag tacctaacat ttatgtctatt 300
 ggagatatac caggaaaatg gcaacttgcc catgtagctt ctcatcaagg aatcattgca 360
 gcaaggtaata taggtggcca taaagaggaa atcgattact ctgctgtccc ttctgtgac 420
 ttactcttcc ctgaagtcgc ttacgtagggc cgtcccccaa cag 463

<210> 56
 <211> 829
 <212> DNA
 <213> Chlamydia trachomatis

<400> 56
 gtactatggg atcattagtt ggaagacagg ctcoggattt ttctggtaaa gccgttgttt 60
 gtggagaaga gaaagaaatt tctctagcag acttttctgtg taagtatgta gtgctctctt 120
 ttatctctaa agattttacc tatgtttgtc ctacagaatt acatgtcttt caagatagat 180
 tggtagattt tgaagagcat ggtgcagtcg tcttctgttg ctccgtgtgac gacattgaga 240
 cacattctcg ttggctcact gttagcgagag atgcaaggagg gatagaggga acagaataac 300
 ctctgttagc agaccctctt tttaaaatat cagaagcttt tgggtgtttg aatcctgaag 360
 gatcgtctcg tttaagagct actttcctta tggataaaaa tggggttatt cgtcatgcgg 420
 ttatcaatga tcttctctta gggcgttcca ttgacaggga attgcgtatt ttatagatcat 480
 tgaatctctt tgagaaccac ggaatgggtt gtccagctaa ctggcgttct ggagagcgtg 540
 gaatgggtgc ttctgaagag ggatataaag aataactcca gacgatggat taagcatctt 600
 tgaaagttaag aaagtgcgtac agatcttgat ctgaaaaag aagaagcctt tttaatttcc 660
 tgcagagagc cagcaggagct tcaataatgt tgaagtctcc gacaccaggc aatgctaagg 720
 cgacgatatt agttagtga gttctgagat taaggaaatg aaggccaaag aaatagcat 780
 caataaagaa gccttcttcc ttgactctaa agaattagat gtctgatcc 829

<210> 57
 <211> 1537
 <212> DNA
 <213> Chlamydia trachomatis

<400> 57

acatcaagaa	atagcggagt	cgcctttagt	gaaaaaagct	gaggagcaga	ttaatcaagc	60
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tggttgatcgt	gcttccgcag	gaagtgcggc	aggagcgttg	aaatcctcta	acaattcagg	180
aagaattcttc	ttgtttgcttg	atgatgtaga	caatgaaatg	gcagcgattg	caatgcaagg	240
ttttcgatct	atgatcgaaac	aatttaattg	aaacaatcct	gcaacagcta	aaggcgctaca	300
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aaactggaac	tctttatatt	ccgaaagcag	aagcggcggtg	cagtcagcta	ttagtcaaac	660
tgcaaatccc	gogctttcca	gaagcgtttc	tcgttctggc	atagaaagtc	aaggacgcag	720
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ttagtctcaa	aaagaagaaa	tataataaag	aaaaaactcc	taattcattt	aaaaagtgct	1260
cggcagactt	cgtggaaaat	gtctgtaaa	ctggagggga	atcagcagaa	agatgcaga	1320
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<210> 58

<211> 463

<212> DNA

<213> Chlamydia trachomatis

<400> 58

ttctcaaatcc	ttgctttgaa	taatccagat	atttcaaaaa	ccatgttoga	taaattcacc	60
cgacaaggac	tcogtttcgt	actagaagcc	tctgtatcaa	atattgagga	tataggagat	120
cgcgttcogt	taactatcaa	tgggaatgtc	gaagaatacg	attactgtct	cgtatctata	180
ggaagccgct	tgaattacaga	aaatattggc	ttggataaag	ctgggtttat	tttgtatgaa	240
cgccggagtca	tcctatccga	tgcacaaatg	cgcaacaaag	tccttaacat	ttaatgctatt	300
cgagatataca	caggaaaatg	gcaacttggc	catgtatgct	actcatcagg	aatcaattgca	360
gcacgggaata	taggtggcca	taaaagggaa	atcgattact	ctgctgtccc	ttctgtgtac	420
tttaacttcc	ctgaagtgcg	ttcagttagc	ctctccocaa	cag		463

<210> 59

<211> 552

<212> DNA

<213> Chlamydia trachomatis

<400> 59

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acggaaatttt	acacgtttct	gctaaagatg	ctgctagtgg	acgcgaacaa	aaatccgta	120
ttgaagcaag	ctctggatta	aaagaagatg	aatgatccgc	aatgatccgc	tgatcagagc	180
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gaatgatctt	tagagccgaa	aaagctgtga	aagattacca	cgacaaaatt	cctgcagaac	300
ttgttaaaga	aattgaaag	catattgaga	aagtacgcca	agcaatcaaa	gaagatgctt	360
ccacaacagc	tatcaaaagc	gcttctgatg	agttgagtac	tcgtatgcaa	aaatccggag	420
aagctatgca	ggctcaatcc	gcacccgcag	cagcatcttc	tgcagcgaat	gctcaaggag	480
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gaggaagcgc	ct					552

<210> 60

<211> 1180
 <212> DNA
 <213> Chlamydia trachomatis

<400> 60
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 acaacttttt catcttgtag agagttagtt tttagaacta agtcttctgc ttacaatgct 180
 cttgcataatt acgagctttt tataaaacct cccaacccaa ctctacaaaa agagtttcaa 240
 tcgatccctc ataaactccg atatatatttg gccgtatgaa aaggcgattt aaaaaacaa 300
 gtogatgtga tagggaaagt atgtggaatc tctgtccgaa ttccggcacga gccgcacgag 360
 gatgtagagt aatttagtta agagctgcat aattatgaca aagcatggaa aacgcattcg 420
 tggatccaa gagacttacg atttagctaa gtctattct ttgggtgaag cgatagatat 480
 tttaaaacag tgcctactg tgcgtttoga tcaaacggtt gatgtgtctg ttaaatagg 540
 gatcgatoca agaaagagtg atcagcaaat tctgtggtcg gtttctttac ctacggtac 600
 aggtaaagtt ttgcgaattt tagtttttgc tctgtggagt aaggctgcag aggtattga 660
 agcaggagcg gactttgttg gtacgcagca cttggtagaa aaaatcaag gtggatgggt 720
 tgacttcgat gttgcggttg ccactccga tatgatgaga gaggtcggaa agctaggaaa 780
 agttttaggt ccaagaaacc ttatgctac gctaaaagcc ggaactgtaa caacagatgt 840
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 gtgatgcaac gtccgagttg cgaagcttct ttctgatgt gcgcaaatca gcaaaaatgt 960
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 agttaatttc actatttctt cgaccattgg ccagggggtt accgtggata tccaggagtt 1080
 gattgcgtta taattctaac tttaaagagg aaaaatgaaa gaagagaaaa agttgctgct 1140
 tcgcgaggtt gaagaaaaga taaccgcttc tcggcacgag 1180

<210> 61
 <211> 1215
 <212> DNA
 <213> Chlamydia trachomatis

<400> 61
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 aaatggggag attgttgcta cgcaaggaaa agctttgaa acacacgcca agcgggatgc 180
 aaagatttt gttgttgga accctgtgaa taocaattgc tggatagcaa tgaatcatgc 240
 tccacagatta ttgagaaga actttcatgc gatgctacga ttggaccaga atcgatagca 300
 tagcatgtta tgcataagag cagaagtacc ttatcggct gtatcacaag ttgtggttgc 360
 gggaaaacac tccgcgaac aagtgctga tttacgcga gctctgatta atgaccgtcc 420
 tgcgcagag acgatagcgg atcgtgatg gttagaagat ttatagctgc ttgcgaatgc 480
 gagtctgtgt agtgacgtaa ttgaagcagc agggaaagct tcggcgactc ctgcagcagc 540
 agcttttaga gaggtctgct gatcaata taagcaaaaa gaaggactcg tgcgcaattc 600
 ggcaacagta tgcgaattgc aggcatttct agtgaatggt cgtatgctta taaactaagt 660
 ggatcagact tgaagcttca aaagtttgct acagattctt acatgcagca cctctgtaac 720
 aagaatatct actccctca actatttga tcccttaaac aagaaaagga ttacgcattt 780
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 aaaaattact tcaattatga aatgcattgt cggctattca cccgagatcc gtcctccagc 900
 gtttccatct ctggaacttt ccttggtatc atcgaaaaaa tagaccacct caaacaacta 960
 ggcgttcatg cagttgaact ccttccattt ttccgaattg atgaaacogt caatccattt 1020
 aaaaatcagg acttccocca cctgtgtaac ttatggggga tttgggggtt agattttttc 1080
 tgcccccctc gccgttatat ttatggggga gacccctgag ctccggcccg agagtttcaa 1140
 actctgttca aagcgttaca ccgtgcggga atcgaagcca tctcgatgt ogttttcatt 1200
 catcagagct ttgaa 1215

<210> 62
 <211> 688
 <212> DNA
 <213> Chlamydia trachomatis

<400> 62
 gtggatccaa aaagaatct aaaaagcat aaaaagattg ogttacttct tgcgatgctc 60

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ctaactcattt atcagcgtaa tctttgagaa gcattctcaat gagcgctttt tcttctctag 120
caatgcgcac atccgcttct tcatgtttctg tgaatbatgc atagtctcca ggattggaaa 180
atccaaagta ctacgtcaaat ocaogaattt tctctctago gatagctgga atttgactct 240
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cttctccat caagttatct aacaataact taocgcgctc taaatcatcg caacgactat 480
gaatcgagaa taaattatta ggaagagctt tgatatgtaa ataatagtct ttggcacagag 540
cotgtlaattg ctcttttagta agctccocct tcgaccattt cacataaaac gtgtgttcta 600
goattatgct attttgaata attaaatcta actgatctaa aaaattcata aacacctcca 660
tcatttcttt tcttgactcc acgttaacc

```

<210> 63

<211> 269

<212> DNA

<213> Chlamydia trachomatis

<400> 63

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gtgaagcaga gttcgtacgc agtgatccag cgacaacctc ggttaagctag 180
tttggaaaaa tgaccgctta ggacaaggcg aaaaagtaga aattactgta tgggtaaaac 240
ctcttaaga aggttgcgtc ttacagct

```

<210> 64

<211> 1339

<212> DNA

<213> Chlamydia trachomatis

<400> 64

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cttttattat ggcctctggg gatgatgtca acgatatoga cctgctatct cgaggagatt 60
ttaaaattgt tatcacagcg gctccagagg agatgcatgg attagcggac tttttggctc 120
ccccggcgaa ggaatcttgg attctctccg cctgggaagc tgggtgagctg cgttacaaac 180
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tgccgcctact tgcctcagct ccatttgaga aggtagtgga gccagctctt ggttagtaac 360
caccattctc tcaataaatc caatagcttt tctgcacgg ctagttaatg gccctgcoga 420
gataglatto actcggactc ccaaacgtgc gccggtctcc caagccagta tctttgtatc 480
aotttctaaa gacgtttttg ctgogttoa tctccgcoca taacctggaa cagcagcat 540
ggaagcaaga taagttagag agatgggtgct agctcctgca ttcataattg ggccaaaatg 600
agagagaagg ctgataaagg agtagctgga tgtacttaag cgggcaagat agcctttacg 660
agaggtatca agtaatggtt tagcaatttc cggactgttt gctaaagagt gaacagaagt 720
atcaatgtgt ccaaaatctt tttcacctg tctacaact tcggatcacg gtatccoga 780
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aaagagtttc ctgtgcaaat tcttatatg gttagatgaa tcaactgttt tcaagtgtat 1260
tatgtttatt taaaataaat ttgttttaac aactgtttaa tagttttaat ttttaaaagt 1320
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<210> 65

<211> 195

<212> PRT

<213> Chlamydia trachomatis

<400> 65

Met Gly Ser Leu Val Gly Arg Gln Ala Pro Asp Phe Ser Gly Lys Ala

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Val	Val	Cys	Gly	Glu	Glu	Lys	Glu	Ile	Ser	Leu	Ala	Asp	Phe	Arg	Gly
			20					25					30		
Lys	Tyr	Val	Val	Leu	Phe	Phe	Tyr	Pro	Lys	Asp	Phe	Thr	Tyr	Val	Cys
		35					40					45			
Pro	Thr	Glu	Leu	His	Ala	Phe	Gln	Asp	Arg	Leu	Val	Asp	Phe	Glu	Glu
		50				55					60				
His	Gly	Ala	Val	Val	Leu	Gly	Cys	Ser	Val	Asp	Asp	Ile	Glu	Thr	His
65				70					75					80	
Ser	Arg	Trp	Leu	Thr	Val	Ala	Arg	Asp	Ala	Gly	Gly	Ile	Glu	Gly	Thr
			85						90					95	
Glu	Tyr	Pro	Leu	Leu	Ala	Asp	Pro	Ser	Phe	Lys	Ile	Ser	Glu	Ala	Phe
		100					105						110		
Gly	Val	Leu	Asn	Pro	Glu	Gly	Ser	Leu	Ala	Leu	Arg	Ala	Thr	Phe	Leu
		115					120					125			
Ile	Asp	Lys	His	Gly	Val	Ile	Arg	His	Ala	Val	Ile	Asn	Asp	Leu	Pro
	130					135					140				
Leu	Gly	Arg	Ser	Ile	Asp	Glu	Glu	Leu	Arg	Ile	Leu	Asp	Ser	Leu	Ile
145				150					155						160
Phe	Phe	Glu	Asn	His	Gly	Met	Val	Cys	Pro	Ala	Asn	Trp	Arg	Ser	Gly
			165						170					175	
Glu	Arg	Gly	Met	Val	Pro	Ser	Glu	Glu	Gly	Leu	Lys	Glu	Tyr	Phe	Gln
		180					185						190		
Thr	Met	Asp													
		195													

<210> 66
 <211> 520
 <212> DNA
 <213> Chlamydia

<400> 66
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 tgatgtaaat tagcgcaatt agagggggat gaggttactt ggaaatataa ggagcgaagc 180
 gatgaaggag atgtatttgc tctggaagca aaggtttctg aagctaacag aacattgcgt 240
 cctccaacaa tcgcctgagg attctggctc atcagttgat gctttgctg aatgagagcg 300
 gacttaagtt tcccatcaga gggagctatt tgaattagat aatcaagagc tagatccttt 360
 attgtgggat cagaaaattt acttgtagac gcatacgaga ttctgtcaga agaagaatca 420
 tcatacgaac aatttttcaa tcttcgaaaa tcttctccag agacttcgga aagatctctt 480
 gtgaaacgat cttcaagagg agtatcgctt ttttctctct 520

<210> 67
 <211> 276
 <212> DNA
 <213> Chlamydia

<400> 67

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gatccgaatt cggcacgagg tattgaagga gaaggatctg actcgatcta tgaatcatg 60
atgcotact atgaagttat gaatatggat ctagaacac gaagatcttt tgcggtacag 120
caagggaact atcaggaccc aagagcttca gattatgacc tcccacgtgc tagcgactat 180
gaatttgcta gaagcccata tctactcca cctttgocct ctagatatca gctacagaat 240
atggaatgtag aagcagggtt ccgtgaggca gtttat 276

```

<210> 68
 <211> 248
 <212> DNA
 <213> Chlamydia

```

<400> 68
gatccgaatt cggcacgagg tgttcaagaa tatgtccttc aagaatgggt taaattgaaa 60
gatctacggt tagaagagtt gctagaaaaa cगतatcaga aattccgaac gataggtcta 120
tatgaaactt ctctgaaag cgattctgag gcataagaag catttagttt tattcggttt 180
ttctctttta tccatattag ggctaacgat aacgtctcaa gcagaaattt ttctcttag 240
tcttattg 248

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<210> 69
 <211> 715
 <212> DNA
 <213> Chlamydia

<220>
 <221> misc_feature
 <222> 34
 <223> n=A,T,C or G

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<400> 69
gatccgaatt cggcacgaga aggtagatcc gatntcagca aaagtgtcc taaaggaaga 60
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attttcatat agttttcgac ggaactcttt attaaactcc caaaaccgaa ttgttagtcgt 180
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ttgtacgaga aaattatgta atgcagggac ctctgggggg aagtatgcat ctgagtcttc 300
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tacggtgaaga gctgtcctcg gagagcctaa tttaaatcg atgattgagg ttggaatttg 480
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gaaaacatcc acggtaatat ccmaaatag taagaaggag atagggctgg aactctgaa 600
tggtagagcc ggtatagcgc tctagcatgt cacaggcgat tgtttcttcg ctgattttt 660
tatgtgatg ggtcataaat cacagatatt ataattggtta gagaatcttt ttttc 715

```

<210> 70
 <211> 323
 <212> DNA
 <213> Chlamydia

```

<400> 70
gatccgaatt cggcacgagc agaacgtaaa cagcacactt aaaccgtgta tgagggtttaa 60
cactgttttg caagcaaaaa accattcttc ttccacatc gtctctacca ataccttga 120
ggagcaatcc aactctctct cctgcacgac ctctctggag ttctttctg aactattcaa 180
cccaagtaac aatcgtttct tttagtatct taagaccgac caactgaact ttatcggaaa 240
ctttaacaat tccacgtcct atacgtccag ttactacagt tctcgtccg gagatagaga 300
acacgtcttc aatgggcatt aag 323

```

<210> 71
 <211> 715
 <212> DNA
 <213> Chlamydia

<400> 71

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gatccgaatt  cggcaacgagg  aaaaaaagat  tctctaacca  ttataatatc  tgtgatttat  60
gaccocatcaa  cataaaaaaa  tcagcgaaga  aacaatcgcc  tgtgacatgc  tagagcggct  120
ataccggctc  taccattcaa  gagttccagc  cctatctcct  tcttactaat  tttgggtatt  180
acgtggatgt  ttctcgctgaa  atctatcagg  tccctgtttc  tcgaggatcc  atgttttcgg  240
gcagcgcagt  cgccctcaaat  tcacacctca  atcatcgatt  ttaaaattagg  ctctccaggga  300
gcagctcatt  ccgtagatct  gtgttctttc  ctccccaatg  ctacacgacg  gatcatgttg  360
ggcatgtgcg  gaggtcttaag  atcccaactac  caaataggag  attattttgt  cctgtgtgct  420
agcatccgaa  aagatggaac  atcagatgca  tacttcccc  cagaggtccc  tgcattagct  480
aattttgtcg  tacaaaaaat  gatcaccaat  attctcgag  ccaaaaaacct  ccttaccat  540
ataggcatca  cccacacgac  taacattcgg  ttttgggagt  ttaataaaga  gttccgtcga  600
aaactatagt  aaaaataaagc  tcaaacctgtc  gagatggagt  gtgccacct  atttgcgtca  660
ggataccgaa  ggaatcttcc  tttaggagca  cttttgtcga  tatcgatct  acctt  715

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```

<210> 72
<211> 641
<212> DNA
<213> Chlamydia

```

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<220>
<221> misc feature
<222> 550,559,575,583,634,638
<223> n=A,T,C or G

```

```

<400> 72
gatccgaatt  cggcaacgaga  tctcctcgag  ctogatcaaa  ccacacattg  ggacaagtagc  60
ctacaacata  acggtccgct  aaaaacttcc  cttctctctc  agaatacagc  tgttcgggtca  120
cctgattctc  taccagtcgc  cgltctcgca  agtttcgata  gaaatcttgc  acaatagcag  180
gatgataaag  gttcgttagtt  ctggaaaaga  aatctacaga  aattcccaat  ttcttgaagg  240
tatctttatg  aagccttatga  tacatgtcga  cataattcttg  ataccoccat  cctgcccaact  300
ctgcattaa  ggttaattg  attccgtatt  catcagaacc  acaaatatac  aaaaaccttt  360
tgcccttagt  tctctgaaaa  cgcgcataaa  catctcgagg  caataaagca  ccggttaatat  420
gtocaaaat  caaagaccca  ttgctgaag  gcaacgcaga  agtaataaga  atacgggaag  480
attccaatat  tcccgctgc  tccagttgta  cagagaagga  tctttctctc  tggatgttcc  540
gaaaccttgn  tctctctgnc  tctctctctg  agcanacaaa  tgnctctctc  gacatctctt  600
tcagcgtatt  cggactgatg  ccctaaagat  ccnggngagt  t  641

```

```

<210> 73
<211> 584
<212> DNA
<213> Chlamydia

```

```

<220>
<221> misc feature
<222> 460,523,541,546
<223> n=A,T,C or G

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<400> 73
gaattcgcca  cgagacattt  ctagaatgga  accggcaaca  aacaaaaact  ttgtatctga  60
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gacttattac  ggaacgagta  aggcggagat  ttctagagtt  tctgaaaagc  gtagaocctg  180
catagccgtg  attgatgtac  aaggagcttt  ggctctgaa  aagcaaatgc  cgcgcgtcac  240
tatttttatt  caagctccct  ctcaagaaga  acttgagcgc  actttgaatg  ctccggtattc  300
agagaagat  ttccagaaga  aagaaagatt  agagcatagc  gctgtcgaaa  ttgtcgcgcg  360
tagcgaattt  gatttatgtt  tggttaatga  tgattttgatt  acagcatatc  aagttttaag  420
aagtattttt  atagctgaag  aacataggat  gagtcatggn  tagaaaaaat  cgttttaacta  480
atgaaaagct  gaataagcta  tttgatagcc  cctttagttt  gntaatatc  gtaattaagc  540
nagctnagaa  caaaattgct  agaggagatg  ttcgttcttc  taac

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```

<210> 74
<211> 465
<212> DNA

```

<213> Chlamydia

<400> 74

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taagaattta	ttttcgagtg	aaagagctag	gcgtaatcat	tacagatagc	catactactc	120
caatgcggcg	tgagctactg	ggtatcgggc	tgtgttggtg	tggattttct	coattacaca	180
actatatagc	atcgctagat	tgtttcggtc	gtccottaca	gatgacgcga	agtaactctg	240
tagatgcctt	agcagttgag	gctgtttgtt	gtatggggaga	ggggaaatgag	caaacaccgt	300
tagcgggtat	agagcaaggca	cctaataatg	tctaccattc	atatcctact	tctcgagaag	360
agtattgttc	tttgcgcata	gatgaacacg	aggacttata	cggacctttt	ttgcaagcgg	420
ttacgttggg	gtcaagaaaa	gaaatgatgg	aggtgtttat	gaatt		465

<210> 75

<211> 545

<212> DNA

<213> Chlamydia

<400> 75

gaattctggca	cgagatgaaa	agttagcgtc	acaggggatt	ctcctaccac	agaattccga	60
aaagttttct	tccaaaaacc	tcttctcttc	ttgatttagt	atccccctgc	aactacttta	120
ctatatgttc	tgtgaatat	gcatagtctt	caggatttga	aaatcccaat	tactcagcca	180
atccacgaat	tttctctcta	gcgatacgtg	gaatttgact	ctcacaagaa	tacaaagcag	240
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ttgtcgtctc	actaggctca	tgagcctcta	actctctcgg	agtaactcct	agagcaaaac	360
caaaactgctt	ccacaaatca	atatgattag	ggtaaccggt	ctcttcaccc	atcaagttaa	420
ctaacaataa	cttacgcgcc	tctaaatcat	cgcaacgcct	atgaatcgca	gataaatatt	480
taggaaagcg	tttgatatgt	aaataatagt	ctttggcata	cgctgtgtaa	tgtctcttag	540
taagc						545

<210> 76

<211> 797

<212> DNA

<213> Chlamydia

<220>

<221> misc_feature

<222> 788,789

<223> n=A,T,C or G

<400> 76

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actgtaataa	aaagagcgcg	cttctcttat	gcaaaatcaa	tttgaacaa	tctctactga	240
attaggagct	caaatcaaca	gcctctttac	tctgtattcc	aataatgcct	gtatagtctg	300
ctttggatac	aaccaatggt	ctgtacaaat	tgaagaggat	ggtaattcag	gatttttagt	360
tgctggagtc	atgcttggaa	aacttcacga	gaataacctt	agacaaaaaa	ttttcaaaag	420
tgctttgtct	atcaatggat	ctccgcgaat	taataattaa	ggcactctag	gatacgggtga	480
aatctctaac	caactctatc	tctgtgatcg	gcttaacatg	acctatctaa	atggagaaaa	540
gctcgcccg	tacttagttc	ttttttcgca	gcacgcgaat	atctggatgc	aactctatctc	600
aaaaggagaa	cttccagatt	tacatgctct	aggtatgtat	caactgtaaa	ttatgcgcgtc	660
attatcccaa	ttccgcagta	tcatccagca	atcttccatt	cgaaagattt	ggaatcagat	720
agatacttct	cctaagcatg	ggggtatgct	tacoggttat	ttttctcttc	atactcaaaa	780
aaagctgnng	gggaata					797

<210> 77

<211> 399

<212> DNA

<213> Chlamydia

<400> 77

catatgcac	accatcacca	tcacatgcc	cgcatcattg	gaattgatat	tctcgcaag	60
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atcattaaaa	agttgaagtt	agatcctgag	gcaagagcct	ctgaattaac	tgaagaaaga	180
gtaggacgac	tgaactctct	gctacaatca	gaatataccg	tagaaggagg	tttgcgagct	240
cgtgttcaat	cgatatcaaa	aagattgac	gccatccatt	cttatcgagg	tcagagacat	300
agactttctt	taccagtaag	aggacaagct	acaaaaacta	attctcgtag	tcgaaaaggt	360
aaaagaaaaa	cagtcgcagg	taagaagaaa	taagaatto			399

<210> 78
 <211> 285
 <212> DNA
 <213> Chlamydia

atgcataacc	atcaccatca	catgagtcac	aaaaataaaa	actctgcttt	tatgcattcc	60
gtgaataatt	ccacagattt	agcagttata	gttggcaagg	gacctatgcc	cagaaccgaa	120
attgtataaa	aagtttggga	atacattaaa	aaacacaaact	gtcaggatca	aaaaataaaa	180
cgtaataacc	ttcccgatgc	gaattctgcc	aaagctcttg	gctctagtga	tcctatcgac	240
atgtttccaa	tgaccaaaag	cctttccaaa	catattgtaa	aataa		285

<210> 79
 <211> 950
 <212> DNA
 <213> Chlamydia

aaattaaact	gagcacaaa	tacggcaatt	gctgagcaaa	agatgaagga	catggatgct	60
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gtagagtaat	tagttaaaag	gctgcataat	tatgacaaa	catggaaaa	gcattcgtgg	180
tatccaaag	acttaacgatt	tagctaaagt	gtattctttg	ggtagaagca	tagatatttt	240
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aggagcggac	ttgttttggt	gagcagactt	ggtagaataa	atcaaaaggt	gatgggttga	480
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taatttcaact	atttctcoga	ccatggggcc	aggggttacc	gtggatacta	ggaggttagt	840
tgcgttataa	ttctaaagt	aaagagaaga	aatgaagaag	gagaaaaagt	tgctgcttgc	900
cgagggtgaa	gaaaagataa	cgcgtttcca	aggtttttat	ttgttgagat		950

<210> 80
 <211> 395
 <212> DNA
 <213> Chlamydia

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agtaggtgtt	cctaacttcg	atagcatcgt	tctagtctct	gatatccaca	ggttgttata	180
gctaactcca	tcaaaagcga	ctagattcat	tttatcgttg	agcaagccct	ggttgactgt	240
gcagcttgac	attttagatc	ccagatactg	gttcgcatag	aaatgattgt	ctctaggtac	300
ataagcccat	tgtctataag	agtcataatt	ccagagcgct	gagatcgctc	cattttttagt	360
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<210> 81
 <211> 2085
 <212> DNA
 <213> Chlamydia

<400> 81
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 agtctcagtt agaaacaattt gctcaagtag gtttagatac aagttggcaa gttgttttgc 180
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 aaaaagcaa gtactactt tcatcggtg gtgtacagga gattccttag ctgcaggagt 2040
 ggctgctttg tattcttatg agagtcaaat tccacgtatc gctc 2085

<210> 82
 <211> 405
 <212> DNA
 <213> Chlamydia

<400> 82
 ttcatcggtc tagtctcgta ttctactctc caatggttcc gcaatttttg gcagagcttc 60
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 attggtcca taaggaggag agaaaaactc gatataggga atcgtatcaa ggtgaaagta 360
 gcaaaaaata aattagctcc tccattccga actgcagaa ttgat 405

<210> 83
 <211> 379
 <212> DNA
 <213> Chlamydia

<400> 83
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gaagcgttca	tgaatttcc					379

<210> 84
 <211> 715
 <212> DNA
 <213> Chlamydia

<400> 84						
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caatagtatc	agcaattcca	ccaagaattt	gatctcccaa	ctttctctaga	ataagctggg	420
aagcttttct	cgcatccaaa	ccaattgtaa	tagaagcatt	ggttgatgga	tattgggaa	480
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<210> 85
 <211> 476
 <212> DNA
 <213> Chlamydia

<400> 85						
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cgattacgtt	tatcatggat	aagcgttaatt	ggatagaaac	cgagtctgaa	caggtacaag	120
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atattttgaa	gaattttagc	gogatttctg	ttctctgtac	tttatgtacg	acotcagatt	360
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<210> 86
 <211> 1551
 <212> DNA
 <213> Chlamydia

<400> 86						
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<210> 87
 <211> 3031
 <212> DNA
 <213> Chlamydia

<400> 87						
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aagatagtca	ggctgaagga	cagtataggt	taattgtagg	agatccaaagt	tctttccaag	120
agaaaagatgc	agatactctt	cccggaag	tagagcaaag	tactttgttc	tcagtaacca	180
atcccggtgt	tttccaaagt	gtggaccaac	aggatcaagt	ctcttcccaa	gggttaattt	240
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<210> 88
 <211> 976
 <212> DNA
 <213> Chlamydia

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<210> 89
 <211> 94
 <212> PRT
 <213> Chlamydia

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<400> 89
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          5                      10                      15

Phe Met His Pro Val Asn Ile Ser Thr Asp Leu Ala Val Ile Val Gly
          20                      25                      30

Lys Gly Pro Met Pro Arg Thr Glu Ile Val Lys Lys Val Trp Glu Tyr
          35                      40                      45

Ile Lys Lys His Asn Cys Gln Asp Gln Lys Asn Lys Arg Asn Ile Leu
          50                      55                      60

Pro Asp Ala Asn Leu Ala Lys Val Phe Gly Ser Ser Asp Pro Ile Asp
          65                      70                      75                      80

Met Phe Gln Met Thr Lys Ala Leu Ser Lys His Ile Val Lys
          85                      90

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<210> 90
 <211> 474
 <212> PRT
 <213> Chlamydia

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			20					25					30	
Ala	Gln	Ala	Gly	Leu	Lys	Thr		Leu	Ile	Glu	Lys	Arg	Glu	Ala
		35					40					45		
Gly	Thr	Cys	Leu	Asn	Arg	Gly	Cys	Ile	Pro	Ser	Lys	Ala	Leu	Leu
						55					60			
Gly	Ala	Glu	Val	Val	Thr	Gln	Ile	Arg	His	Ala	Asp	Gln	Phe	Gly
					70					75				80
His	Val	Glu	Gly	Phe	Ser	Ile	Asn	Tyr	Pro	Ala	Met	Val	Gln	Arg
				85					90					95
Asp	Ser	Val	Val	Arg	Ser	Ile	Arg	Asp	Gly	Leu	Asn	Gly	Leu	Ile
			100					105					110	
Ser	Asn	Lys	Ile	Thr	Val	Phe	Ser	Gly	Arg	Gly	Ser	Leu	Ile	Ser
		115					120					125		
Thr	Glu	Val	Lys	Ile	Leu	Gly	Glu	Asn	Pro	Ser	Val	Ile	Lys	Ala
		130				135					140			
Ser	Ile	Ile	Leu	Ala	Thr	Gly	Ser	Glu	Pro	Arg	Ala	Phe	Pro	Gly
					150					155				160
Pro	Phe	Ser	Ala	Glu	Ser	Pro	Arg	Ile	Leu	Cys	Ser	Thr	Gly	Val
				165					170				175	
Asn	Leu	Lys	Glu	Ile	Pro	Gln	Lys	Met	Ala	Ile	Ile	Gly	Gly	Val
			180					185					190	
Ile	Gly	Cys	Glu	Phe	Ala	Ser	Leu	Phe	His	Thr	Leu	Gly	Ser	Glu
			195				200					205		
Ser	Val	Ile	Glu	Ala	Ser	Ser	Gln	Ile	Leu	Ala	Leu	Asn	Asn	Pro
						215					220			
Ile	Ser	Lys	Thr	Met	Phe	Asp	Lys	Phe	Thr	Arg	Gln	Gly	Leu	Arg
				230						235				240
Val	Leu	Glu	Ala	Ser	Val	Ser	Asn	Ile	Glu	Asp	Ile	Gly	Asp	Arg
				245					250				255	
Arg	Leu	Thr	Ile	Asn	Gly	Asn	Val	Glu	Glu	Tyr	Asp	Tyr	Val	Leu
			260					265					270	
Ser	Ile	Gly	Arg	Arg	Leu	Asn	Thr	Glu	Asn	Ile	Gly	Leu	Asp	Lys
		275					280					285		
Gly	Val	Ile	Cys	Asp	Glu	Arg	Gly	Val	Ile	Pro	Thr	Asp	Ala	Thr
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Arg	Thr	Asn	Val	Pro	Asn	Ile	Tyr	Ala	Ile	Gly	Asp	Ile	Thr	Gly
					310					315				320

Trp	Gln	Leu	Ala	His	Val	Ala	Ser	His	Gln	Gly	Ile	Ile	Ala	Ala	Arg
				325					330					335	
Asn	Ile	Gly		Gly	His	Lys	Glu	Glu	Ile	Asp	Tyr	Ser	Ala	Val	Pro
				340					345					350	Ser
Val	Ile	Phe	Thr	Phe	Pro	Glu	Val	Ala	Ser	Val	Gly	Leu	Ser	Pro	Thr
				355				360						365	
Ala	Ala	Gln	Gln	Gln	Lys	Ile	Pro	Val	Lys	Val	Thr	Lys	Phe	Pro	Phe
							375					380			
Arg	Ala	Ile	Gly	Lys	Ala	Val	Ala	Met	Gly	Glu	Ala	Asp	Gly	Phe	Ala
						390					395				400
Ala	Ile	Ile	Ser	His	Glu	Thr	Thr	Gln	Gln	Ile	Leu	Gly	Ala	Tyr	Val
				405					410						415
Ile	Gly	Pro	His	Ala	Ser	Ser	Leu	Ile	Ser	Glu	Ile	Thr	Leu	Ala	Val
				420					425					430	
Arg	Asn	Glu		Leu	Thr	Leu	Pro	Cys	Ile	Tyr	Glu	Thr	Ile	His	Ala
				435				440					445		His
Pro	Thr	Leu	Ala	Glu	Val	Trp	Ala	Glu	Ser	Ala	Leu	Leu	Ala	Val	Asp
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<210> 91
<211> 129
<212> PRT
<213> Chlamydia

<400> 91																		
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Gly	Ser	Ala	Arg	Ser	35	Asp	Glu	Ile	40	Ile	Lys	Lys	Leu	Lys	45	Leu	Asp	Pro
Glu	Ala	Arg	Ala	Ser	50	Glu	Leu	55	Thr	Glu	Glu	Glu	Val	60	Gly	Arg	Leu	Asn
Ser	Leu	Leu	Gln	Ser	65	Glu	70	Tyr	Thr	Val	Glu	Gly	75	Asp	Leu	Arg	Arg	80
Val	Gln	Ser	Asp	Ile	85	Lys	Arg	Leu	Ile	Ala	90	Ile	His	Ser	Tyr	Arg	95	Gly
Gln	Arg	His	Arg	100	Leu	Ser	Leu	Pro	Val	105	Arg	Gly	Gln	Arg	Thr	Lys	Thr	
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Lys

<210> 92
 <211> 202
 <212> PRT
 <213> Chlamydia

<400> 92
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 35 40 45
 Lys Asp Phe Thr Tyr Val Cys Pro Thr Glu Leu His Ala Phe Gln Asp
 50 55 60
 Arg Leu Val Asp Phe Glu Glu His Gly Ala Val Val Leu Gly Cys Ser
 65 70 75 80
 Val Asp Asp Ile Glu Thr His Ser Arg Trp Leu Thr Val Ala Arg Asp
 85 90 95
 Ala Gly Gly Ile Glu Gly Thr Glu Tyr Pro Leu Leu Ala Asp Pro Ser
 100 105 110
 Phe Lys Ile Ser Glu Ala Phe Gly Val Leu Asn Pro Glu Gly Ser Leu
 115 120 125
 Ala Leu Arg Ala Thr Phe Leu Ile Asp Lys His Gly Val Ile Arg His
 130 135 140
 Ala Val Ile Asn Asp Leu Pro Leu Gly Arg Ser Ile Asp Glu Glu Leu
 145 150 155 160
 Arg Ile Leu Asp Ser Leu Ile Phe Phe Glu Asn His Gly Met Val Cys
 165 170 175
 Pro Ala Asn Trp Arg Ser Gly Glu Arg Gly Met Val Pro Ser Glu Glu
 180 185 190
 Gly Leu Lys Glu Tyr Phe Gln Thr Met Asp
 195 200

<210> 93
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> made in a lab

<400> 93

Glu Asn Ser Leu Gln Asp Pro Thr Asn Lys Arg Asn Ile Asn Pro Asp
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 Asp Lys Leu

<210> 94
 <211> 20
 <212> FRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 94
 Asp Pro Thr Asn Lys Arg Asn Ile Asn Pro Asp Asp Lys Leu Ala Lys
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 Val Phe Gly Thr
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<210> 95
 <211> 20
 <212> FRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 95
 Lys Arg Asn Ile Asn Pro Asp Asp Lys Leu Ala Lys Val Phe Gly Thr
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<210> 96
 <211> 20
 <212> FRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 96
 Asp Asp Lys Leu Ala Lys Val Phe Gly Thr Glu Lys Pro Ile Asp Met
 1 5 10 15
 Phe Gln Met Thr
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<210> 97
 <211> 20
 <212> FRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 97
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 Met Val Ser Gln
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<210> 98
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 98
Asn Lys Arg Asn Ile Asn Pro Asp Asp Lys Leu Ala Lys Val Phe Gly
1 5 10 15
Thr Glu Lys Pro
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<210> 99
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 99
Asn Lys Arg Asn Ile Leu Pro Asp Ala Asn Leu Ala Lys Val Phe Gly
1 5 10 15

<210> 100
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 100
Lys Met Trp Asp Tyr Ile Lys Glu Asn Ser Leu Gln Asp Pro Thr
1 5 10 15

<210> 101
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 101
Thr Glu Ile Val Lys Lys Val Trp Glu Tyr Ile Lys Lys His Asn Cys
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Gln Asp Gln Lys
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<210> 102
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 102

Lys Val Trp Glu Tyr Ile Lys Lys His Asn Cys Gln Asp Gln Lys Asn
 1 5 10 15

Lys Arg Asn Ile
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<210> 103

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 103

Lys Val Trp Glu Tyr Ile Lys Lys His Asn Cys Gln Asp Gln Lys
 1 5 10 15

<210> 104

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 104

Ala Glu Leu Thr Glu Glu Glu Val Gly Arg Leu Asn Ala Leu Leu Gln
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Ser Asp Tyr Val
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<210> 105

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 105

Leu Gln Ser Asp Tyr Val Val Glu Gly Asp Leu Arg Arg Arg Val Gln
 1 5 10 15

Ser Asp Ile Lys Arg
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<210> 106

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 106

Met Pro Arg Ile Ile Gly Ile Asp Ile Pro Ala Lys Lys Lys Leu Lys
 1 5 10 15

Ile Ser Leu Thr
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<210> 107

<211> 20

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 107
 Ala Glu Leu Thr Glu Glu Glu Val Gly Arg Leu Asn Ala Leu Leu Gln
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 Ser Asp Tyr Val
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<210> 108
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 108
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 Arg Arg Val Gln
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<210> 109
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 109
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 Arg Arg Val Gln
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<210> 110
 <211> 1461
 <212> DNA
 <213> Chlamydia

<400> 110
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ggacagatta	gagaaaaatg	agcaagcttt	attgtccgat	gtgcgcttag	ttttatctag	1440
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<210> 111

<211> 267

<212> DNA

<213> Chlamydia

<400> 111

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gaaaagctat	gttggaagac	atcgctatct	taactggcgg	tcaactcatt	agcgaagagt	180
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<210> 112

<211> 698

<212> DNA

<213> Chlamydia

<400> 112

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<210> 113

<211> 1142

<212> DNA

<213> Chlamydia

<400> 113

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ca						1142

<210> 114

<211> 976

<212> DNA

<213> Chlamydia

<400> 114

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cagagcttcg	caatcattat	gcaacgagt	gtttgaaaag	cggttacaat	attgggagta	420
ccgatgggtt	ttccctgttc	attgggctgt	ttatgtggga	gtcggagggt	cttttccggc	480
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aaacgaacaa	cccaggtggt	agtgtccttt	atctttatgc	actgctttcc	atgttgaacg	720
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tgggagacaa	catggaagga	tatactgtgg	atctacaggt	tgccgagtat	ttaaaaagct	900
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<210> 115

<211> 995

<212> DNA

<213> Chlamydia

<400> 115

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ccctctcaaaa	gttgctctcta	actcgaaagg	agatcgogtc	tttgatgtgg	taacagattc	360
gtacactcca	gaagaaatcg	gcgctcagat	ccctcatgaag	atgaaggaaa	ctgctgagcc	420
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tgggtgatcg	tctactgaaa	tcaatcagcc	atctcatcact	atcgagccta	atggacctaa	900
acatttggct	ttaactctaa	ctcgcgctca	attcgaaacac	ctagcttctc	ctctcatgta	960
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<210> 116

<211> 437

<212> DNA

<213> Chlamydia

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 ggaaccctta cttgttaaaaa ctctcacogt ctacaatttt tgaaaaaact tcccgataaa 180
 caaggtggag gaactctacgg agaagacaac atcacccat ctcaatttgac aggggaagact 240
 ctatttccaa agaatactgc aaaaaaagag ggccgtggac tttctcataaa aggtacagat 300
 aaagctctta caatgacagg actggatagt ttctgtttaa ttaataaacac atcagaaaaa 360
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 acaattccag gaatcac 437

<210> 117
 <211> 446
 <212> DNA
 <213> Chlamydia

<400> 117
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 agggacaatat taccgaaaaa gttaagggtg gtttgatcgt agatatttgt atgggaacct 180
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 aggtttgtga gttcaaaatt ctcaaaatca acgtggatcg tcggaacctt gttgatcta 300
 gaagagaact tctogaagct gaacgcattt ctaagaaagc agagttgatc gagcaaatca 360
 ctatcgggtga acgtcgcaaa ggtatcgtta agaatacac agatttcgga gtattctgtg 420
 atcttgatgg cattgacggc ctactc 446

<210> 118
 <211> 951
 <212> DNA
 <213> Chlamydia

<400> 118
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 tgaaggggaa atgatcgata agttgcaaga tgcctatgat agaaagttgt tggattctcg 240
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 aggttctgtt gatctgggtt ttgctgtttg ggaccaaat aaaaatgatc ttctctcttt 420
 gactcaagtt gttcaaggtt tagcaagcat tatgggatct gtattgagtt tttgtcgtt 480
 tccaggaaag actttttgcta cgcctcatgc gcgcattatg attcaaccag cttctattgg 540
 aggaaccact agttttcga cccaggaact ggaattcat gctcgtgaaa ttttaaaac 600
 aaagacagc attatttgat tgtatgtoga gccactgga caatctccag aggtgataga 660
 gaaagctatc gatcgagata tgggtgatgg tcaaatgaa gcaatggagt ttgactgttt 720
 agatgggatt ctctctctct ttaacgactt tgatgatct tttatattct ggagcaggaa 780
 acagtttcat tttggagaa tcatgacct ctcttgagga tttctgttt ttatgccagg 840
 aagagatggt tgaatgggtt ttatgtgtag agtctctc aatagcagat gctaaactca 900
 ctgtttttaa tagtgatgga tctatcgct ctatgtgcgg gaattgggttg c 951

<210> 119
 <211> 953
 <212> DNA
 <213> Chlamydia

<400> 119
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 ataatccatc aaacaaatgc tctattacaa ttggttttga tgcggaaaaa gcttaccagc 180
 ttaattctaga aaagtggga galcaaatc ttggtggaat tgcgtgact attgttgata 240
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 ctlttaacaa ctttcaatc actaatgaaa ttcaatgcaa cgggttatc atccccagga 360
 acattgaaac ttatttagga ggaactgaaa taggaaatc cacagtcaac cccaaaagct 420

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caggcggttcc taattttatgt agtctaagaa ccagaattat taatacagga ttgactccga 600
caacgtatttc attacgtgta ggcgggttag aaagcgggtg ggtatgggtt aatgcccttt 660
ctaattggcaa tgaattttta ggaataacaa atactcttaa tgtatctttt ttggaggtaa 720
tacctcaaac aaacgcttaa acaattttta ttggattttt cttataggtt ttatatttag 780
agaaaaaagt tgaatttacg gggtttggtta tgcataataa aagcaaaagt agggacgatt 840
ttattaaaaa tgttaaagat tcttggtatc ggtctgcgat tccgactcgt ccaactcaaa 900
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<210> 120

<211> 897

<212> DNA

<213> Chlamydia

<220>

<221> misc_feature

<222> 395

<223> n = A,T,C or G

<400> 120

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<210> 121

<211> 298

<212> PRT

<213> Chlamydia

<400> 121

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Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala
35 40 45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
50 55 60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
65 70 75 80
Thr Val Leu Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
85 90 95
Val Gln Ser Ala Gln Ser Phe Phe Ser Tyr Met Lys Ala Ala Ser Gln
100 105 110
Lys Pro Gln Glu Gly Asp Glu Gly Leu Val Ala Asp Leu Cys Val Ser
115 120 125
His Lys Arg Arg Ala Ala Ala Val Cys Ser Phe Ile Gly Gly Ile

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130 135 140
 Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
 145 150 155 160
 Lys Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Ile Lys Ala Asn Met
 165 170 175
 Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Phe Val
 180 185 190
 Val Gly Ser Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
 195 200 205
 Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Ser Leu Glu Leu Ser Gly
 210 215 220
 Glu Glu Asn Ala Cys Glu Arg Arg Val Ala Gly Glu Lys Ala Lys Thr
 225 230 235 240
 Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
 245 250 255
 Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
 260 265 270
 Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Val
 275 280 285
 Ile Gly Leu Trp Thr Phe Cys Ala Arg Ala
 290 295

 <210> 122
 <211> 897
 <212> DNA
 <213> Chlamydia

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 gtttaggtcg ccaagtctgc tgcgaattg accgcaaat ttttgaaca agctggagcc 180
 gcgggtcttt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatacaga 240
 actgtgttcg ctittaggaa tgcctttaac ggagcgttgc caggaacagt tcaaatggcg 300
 caaagctctt tctctcacat gaaagctgct agtcagaaaa cgcaagaagg ggaatgaggg 360
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 aaaaatgctg tgaaccgctt tctttcttcc caaactaaag caaatatggg atcttctgtt 540
 agctatatat tggcggctaa ccatgcagcg tctgtgtgtg gtgctggact cgtatcagt 600
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 gaagtgtcgg gagagaaaa tgcttgcgag aagagagtgc ctgagagaa agccaagagc 720
 ttcaacggca tcaagtatgc actccacact atgctcgaga agtttttggg atgctgtgcc 780
 gacgttttca aattggtgcc gctgcctatt acaatgggta ttctgtcgat tgtggtgct 840
 ggaatgacgt tcaattctgc aattattgga ttgtgcactt tctgcgccag agcataa 897

 <210> 123
 <211> 298
 <212> PRT
 <213> Chlamydia

 <400> 123
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 20 25 30
 Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala
 35 40 45
 Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
 50 55 60
 Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Thr Arg
 65 70 75 80
 Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr

Val	Gln	Ser	Ala	Gln	Ser	Phe	Phe	Ser	His	Met	Lys	Ala	Ala	Ser	Gln
Lys	Thr	Gln	Glu	Gly	Asp	Glu	Gly	Leu	Thr	Ala	Asp	Leu	Cys	Val	Ser
His	Lys	Arg	Arg	Ala	Ala	Ala	Ala	Val	Cys	Gly	Phe	Ile	Gly	Gly	Ile
Thr	Tyr	Leu	Ala	Thr	Phe	Gly	Val	Ile	Arg	Pro	Ile	Leu	Phe	Val	Asn
145	Met	Leu	Val	Asn	Pro	Phe	Leu	Ser	Ser	Gln	Thr	Lys	Ala	Asn	Met
Lys	Ser	Ser	Val	Ser	Tyr	Ile	Met	Ala	Ala	Asn	His	Ala	Ala	Ser	Val
Val	Gly	Ala	Gly	Leu	Ala	Ile	Ser	Ala	Glu	Arg	Ala	Asp	Cys	Glu	Ala
Arg	Cys	Ala	Arg	Ile	Ala	Arg	Glu	Glu	Ser	Leu	Leu	Glu	Val	Ser	Gly
Glu	Glu	Asn	Ala	Cys	Glu	Lys	Arg	Val	Ala	Gly	Gly	Lys	Ala	Lys	Thr
225	Phe	Thr	Arg	Ile	Lys	Tyr	Ala	Leu	Leu	Thr	Met	Leu	Glu	Lys	Phe
Glu	Cys	Val	Ala	Asp	Val	Phe	Lys	Leu	Val	Pro	Leu	Pro	Ile	Thr	Met
Gly	Ile	Arg	Ala	Ile	Val	Ala	Ala	Gly	Cys	Thr	Phe	Thr	Ser	Ala	Ile
Ile	Gly	Leu	Cys	Thr	Phe	Cys	Ala	Arg	Ala						

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 50 55 60
 Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
 65 70 75 80
 Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
 85 90 95
 Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
 100 105 110
 Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser
 115 120 125
 His Lys Arg Arg Ala Ala Ala Val Cys Ser Ile Ile Gly Gly Ile
 130 135 140
 Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
 145 150 155 160
 Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
 165 170 175
 Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
 180 185 190
 Val Gly Ala Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
 195 200 205
 Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Pro Gly
 210 215 220
 Glu Glu Asn Ala Cys Glu Lys Lys Val Ala Gly Glu Lys Ala Lys Thr
 225 230 235 240
 Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
 245 250 255
 Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
 260 265 270
 Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
 275 280 285
 Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
 290 295

<210> 126

<211> 897

<212> DNA

<213> Chlamydia

<400> 126

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 caaagcttct tctctcacat gaaagctgct agtcagaaaa cgcaagaagg ggatgagggg 360
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<210> 127

<211> 298

<212> FRT

<213> Chlamydia

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 Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
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 Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
 65 70 75 80
 Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
 85 90 95
 Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
 100 105 110
 Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser
 115 120 125
 His Lys Arg Arg Ala Ala Ala Val Cys Ser Ile Ile Gly Gly Ile
 130 135 140
 Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
 145 150 155 160
 Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
 165 170 175
 Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
 180 185 190
 Val Gly Ala Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
 195 200 205
 Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Pro Gly
 210 215 220
 Glu Glu Asn Ala Cys Glu Lys Lys Val Ala Gly Glu Lys Ala Lys Thr
 225 230 235 240
 Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
 245 250 255
 Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
 260 265 270
 Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
 275 280 285
 Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
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<210> 128
 <211> 897
 <212> DNA
 <213> Chlamydia

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 aaaatgctgg tgaaccogtt tctttcttcc caaactaaag caaatatggg atcttctgtt 540
 agctatattt tggcggtctaa ccattgcagcg cctgtgtgtg gtgctggact cgctatcagt 600
 gcggaaagag cagattgcga agcccgcgtgc gctcgtattg cgagagaaga gtcgttactc 660
 gaagtgtcgg gagaggaaaa tgcttgccga aagagagtcg ctggagagaa agccaagacg 720
 ttacgcgcga tcaagtatgc actctcactc atgctcgaga agtttttggg atgcgttgcc 780
 gacgttttca aattgggtgc gctgcctatt acaatgggta ttcgtgcgat tgtgtgcgt 840
 ggaatgacgt tcacttctgc aattattgga ttgtgcactt tctgcgccag agcataa 897

<210> 129
 <211> 298
 <212> PRT
 <213> Chlamydia

<400> 129
 Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
 1 5 10 15
 Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val Val Asn
 20 25 30
 Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala
 35 40 45
 Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
 50 55 60
 Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Thr Arg
 65 70 75 80
 Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
 85 90 95
 Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
 100 105 110
 Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser
 115 120 125
 His Lys Arg Arg Ala Ala Ala Val Cys Gly Phe Ile Gly Gly Ile
 130 135 140
 Thr Tyr Leu Ala Thr Phe Gly Val Ile Arg Pro Ile Leu Phe Val Asn
 145 150 155 160
 Lys Met Leu Val Asn Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
 165 170 175
 Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
 180 185 190
 Val Gly Ala Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
 195 200 205
 Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Ser Gly
 210 215 220
 Glu Glu Asn Ala Cys Glu Lys Arg Val Ala Gly Glu Lys Ala Lys Thr
 225 230 235 240
 Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
 245 250 255
 Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
 260 265 270
 Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
 275 280 285
 Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
 290 295

<210> 130
 <211> 897
 <212> DNA
 <213> Chlamydia

<400> 130
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 gtttaaggctgc ccaagctctgc tgcgcaattg acgcgaaata ttttggaaaca agctggaggc 180
 gcgggctctt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatgcgaga 240
 actgttctgc ctttagggaat tgcctttaac ggagcgttgc caggaacagt tcaaaagtgcg 300
 caaagctctt tctcttacat gaaagctgct agtcagaaac cgcaagaaagg ggatgagggg 360
 ctctgtagcag atcttttgtt gtctcataag cgcagagcgg ctgcggtgt ctgtagcttc 420
 atcggaggaa ttacctacat cgcgacatic ggagctatcc gtccgattct gttttgcaac 480
 aaaatgctgg cgcaaccggt tctttcttcc caaactaaag caaatatggg atcttctgtt 540

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agctatatta tggcgcttaa ccatgcagcg ttgtgtgttg gttctggact cgctatcagt 600
gcggaaagag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtcgtcactc 660
gaattgtcgg gagaggaaaa tgcttgogag aggggagtcg ctggagagaa agccaagacg 720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttggg atgcgttgcc 780
gacgttttca aattgggtgc gttgcctatt acaatgggta tctcgtgcaat tgtggctgcg 840
ggaatgacgt tcaattctgc agttattgga ttgtggactt tctgcaacag agtataaa 897

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<210> 131

<211> 298

<212> PR1

<213> Chlamydia

<400> 131

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Met Ala Ala Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
1      5      10      15
Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val Val Asn
20      25      30
Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala
35      40      45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
50      55      60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
65      70      75      80
Thr Val Leu Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
85      90      95
Val Gln Ser Ala Gln Ser Phe Phe Ser Tyr Met Lys Ala Ala Ser Gln
100     105     110
Lys Pro Gln Glu Gly Asp Glu Gly Leu Val Ala Asp Leu Cys Val Ser
115     120     125
His Lys Arg Arg Ala Ala Ala Val Cys Ser Phe Ile Gly Gly Ile
130     135     140
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
145     150     155     160
Lys Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
165     170     175
Gly Ser Ser Val Ser Tyr Ile Met Ala Asn His Ala Ala Phe Val
180     185     190
Val Gly Ser Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
195     200     205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Ser Leu Glu Leu Ser Gly
210     215     220
Glu Glu Asn Ala Cys Glu Arg Gly Val Ala Gly Glu Lys Ala Lys Thr
225     230     235     240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
245     250     255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
260     265     270     275
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Val
280     285
Ile Gly Leu Trp Thr Phe Cys Asn Arg Val
290     295

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<210> 132

<211> 897

<212> DNA

<213> Chlamydia

<400> 132

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acacagccca gcaataaaat ggcaagggtg gtaataaga cgaagggaat ggataagact 120
gtaaggtgoc ccaagtctgc tgccgaattg accgcaataa ttttggaaca agctggaggc 180

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gccccgtctt cgcacacat tacagcttcc caagtgtcca aaggattagg ggaatgcaga 240
actgttctcg ctttagggaa tgcctttaac ggagcgttgc caggaacagt tcaaagtgcg 300
caaaagcttc tctcttacat gaaagctgct agtcagaaac cgcaagaagg ggaatgaggg 360
ctcgtaggag atcttttgtt gtcctcaaa cgcagagcgg ctgcggctgt ctgtagcttc 420
atcgaggagaa ttacctacct cgcgacattc ggagctatcc gtccgattct gtttgcacac 480
aaaatgctgg cgcacacggt tctttcttcc caaactaaag caaatatggg atcttctggt 540
agctatatata tggcggctaa ccaatgcagcg tttgtgtggg gttctggact cgctatcagt 600
gcggaagaag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtccgtcact 660
gaattgtcgg gagaggaaaa tgcttgtgag aggaagatcg ctggagagaa agccaagacg 720
ttcacgcgca tcaagatagc actcctcact atgctcgaga agtttttgga atgcgttgcc 780
gacgttttca aattgggtgc gttgcctatt acaatgggta ttcgtgcaat ttggctgcg 840
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<210> 133
 <211> 298
 <212> PRT
 <213> Chlamydia

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<400> 133
Met Ala Ala Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
1 5 10 15
Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val Val Asn
20 25 30
Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala
35 40 45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
50 55 60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
65 70 75 80
Thr Val Leu Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
85 90 95
Val Gln Ser Ala Gln Ser Phe Phe Ser Tyr Met Lys Ala Ala Ser Gln
100 105 110
Lys Pro Gln Glu Gly Asp Glu Gly Leu Val Ala Asp Leu Cys Val Ser
115 120 125
His Lys Arg Arg Ala Ala Ala Val Cys Ser Phe Ile Gly Gly Ile
130 135 140
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
145 150 155 160
Lys Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
165 170 175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Phe Val
180 185 190
Val Gly Ser Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
195 200 205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Ser Leu Glu Leu Ser Gly
210 215 220
Glu Glu Asn Ala Cys Glu Arg Arg Val Ala Gly Glu Lys Ala Lys Thr
225 230 235 240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
245 250 255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
260 265 270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Val
275 280 285
Ile Gly Leu Trp Thr Phe Cys Asn Arg Val
290 295

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<210> 134
 <211> 897
 <212> DNA

<213> Chlamydia

<400> 134

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attaagggttg	coaagtctgc	lgccgaatttg	accgcacaata	ttttggaaca	agctgggagc	180
gggggtctct	cgccacacat	tacagcttcc	caagtgtcca	aaggattagg	ggatgcgaga	240
actgtgtctg	cttttagggaa	tgctcttaac	ggagcgttgc	caggaacagt	tcaaagtgcg	300
caaagcttct	tcctctacat	gaaagctgct	agtcagaaaa	cgcaagaagg	ggatgagggg	360
ctcacagcag	atcttttgtt	gtctcataag	cgcagagcgg	ctgcggctgt	ctgtagatct	420
atcgaggaaa	ttacctacct	cgcgacattc	ggagctatcc	gtccgattct	gtttgtcaac	480
aaaatgctgg	caaaacogtt	tctttcttcc	caaaactaaag	caaatatggg	atcttctgtt	540
agctatatta	tgccggctaa	ccatgcagcg	tctgtgtgtg	gtgctggact	cgcatacagt	600
gcggaagaag	cagattgcga	agcccgctgc	gctcgtattg	cgagagaaga	gtcgttactc	660
gaaatgccgg	gagaggaaaa	tgcttgcgag	aagaaagtgc	ctggagagaa	agccaagacg	720
ttcacgcgca	tcaagtatgc	actcctcact	atgctcgaga	agtttttggg	atgcgttgcc	780
gacgttttca	aattggtgcc	gctgcctatt	acaatgggta	ttcgtgcgat	tggtgctgct	840
ggatgtacgt	tcacttctgc	aattattgga	ttgtgcactt	tctgcgccag	agcataa	897

<210> 135

<211> 298

<212> PRT

<213> Chlamydia

<400> 135

Met	Ala	Ser	Ile	Cys	Gly	Arg	Leu	Gly	Ser	Gly	Thr	Gly	Asn	Ala	Leu
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Lys	Ala	Phe	Phe	Thr	Gln	Pro	Asn	Asn	Lys	Met	Ala	Arg	Val	Val	Asn
				20				25					30		
Lys	Thr	Lys	Gly	Met	Asp	Lys	Thr	Ile	Lys	Val	Ala	Lys	Ser	Ala	Ala
		35					40					45			
Glu	Leu	Thr	Ala	Asn	Ile	Leu	Glu	Gln	Ala	Gly	Gly	Ala	Gly	Ser	Ser
	50					55					60				
Ala	His	Ile	Thr	Ala	Ser	Gln	Val	Ser	Lys	Gly	Leu	Gly	Asp	Ala	Arg
65					70				75				80		
Thr	Val	Val	Ala	Leu	Gly	Asn	Ala	Phe	Asn	Gly	Ala	Leu	Pro	Gly	Thr
				85					90				95		
Val	Gln	Ser	Ala	Gln	Ser	Phe	Phe	Ser	His	Met	Lys	Ala	Ala	Ser	Gln
			100					105					110		
Lys	Thr	Gln	Glu	Gly	Asp	Glu	Gly	Leu	Thr	Ala	Asp	Leu	Cys	Val	Ser
		115					120					125			
His	Lys	Arg	Arg	Ala	Ala	Ala	Ala	Val	Cys	Ser	Ile	Ile	Gly	Gly	Ile
	130				135							140			
Thr	Tyr	Leu	Ala	Thr	Phe	Gly	Ala	Ile	Arg	Pro	Ile	Leu	Phe	Val	Asn
145					150					155				160	
Lys	Met	Leu	Ala	Lys	Pro	Phe	Leu	Ser	Ser	Gln	Thr	Lys	Ala	Asn	Met
			165						170				175		
Gly	Ser	Ser	Val	Ser	Tyr	Ile	Met	Ala	Ala	Asn	His	Ala	Ala	Ser	Val
			180					185					190		
Val	Gly	Ala	Gly	Leu	Ala	Ile	Ser	Ala	Glu	Arg	Ala	Asp	Cys	Glu	Ala
	195						200					205			
Arg	Cys	Ala	Arg	Ile	Ala	Arg	Glu	Glu	Ser	Leu	Leu	Glu	Met	Pro	Gly
	210				215							220			
Glu	Glu	Asn	Ala	Cys	Glu	Lys	Lys	Val	Ala	Gly	Glu	Lys	Ala	Lys	Thr
225					230					235				240	
Phe	Thr	Arg	Ile	Lys	Tyr	Ala	Leu	Leu	Thr	Met	Leu	Glu	Lys	Phe	Leu
			245						250				255		
Glu	Cys	Val	Ala	Asp	Val	Phe	Lys	Leu	Val	Pro	Leu	Pro	Ile	Thr	Met
	260							265					270		
Gly	Ile	Arg	Ala	Ile	Val	Ala	Ala	Gly	Cys	Thr	Phe	Thr	Ser	Ala	Ile
	275					280							285		

Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
290 295

<210> 136
<211> 882
<212> DNA
<213> Chlamydia

<400> 136

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ataaaagttg	ggaagtctgc	tgctgaatta	acggcgagta	tttttagagca	aactgggggg	180
gcagggactg	atgcacatgt	tacggcggcc	aaggtgtcta	aagcacttgg	ggacgcgcga	240
acagtaatgg	ctctagggaa	tgtcttcaat	gggtctgtgc	cagcaaccat	tcaaaagtcg	300
cgaagctgtc	tcgcccattt	acgagcggcc	ggcaaaagaag	aagaaacatg	ctccaaggtg	360
aaagatctct	gtgtttctca	tagacgaaga	gctcgggtg	aggcttgtaa	tgttattgga	420
ggagcaactt	atattacaac	tttcggagcg	attcgtccga	cattactcgt	taacaagctt	480
cttgccaaac	cattcctttc	ctcccaagcc	aaagaagggt	tgggagcttc	tgttggttat	540
atcatggcag	cgaaccatgc	ggcatctgtg	cttgggtctg	ctttaagtat	tagcgcagaa	600
agagcagact	gtgaagagcg	gtgtgatcgc	attcgtatga	gtgaggatgg	tgaaatttgc	660
gaaggcaata	aattaacagc	tatttcggaa	gagaaggcta	gatcatggac	tctcattaag	720
tacagattcc	ttactatgat	agaaaaacta	tttgagatgg	tgccggatat	cttcaagtta	780
attcctttgc	caatttcgca	tggaattcgt	gctattgttg	ctgcgggatg	tacgttgact	840
tctgcagtta	ttggottagg	tacttttttg	tctagagcat	aa		882

<210> 137
<211> 293
<212> PRT
<213> Chlamydia

<400> 137

Met	Ala	Ser	Val	Cys	Gly	Arg	Leu	Ser	Ala	Gly	Val	Gly	Asn	Arg	Phe
1				5					10					15	
Asn	Ala	Phe	Phe	Thr	Arg	Pro	Gly	Asn	Lys	Leu	Ser	Arg	Phe	Val	Asn
								25					30		
Ser	Ala	Lys	Gly	Leu	Asp	Arg	Ser	Ile	Lys	Val	Gly	Lys	Ser	Ala	Ala
		35						40				45			
Glu	Leu	Thr	Ala	Ser	Ile	Leu	Glu	Gln	Thr	Gly	Gly	Ala	Gly	Thr	Asp
	50					55					60				
Ala	His	Val	Thr	Ala	Ala	Lys	Val	Ser	Lys	Ala	Leu	Gly	Asp	Ala	Arg
	65					70				75				80	
Thr	Val	Met	Ala	Leu	Gly	Asn	Val	Phe	Asn	Gly	Ser	Val	Pro	Ala	Thr
			85						90					95	
Ile	Gln	Ser	Ala	Arg	Ser	Cys	Leu	Ala	His	Leu	Arg	Ala	Ala	Gly	Lys
			100					105					110		
Glu	Glu	Glu	Thr	Cys	Ser	Lys	Val	Lys	Asp	Leu	Cys	Val	Ser	His	Arg
		115				120						125			
Arg	Arg	Ala	Ala	Ala	Glu	Ala	Cys	Asn	Val	Ile	Gly	Gly	Ala	Thr	Tyr
	130				135						140				
Ile	Thr	Thr	Phe	Gly	Ala	Ile	Arg	Pro	Thr	Leu	Leu	Val	Asn	Lys	Leu
	145				150					155				160	
Leu	Ala	Lys	Pro	Phe	Leu	Ser	Ser	Gln	Ala	Lys	Glu	Gly	Leu	Gly	Ala
			165					170						175	
Ser	Val	Gly	Tyr	Ile	Met	Ala	Ala	Asn	His	Ala	Ala	Ser	Val	Leu	Gly
			180					185					190		
Ser	Ala	Leu	Ser	Ile	Ser	Ala	Glu	Arg	Ala	Asp	Cys	Glu	Glu	Arg	Cys
		195				200					205				
Asp	Arg	Ile	Arg	Cys	Ser	Glu	Asp	Gly	Glu	Ile	Cys	Glu	Gly	Asn	Lys
	210				215						220				
Leu	Thr	Ala	Ile	Ser	Glu	Glu	Lys	Ala	Arg	Ser	Trp	Thr	Leu	Ile	Lys
	225				230					235				240	

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<210> 138
<211> 16
<212> PRT
<213> Artificial Sequence
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<220>
<223> Made in a lab

<400> 138
Asp Leu Cys Val Ser His Lys Arg Arg Ala Ala Ala Val Cys Ser
1 5 10 15

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<210> 139
<211> 16
<212> PRT
<213> Artificial Sequence
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<220>
<223> Made in a lab

<400> 139
Arg Ala Ala Ala Ala Val Cys Ser Phe Ile Gly Gly Ile Thr Tyr Leu
1 5 10 15

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<210> 140
<211> 18
<212> PRT
<213> Artificial Sequence
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<220>
<223> Made in a lab

<400> 140
Cys Ser Phe Ile Gly Gly Ile Thr Tyr Leu Ala Thr Phe Gly Ala Ile
1 5 10 15

Arg Pro

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<210> 141
<211> 18
<212> PRT
<213> Artificial Sequence
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<220>
<223> Made in a lab

<400> 141
Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn Lys
1 5 10 15
Met Leu

<210> 142
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 142
 Arg Pro Ile Leu Phe Val Asn Lys Met Leu Ala Gln Pro Phe Leu Ser
 1 5 10 15
 Ser Gln

<210> 143
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 143
 Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met Gly
 1 5 10 15
 Ser

<210> 144
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 144
 Cys Ser Phe Ile Gly Gly Ile Thr Tyr Leu
 1 5 10

<210> 145
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 145
 Ser Phe Ile Gly Gly Ile Thr Tyr Leu
 1 5

<210> 146
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 146

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Phe Ile Gly Gly Ile Thr Tyr Leu
 1           5

<210> 147
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 147
Cys Ser Phe Ile Gly Gly Ile Thr Tyr
 1           5

<210> 148
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 148
Cys Ser Phe Ile Gly Gly Ile Thr
 1           5

<210> 149
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 149
Cys Ser Ile Ile Gly Gly Ile Thr Tyr Leu
 1           5           10

<210> 150
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 150
Cys Gly Phe Ile Gly Gly Ile Thr Tyr Leu
 1           5           10

<210> 151
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 151
Gly Phe Ile Gly Gly Ile Thr Tyr Leu

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```

1           5

<210> 152
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 152
Gln Ile Phe Val Cys Leu Ile Ser Ala Glu Arg Leu Arg Leu Arg Leu
1           5           10           15
Ser Val Ala Ser
                20

<210> 153
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 153
Glu Arg Leu Arg Leu Arg Leu Ser Val Ala Ser Ser Glu Glu Leu Pro
1           5           10           15
Thr Ser Arg His
                20

<210> 154
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 154
Ala Ser Ser Glu Glu Leu Pro Thr Ser Arg His Ser Glu Leu Ser Val
1           5           10           15
Arg Phe Cys Leu
                20

<210> 155
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 155
Arg His Ser Glu Leu Ser Val Arg Phe Cys Leu Ser Thr Lys Cys Trp
1           5           10           15
Arg Asn Arg Phe
                20

<210> 156
<211> 20
<212> PRT

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<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 156

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Leu Ser Thr Lys Cys Trp Arg Asn Arg Phe Phe Leu Pro Lys Leu Lys
 1           5           10           15
Gln Ile Trp Asp
 20

```

<210> 157

<211> 53

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 157

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Ile Phe Val Cys Leu Ile Ser Ala Glu Arg Leu Arg Leu Ser Val Ala
 1           5           10           15
Ser Ser Glu Glu Leu Pro Thr Ser Arg His Ser Glu Leu Ser Val Arg
 20           25           30
Phe Cys Leu Ser Thr Lys Cys Trp Arg Asn Arg Phe Phe Leu Pro Lys
 35           40           45
Leu Lys Gln Ile Trp
 50

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<210> 158

<211> 52

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 158

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Leu Cys Val Ser His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Phe
 1           5           10           15
Ile Gly Gly Ile Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile
 20           25           30
Leu Phe Val Asn Lys Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Ile
 35           40           45
Lys Ala Asn Met
 50

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<210> 159

<211> 24

<212> DNA

<213> Chlamydia

<400> 159

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24

<210> 160

<211> 24

<212> DNA

<213> Chlamydia

<400> 160

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<210> 161	
<211> 24	
<212> DNA	
<213> Chlamydia	
<400> 161	
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<210> 162	
<211> 19	
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 Gly Gly Ala Ile Gln Ala Gln Thr Phe Ser Leu Ser Arg Asn Val Ser
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 Pro Ile Ser Phe Ala Arg Asn Arg Ala Asp Leu Asn Gly Gly Ala Ile
 195 200 205
 Cys Cys Ser Asn Leu Ile Cys Ser Gly Asn Val Asn Pro Leu Phe Phe
 210 215 220
 Thr Gly Asn Ser Ala Thr Asn Gly Gly Ala Ile Cys Cys Ile Ser Asp
 225 230 235 240
 Leu Asn Thr Ser Glu Lys Gly Ser Leu Ser Leu Ala Cys Asn Gln Glu
 245 250 255 260
 Thr Leu Phe Ala Ser Asn Ser Ala Lys Glu Lys Gly Gly Ala Ile Tyr
 265 270 275
 Ala Lys His Met Val Leu Arg Tyr Asn Gly Pro Val Ser Phe Ile Asn
 280 285 290
 Asn Ser Ala Lys Ile Gly Gly Ala Ile Ala Ile Gln Ser Gly Gly Ser
 295 300 305
 Leu Ser Ile Leu Ala Gly Glu Gly Ser Val Leu Phe Gln Asn Asn Ser
 310 315 320
 Gln Arg Thr Ser Asp Gln Gly Leu Val Arg Asn Ala Ile Tyr Leu Xaa
 325 330 335
 Lys Asp Ala Ile Leu Ser Ser Leu Glu Ala Arg Asn Gly Asp Ile Leu
 340 345 350
 Phe Phe Asp Pro Ile Val Gln Glu Ser Ser Ser Lys Glu Ser Pro Leu
 355 360 365
 Pro Ser Ser Leu Gln Ala Ser Val Thr Ser Pro Thr Pro Ala Thr Ala
 370 375 380
 Ser Pro Leu Val Ile Gln Thr Ser Ala Asn Arg Ser Val Ile Phe Ser
 385 390 395 400
 Ser Glu Arg Leu Ser Glu Glu Lys Thr Pro Asp Asn Leu Thr Ser
 405 410 415
 Gln Leu Gln Gln Pro Ile Glu Leu Lys Ser Gly Arg Leu Val Leu Lys
 420 425 430
 Asp Arg Ala Val Leu Ser Ala Pro Ser Leu Ser Gln Asp Pro Gln Ala
 435 440 445
 Leu Leu Ile Met Glu Ala Gly Thr Ser Leu Lys Thr Ser Ser Asp Leu
 450 455 460
 Lys Leu Ala Thr Leu Ser Ile Pro Leu His Ser Leu Asp Thr Glu Lys
 465 470 475 480
 Ser Val Thr Ile His Ala Pro Asn Leu Ser Ile Gln Lys Ile Phe Leu
 485 490 495
 Ser Asn Ser Gly Asp Glu Asn Phe Tyr Glu Asn Val Glu Leu Ser
 500 505 510
 Lys Glu Gln Asn Asn Ile Pro Leu Leu Thr Leu Pro Lys Glu Gln Ser
 515 520 525
 His Leu His Leu Pro Asp Gly Asn Leu Ser Ser His Phe Gly Tyr Gln
 530 535 540
 Gly Asp Trp Thr Phe Ser Trp Lys Asp Ser Asp Glu Gly His Ser Leu
 545 550 555 560
 Ile Ala Asn Trp Thr Pro Lys Asn Tyr Val Pro His Pro Glu Arg Gln
 565 570 575
 Ser Thr Leu Val Ala Asn Thr Leu Trp Asn Thr Tyr Ser Asp Met Gln
 580 585 590
 Ala Val Gln Ser Met Ile Asn Thr Thr Ala His Gly Gly Ala Tyr Leu
 595 600 605
 Phe Gly Thr Trp Gly Ser Ala Val Ser Asn Leu Phe Tyr Val His Asp
 610 615 620
 Ser Ser Gly Lys Pro Ile Asp Asn Trp His His Arg Ser Leu Gly Tyr
 625 630 635 640
 Leu Phe Gly Ile Ser Thr His Ser Leu Asp Asp His Ser Phe Cys Leu


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        645                650                655
Ala Ala Gly Gln Leu Leu Gly Lys Ser Ser Asp Ser Phe Ile Thr Ser
        660                665                670
Thr Glu Thr Thr Ser Tyr Ile Ala Thr Val Gln Ala Gln Leu Ala Thr
        675                680                685
Ser Leu Met Lys Ile Ser Ala Gln Ala Cys Tyr Asn Glu Ser Ile His
        690                695                700
Glu Leu Lys Thr Lys Tyr Arg Ser Phe Ser Lys Glu Gly Phe Gly Ser
        705                710                715                720
Trp His Ser Val Ala Val Ser Gly Glu Val Cys Ala Ser Ile Pro Ile
        725                730                735
Val Ser Asn Gly Ser Gly Leu Phe Ser Ser Phe Ser Ile Phe Ser Lys
        740                745                750
Leu Gln Gly Phe Ser Gly Thr Gln Asp Gly Phe Glu Glu Ser Ser Gly
        755                760                765
Glu Ile Arg Ser Phe Ser Ala Ser Ser Phe Arg Asn Ile Ser Leu Pro
        770                775                780
Ile Gly Ile Thr Phe Glu Lys Lys Ser Gln Lys Thr Arg Thr Tyr Tyr
        785                790                795                800
Tyr Phe Leu Gly Ala Tyr Ile Gln Asp Leu Lys Arg Asp Val Glu Ser
        805                810                815
Gly Pro Val Val Leu Leu Lys Asn Ala Val Ser Trp Asp Ala Pro Met
        820                825                830
Ala Asn Leu Asp Ser Arg Ala Tyr Met Phe Arg Leu Thr Asn Gln Arg
        835                840                845
Ala Leu His Arg Leu Gln Thr Leu Leu Asn Val Ser Cys Val Leu Arg
        850                855                860
Gly Gln Ser His Ser Tyr Ser Leu Asp Leu Gly Thr Thr Tyr Arg Phe
        865                870                875                880

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<210> 176

<211> 982

<212> PRT

<213> Chlamydia

<220>

<221> VARIANT

<222> 981

<223> Xaa = Any Amino Acid

<400> 176

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Met Ile Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val Ser Phe
 1          5          10          15
Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala
 20          25          30
Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Leu Pro
 35          40          45
Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg
 50          55          60
Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala
 65          70          75          80
Ala Leu Ser Asn Ser Ala Ala Asp Gly Leu Phe Thr Ile Glu Gly Phe
 85          90          95
Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val Leu Pro
100          105          110
Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr Thr Ser Thr
115          120          125
Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu Asn
130          135          140
Asn Glu Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp Gly Gly
145          150          155          160

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Ala Ile Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys Leu Cys
 165 170 175
 Val Phe Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys Gln Val
 180 185 190
 Val Thr Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Phe Val
 195 200 205
 Ala Asn Val Ala Gly Val Arg Gly Gly Ile Ala Val Gln Asp
 210 215 220
 Gly Gln Gln Gly Val Ser Ser Thr Ser Thr Glu Asp Pro Val Val
 225 230 235
 Ser Phe Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val Ala Arg
 245 250 255
 Val Gly Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu Asn Asn
 260 265 270
 Gly Lys Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr Ile Ala
 275 280 285
 Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr Ser Asn Asn Tyr
 290 295 300
 Gly Asp Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala Gly Ser
 305 310 315
 Asn Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly Val Val Phe Phe
 325 330 335
 Ser Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile Tyr Ala Lys Lys
 340 345 350
 Leu Ser Val Ala Asn Cys Gly Pro Val Gln Phe Leu Arg Asn Ile Ala
 355 360 365
 Asn Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly Glu Leu Ser Leu
 370 375 380
 Ser Ala Asp Tyr Gly Asp Ile Ile Phe Asp Gly Asn Leu Lys Arg Thr
 385 390 395
 Ala Lys Glu Asn Ala Ala Asp Val Asn Gly Val Thr Val Ser Ser Gln
 405 410 415
 Ala Ile Ser Met Gly Ser Gly Gly Lys Ile Thr Thr Leu Arg Ala Lys
 420 425 430
 Ala Gly His Gln Ile Leu Phe Asn Asp Pro Ile Glu Met Ala Asn Gly
 435 440 445
 Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu Leu Lys Ile Asn Asp Gly
 450 455 460
 Glu Gly Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly Ser Ser Thr Leu
 465 470 475
 Tyr Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val Leu Arg Glu Lys
 485 490 495
 Ala Lys Leu Ser Val Asn Ser Leu Ser Gln Thr Gly Gly Ser Leu Tyr
 500 505 510
 Met Glu Ala Gly Ser Thr Leu Asp Phe Val Thr Pro Gln Pro Pro Gln
 515 520 525
 Gln Pro Pro Ala Ala Asn Gln Leu Ile Thr Leu Ser Asn Leu His Leu
 530 535 540
 Ser Leu Ser Ser Leu Leu Ala Asn Asn Ala Val Thr Asn Pro Pro Thr
 545 550 555
 Asn Pro Pro Ala Gln Asp Ser His Pro Ala Val Ile Gly Ser Thr Thr
 565 570 575
 Ala Gly Ser Val Thr Ile Ser Gly Pro Ile Phe Phe Glu Asp Leu Asp
 580 585 590
 Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu Gly Ser Asn Gln Lys Ile
 595 600 605
 Asn Val Leu Lys Leu Gln Leu Gly Thr Lys Pro Pro Ala Asn Ala Pro
 610 615 620
 Ser Asp Leu Thr Leu Gly Asn Glu Met Pro Lys Tyr Gly Tyr Gln Gly
 625 630 635
 Ser Trp Lys Leu Ala Trp Asp Pro Asn Thr Ala Asn Asn Gly Pro Tyr
 640

645
 Thr Leu Lys Ala Thr Trp Thr Lys Thr Gly Tyr Asn Pro Gly Pro Glu
 660
 Arg Val Ala Ser Leu Val Pro Asn Ser Leu Trp Gly Ser Ile Leu Asp
 675
 Ile Arg Ser Ala His Ser Ala Ile Gln Ala Ser Val Asp Gly Arg Ser
 690
 Tyr Cys Arg Gly Leu Trp Val Ser Gly Val Ser Asn Phe Phe Tyr His
 705
 Asp Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile Ser Gly Gly Tyr
 720
 Ser Leu Gly Ala Asn Ser Tyr Phe Gly Ser Ser Met Phe Gly Leu Ala
 735
 Phe Thr Glu Val Phe Gly Arg Ser Lys Asp Tyr Val Val Cys Arg Ser
 750
 Asn His His Ala Cys Ile Gly Ser Val Tyr Leu Ser Thr Gln Gln Ala
 765
 Leu Cys Gly Ser Tyr Leu Phe Gly Asp Ala Phe Ile Arg Ala Ser Tyr
 780
 Gly Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr Phe Ala Glu Glu
 800
 Ser Asp Val Arg Trp Asp Asn Asn Cys Leu Ala Gly Glu Ile Gly Ala
 815
 Gly Leu Pro Ile Val Ile Thr Pro Ser Lys Leu Tyr Leu Asn Glu Leu
 830
 Arg Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu Ser Phe
 845
 Thr Glu Glu Gly Asp Gln Ala Arg Ala Phe Lys Ser Gly His Leu Leu
 860
 Asn Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser Ser Thr
 875
 His Pro Asn Lys Tyr Ser Phe Met Ala Ala Tyr Ile Cys Asp Ala Tyr
 890
 Arg Thr Ile Ser Gly Thr Glu Thr Thr Leu Leu Ser His Gln Glu Thr
 905
 Trp Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Val Val Arg
 920
 Gly Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His
 935
 945
 Gly Arg Tyr Glu Tyr Arg Asp Ala Ser Arg Gly Tyr Gly Leu Ser Ala
 955
 Gly Ser Lys Val Xaa Phe
 970
 980

<210> 177

<211> 964

<212> PRT

<213> Chlamydia

<400> 177

Met Lys Lys Ala Phe Phe Phe Phe Leu Ile Gly Asn Ser Leu Ser Gly
 1 5 10 15
 Leu Ala Arg Glu Val Pro Ser Arg Ile Phe Leu Met Pro Asn Ser Val
 20 25 30
 Pro Asp Pro Thr Lys Glu Ser Leu Ser Asn Lys Ile Ser Leu Thr Gly
 35 40 45
 Asp Thr His Asn Leu Thr Asn Cys Tyr Leu Asp Asn Leu Arg Tyr Ile
 50 55 60
 Leu Ala Ile Leu Gln Lys Thr Pro Asn Glu Gly Ala Ala Val Thr Ile
 65 70 75 80
 Thr Asp Tyr Leu Ser Phe Phe Asp Thr Gln Lys Glu Gly Ile Tyr Phe

85										90										95									
Ala	Lys	Asn	Leu	Thr	Pro	Glu	Ser	Gly	Gly	Ala	Ile	Gly	Tyr	Ala	Ser														
Pro			Asn	Ser	Pro	Thr	Val	Glu	Ile	Arg	Asp	Thr	Ile	Gly	Pro	Val	Ile												
Phe			Glu	Asn	Asn	Thr	Cys	Cys	Arg	Leu	Phe	Thr	Trp	Arg	Asn	Pro	Tyr												
Ala			Ala	Asp	Lys	Ile	Arg	Glu	Gly	Gly	Ala	Ile	His	Ala	Gln	Asn	Leu												
Tyr			Ile	Asn	His	Asn	His	Asp	Val	Val	Gly	Phe	Met	Lys	Asn	Phe	Ser												
Tyr			Val	Gln	Gly	Gly	Ala	Ile	Ser	Thr	Ala	Asn	Thr	Phe	Val	Val	Ser												
Glu			Asn	Gln	Ser	Cys	Phe	Leu	Phe	Met	Asp	Asn	Ile	Cys	Ile	Gln	Thr												
Asn			Thr	Ala	Gly	Lys	Gly	Gly	Ala	Ile	Tyr	Ala	Gly	Thr	Ser	Asn	Ser												
Phe			Glu	Ser	Asn	Asn	Cys	Asp	Leu	Phe	Phe	Ile	Asn	Asn	Ala	Cys	Cys												
Ala			Gly	Gly	Ala	Ile	Phe	Ser	Pro	Ile	Cys	Ser	Leu	Thr	Gly	Asn	Arg												
Gly			Asn	Ile	Val	Phe	Tyr	Asn	Asn	Arg	Cys	Phe	Lys	Asn	Val	Glu	Thr												
Ala			Ser	Ser	Glu	Ala	Ser	Asp	Gly	Gly	Ala	Ile	Lys	Val	Thr	Thr	Arg												
Leu			Asp	Val	Thr	Gly	Asn	Arg	Gly	Arg	Ile	Phe	Phe	Ser	Asp	Asn	Ile												
Thr			Lys	Asn	Tyr	Gly	Gly	Ala	Ile	Tyr	Ala	Pro	Val	Val	Thr	Leu	Val												
Asp			Asn	Gly	Pro	Thr	Tyr	Phe	Ile	Asn	Asn	Ile	Ala	Asn	Asn	Lys	Gly												
Gly			Ala	Ile	Tyr	Ile	Asp	Gly	Thr	Ser	Asn	Ser	Lys	Ile	Ser	Ala	Asp												
Arg			His	Ala	Ile	Ile	Phe	Asn	Glu	Asn	Ile	Val	Thr	Asn	Val	Thr	Asn												

Gln Pro Met Leu Ser Ile Ser Glu Ala Ser Asp Asn Gln Leu Gln Ser
 580 585 590
 Glu Asn Ile Asp Phe Ser Gly Leu Asn Val Pro His Tyr Gly Trp Gln
 595 600 605
 Gly Leu Trp Thr Trp Gly Trp Ala Lys Thr Gln Asp Pro Glu Pro Ala
 610 615 620
 Ser Ser Ala Thr Ile Thr Asp Pro Gln Lys Ala Arg Phe His Arg
 625 630 635 640
 Thr Leu Leu Leu Thr Trp Leu Pro Ala Gly Tyr Val Pro Ser Pro Lys
 645 650 655
 His Arg Ser Pro Leu Ile Ala Asn Thr Leu Trp Gly Asn Met Leu Leu
 660 665 670
 Ala Thr Glu Ser Leu Lys Asn Ser Ala Glu Leu Thr Pro Ser Gly His
 675 680 685
 Pro Phe Trp Gly Ile Thr Gly Gly Gly Leu Gly Met Met Val Tyr Gln
 690 695 700
 Asp Pro Arg Glu Asn His Pro Gly Phe His Met Arg Ser Ser Gly Tyr
 705 710 715 720
 Ser Ala Gly Met Ile Ala Gly Gln Thr His Thr Phe Ser Leu Lys Phe
 725 730 735
 Ser Gln Thr Tyr Thr Lys Leu Asn Glu Arg Tyr Ala Lys Asn Asn Val
 740 745 750
 Ser Ser Lys Asn Tyr Ser Cys Gln Gly Glu Met Leu Phe Ser Leu Gln
 755 760 765
 Glu Gly Phe Leu Leu Thr Lys Leu Val Gly Leu Tyr Ser Tyr Gly Asp
 770 775 780
 His Asn Cys His His Phe Tyr Thr Gln Gly Glu Asn Leu Thr Ser Gln
 785 790 795 800
 Gly Thr Phe Arg Ser Gln Thr Met Gly Gly Ala Val Phe Phe Asp Leu
 805 810 815
 Pro Met Lys Pro Phe Gly Ser Thr His Ile Leu Thr Ala Pro Phe Leu
 820 825 830
 Gly Ala Leu Gly Ile Tyr Ser Ser Leu Ser His Phe Thr Glu Val Gly
 835 840 845
 Ala Tyr Pro Arg Ser Phe Ser Thr Lys Thr Pro Leu Ile Asn Val Leu
 850 855 860
 Val Pro Ile Gly Val Lys Gly Ser Phe Met Asn Ala Thr His Arg Pro
 865 870 875 880
 Gln Ala Trp Thr Val Glu Leu Ala Tyr Gln Pro Val Leu Tyr Arg Gln
 885 890 895
 Glu Pro Gly Ile Ala Thr Gln Leu Leu Ala Ser Lys Gly Ile Trp Phe
 900 905 910
 Gly Ser Gly Ser Pro Ser Ser Arg His Ala Met Ser Tyr Lys Ile Ser
 915 920 925
 Gln Gln Thr Gln Pro Leu Ser Trp Leu Thr Leu His Phe Gln Tyr His
 930 935 940
 Gly Phe Tyr Ser Ser Thr Phe Cys Asn Tyr Leu Asn Gly Glu Ile
 945 950 955 960
 Ala Leu Arg Phe

<210> 178
 <211> 1530
 <212> PRT
 <213> Chlamydia

<400> 178
 Met Ser Ser Glu Lys Asp Ile Lys Ser Thr Cys Ser Lys Phe Ser Leu
 1 5 10 15
 Ser Val Val Ala Ile Leu Ala Ser Val Ser Gly Leu Ala Ser Cys
 20 25 30

Val Asp Leu His Ala Gly Gly Gln Ser Val Asn Glu Leu Val Tyr Val
 35 40 45
 Gly Pro Gln Ala Val Leu Leu Leu Asp Gln Ile Arg Asp Leu Phe Val
 50 55 60
 Gly Ser Lys Asp Ser Gln Ala Glu Gly Gln Tyr Arg Leu Ile Val Gly
 65 70 75 80
 Asp Pro Ser Ser Phe Gln Glu Lys Asp Ala Asp Thr Leu Pro Gly Lys
 85 90 95
 Val Glu Gln Ser Thr Leu Phe Ser Val Thr Asn Pro Val Val Phe Gln
 100 105 110
 Gly Val Asp Gln Gln Asp Gln Val Ser Ser Gln Gly Leu Ile Cys Ser
 115 120 125
 Phe Thr Ser Ser Asn Leu Asp Ser Pro Arg Asp Gly Glu Ser Phe Leu
 130 135 140
 Gly Ile Ala Phe Val Gly Asp Ser Ser Lys Ala Gly Ile Thr Leu Thr
 145 150 155 160
 Asp Val Lys Ala Ser Leu Ser Gly Ala Ala Leu Tyr Ser Thr Glu Asp
 165 170 175
 Leu Ile Phe Glu Lys Ile Lys Gly Gly Leu Glu Phe Ala Ser Cys Ser
 180 185 190
 Ser Leu Glu Gln Gly Gly Ala Cys Ala Ala Gln Ser Ile Leu Ile His
 195 200 205
 Asp Cys Gln Gly Leu Gln Val Lys His Cys Thr Thr Ala Val Asn Ala
 210 215 220
 Glu Gly Ser Ser Ala Asn Asp His Leu Gly Phe Gly Gly Ala Phe
 225 230 235 240
 Phe Val Thr Gly Ser Leu Ser Gly Glu Lys Ser Leu Tyr Met Pro Ala
 245 250 255
 Gly Asp Met Val Val Ala Asn Cys Asp Gly Ala Ile Ser Phe Glu Gly
 260 265 270
 Asn Ser Ala Asn Phe Ala Asn Gly Gly Ala Ile Ala Ala Ser Gly Lys
 275 280 285
 Val Leu Phe Val Ala Asn Asp Lys Lys Thr Ser Phe Ile Glu Asn Arg
 290 295 300
 Ala Leu Ser Gly Gly Ala Ile Ala Ala Ser Ser Asp Ile Ala Phe Gln
 305 310 315 320
 Asn Cys Ala Glu Leu Val Phe Lys Gly Asn Cys Ala Ile Gly Thr Glu
 325 330 335
 Asp Lys Gly Ser Leu Gly Gly Gly Ala Ile Ser Ser Leu Gly Thr Val
 340 345 350
 Leu Leu Gln Gly Asn His Gly Ile Thr Cys Asp Lys Asn Glu Ser Ala
 355 360 365
 Ser Gln Gly Gly Ala Ile Phe Gly Lys Asn Cys Gln Ile Ser Asp Asn
 370 375 380
 Glu Gly Pro Val Val Phe Arg Asp Ser Thr Ala Cys Leu Gly Gly Gly
 385 390 395 400
 Ala Ile Ala Ala Gln Glu Ile Val Ser Ile Gln Asn Asn Gln Ala Gly
 405 410 415
 Ile Ser Phe Glu Gly Gly Lys Ala Ser Phe Gly Gly Ile Ala Cys
 420 425 430
 Gly Ser Phe Ser Ser Ala Gly Gly Ala Ser Val Leu Gly Thr Ile Asp
 435 440 445
 Ile Ser Lys Asn Leu Gly Ala Ile Ser Phe Ser Arg Thr Leu Cys Thr
 450 455 460
 Thr Ser Asp Leu Gly Gln Met Glu Tyr Gln Gly Gly Gly Ala Leu Phe
 465 470 475 480
 Gly Glu Asn Ile Ser Leu Ser Glu Asn Ala Gly Val Leu Thr Phe Lys
 485 490 495
 Asp Asn Ile Val Lys Thr Phe Ala Ser Asn Gly Lys Ile Leu Gly Gly
 500 505 510
 Gly Ala Ile Leu Ala Thr Gly Lys Val Glu Ile Thr Asn Asn Ser Gly

[illegible]

Thr Leu Cys Ser Tyr Gly Phe Lys Gln Asp Ala Gly Ala Lys Leu Val
 1010 1015 1020
 Leu Ala Ala Gly Ser Lys Leu Lys Ile Leu Asp Ser Gly Thr Pro Val
 1025 1030 1035 1040
 Gln Gly His Ala Ile Ser Lys Pro Glu Ala Glu Ile Glu Ser Ser Ser
 1045 1050 1055
 Glu Pro Glu Gly Ala His Ser Leu Trp Ile Ala Lys Asn Ala Gln Thr
 1060 1065 1070
 Thr Val Pro Met Val Asp Ile His Thr Ile Ser Val Asp Leu Ala Ser
 1075 1080 1085
 Phe Ser Ser Ser Gln Gln Glu Gly Thr Val Glu Ala Pro Gln Val Ile
 1090 1095 1100
 Val Pro Gly Gly Ser Tyr Val Arg Ser Gly Glu Leu Asn Leu Glu Leu
 1105 1110 1115 1120
 Val Asn Thr Thr Gly Thr Gly Tyr Glu Asn His Ala Leu Leu Lys Asn
 1125 1130 1135
 Glu Ala Lys Val Pro Leu Met Ser Phe Val Ala Ser Ser Asp Glu Ala
 1140 1145 1150
 Ser Ala Glu Ile Ser Asn Leu Ser Val Ser Asp Leu Gln Ile His Val
 1155 1160 1165
 Ala Thr Pro Glu Ile Glu Glu Asp Thr Tyr Gly His Met Gly Asp Trp
 1170 1175 1180
 Ser Glu Ala Lys Ile Gln Asp Gly Thr Leu Val Ile Asn Trp Asn Pro
 1185 1190 1195 1200
 Thr Gly Tyr Arg Leu Asp Pro Gln Lys Ala Gly Ala Leu Val Phe Asn
 1205 1210 1215
 Ala Leu Trp Glu Glu Gly Ala Val Leu Ser Ala Leu Lys Asn Ala Arg
 1220 1225 1230
 Phe Ala His Asn Leu Thr Ala Gln Arg Met Glu Phe Asp Tyr Ser Thr
 1235 1240 1245
 Asn Val Trp Gly Phe Ala Phe Gly Gly Phe Arg Thr Leu Ser Ala Glu
 1250 1255 1260
 Asn Leu Val Ala Ile Asp Gly Tyr Lys Gly Ala Tyr Gly Gly Ala Ser
 1265 1270 1275 1280
 Ala Gly Val Asp Ile Gln Leu Met Glu Asp Phe Val Leu Gly Val Ser
 1285 1290 1295
 Gly Ala Ala Phe Leu Gly Lys Met Asp Ser Gln Lys Phe Asp Ala Glu
 1300 1305 1310
 Val Ser Arg Lys Gly Val Val Gly Ser Val Tyr Thr Gly Phe Leu Ala
 1315 1320 1325
 Gly Ser Trp Phe Phe Lys Gly Gln Tyr Ser Leu Gly Glu Thr Gln Asn
 1330 1335 1340
 Asp Met Lys Thr Arg Tyr Gly Val Leu Gly Glu Ser Ser Ala Ser Trp
 1345 1350 1355 1360
 Thr Ser Arg Gly Val Leu Ala Asp Ala Leu Val Glu Tyr Arg Ser Leu
 1365 1370 1375
 Val Gly Pro Val Arg Pro Thr Phe Tyr Ala Leu His Phe Asn Pro Tyr
 1380 1385 1390
 Val Glu Val Ser Tyr Ala Ser Met Lys Phe Pro Gly Phe Thr Glu Gln
 1395 1400 1405
 Gly Arg Glu Ala Arg Ser Phe Glu Asp Ala Ser Leu Thr Asn Ile Thr
 1410 1415 1420
 Ile Pro Leu Gly Met Lys Phe Glu Leu Ala Phe Ile Lys Gly Gln Phe
 1425 1430 1435 1440
 Ser Glu Val Asn Ser Leu Gly Ile Ser Tyr Ala Trp Glu Ala Tyr Arg
 1445 1450 1455
 Lys Val Glu Gly Gly Ala Val Gln Leu Leu Glu Ala Gly Phe Asp Trp
 1460 1465 1470
 Glu Gly Ala Pro Met Asp Leu Pro Arg Gln Glu Leu Arg Val Ala Leu
 1475 1480 1485
 Glu Asn Asn Thr Glu Trp Ser Ser Tyr Phe Ser Thr Val Leu Gly Leu

1490 1495 1500
 Thr Ala Phe Cys Gly Gly Phe Thr Ser Thr Asp Ser Lys Leu Gly Tyr
 1505 1510 1515 1520
 Glu Ala Asn Thr Gly Leu Arg Leu Ile Phe
 1525 1530

<210> 179
 <211> 1776
 <212> PRT
 <213> Chlamydia

<400> 179
 Ala Ile Met Lys Phe Met Ser Ala Thr Ala Val Phe Ala Ala Val Leu
 1 5 10 15
 Ser Ser Val Thr Glu Ala Ser Ser Ile Gln Asp Gln Ile Lys Asn Thr
 20 25 30
 Asp Cys Asn Val Ser Lys Val Gly Tyr Ser Thr Ser Gln Ala Phe Thr
 35 40 45
 Asp Met Met Leu Ala Asp Asn Thr Glu Tyr Arg Ala Ala Asp Ser Val
 50 55 60
 Ser Phe Tyr Asp Phe Ser Thr Ser Ser Gly Leu Pro Arg Lys His Leu
 65 70 75 80
 Ser Ser Ser Ser Glu Ala Ser Pro Thr Thr Glu Gly Val Ser Ser Ser
 85 90 95
 Ser Ser Gly Glu Asn Thr Glu Asn Ser Gln Asp Ser Ala Pro Ser Ser
 100 105 110
 Gly Glu Thr Asp Lys Lys Thr Glu Glu Leu Asp Asn Gly Gly Ile
 115 120 125
 Ile Tyr Ala Arg Glu Lys Leu Thr Ile Ser Glu Ser Gln Asp Ser Leu
 130 135 140
 Ser Asn Pro Ser Ile Glu Leu His Asp Asn Ser Phe Phe Phe Gly Glu
 145 150 155 160
 Gly Glu Val Ile Phe Asp His Arg Val Ala Leu Lys Asn Gly Gly Ala
 165 170 175
 Ile Tyr Gly Glu Lys Glu Val Val Phe Glu Asn Ile Lys Ser Leu Leu
 180 185 190
 Val Glu Val Asn Ile Ser Val Glu Lys Gly Gly Ser Val Tyr Ala Lys
 195 200 205
 Glu Arg Val Ser Leu Glu Asn Val Thr Glu Ala Thr Phe Ser Ser Asn
 210 215 220
 Gly Gly Glu Gln Gly Gly Gly Gly Ile Tyr Ser Glu Gln Asp Met Leu
 225 230 235 240
 Ile Ser Asp Cys Asn Asn Val His Phe Gln Gly Asn Ala Ala Gly Ala
 245 250 255
 Thr Ala Val Lys Gln Cys Leu Asp Glu Glu Met Ile Val Leu Leu Thr
 260 265 270
 Glu Cys Val Asp Ser Leu Ser Glu Asp Thr Leu Asp Ser Thr Pro Glu
 275 280 285
 Thr Glu Gln Thr Lys Ser Asn Gly Asn Gln Asp Gly Ser Ser Glu Thr
 290 295 300
 Lys Asp Thr Gln Val Ser Glu Ser Pro Glu Ser Thr Pro Ser Pro Asp
 305 310 315 320
 Asp Val Leu Gly Lys Gly Gly Gly Ile Tyr Thr Glu Lys Ser Leu Thr
 325 330 335
 Ile Thr Gly Ile Thr Gly Thr Ile Asp Phe Val Ser Asn Ile Ala Thr
 340 345 350
 Asp Ser Gly Ala Gly Val Phe Thr Lys Glu Asn Leu Ser Cys Thr Asn
 355 360 365
 Thr Asn Ser Leu Gln Phe Leu Lys Asn Ser Ala Gly Gln His Gly Gly
 370 375 380
 Gly Ala Tyr Val Thr Gln Thr Met Ser Val Thr Asn Thr Thr Ser Glu

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385                               390                               395                               400
Ser Ile Thr Thr Pro Pro Leu Val Gly Glu Val Ile Phe Ser Glu Asn
405                               410                               415
Thr Ala Lys Gly His Gly Gly Gly Ile Cys Thr Asn Lys Leu Ser Leu
420                               425
Ser Asn Leu Lys Thr Val Thr Leu Thr Lys Asn Ser Ala Lys Glu Ser
435                               440                               445
Gly Gly Ala Ile Phe Thr Asp Leu Ala Ser Ile Pro Thr Thr Asp Thr
450                               455                               460
Pro Glu Ser Ser Thr Pro Ser Ser Ser Ser Pro Ala Ser Thr Pro Glu
465                               470                               475                               480
Val Val Ala Ser Ala Lys Ile Asn Arg Phe Phe Ala Ser Thr Ala Glu
485                               490                               495
Pro Ala Ala Pro Ser Leu Thr Glu Ala Glu Ser Asp Gln Thr Asp Gln
500                               505                               510
Thr Glu Thr Ser Asp Thr Asn Ser Asp Ile Asp Val Ser Ile Glu Asn
515                               520                               525
Ile Leu Asn Val Ala Ile Asn Gln Asn Thr Ser Ala Lys Lys Gly Gly
530                               535                               540
Ala Ile Tyr Gly Lys Lys Ala Lys Leu Ser Arg Ile Asn Asn Leu Glu
545                               550                               555                               560
Leu Ser Gly Asn Ser Ser Gln Asp Val Gly Gly Gly Leu Cys Leu Thr
565                               570                               575
Glu Ser Val Glu Phe Asp Ala Ile Gly Ser Leu Leu Ser His Tyr Asn
580                               585                               590
Ser Ala Ala Lys Glu Gly Gly Val Ile His Ser Lys Thr Val Thr Leu
595                               600                               605
Ser Asn Leu Lys Ser Thr Phe Thr Phe Ala Asp Asn Thr Val Lys Ala
610                               615                               620
Ile Val Glu Ser Thr Pro Glu Ala Pro Glu Glu Ile Pro Pro Val Glu
625                               630                               635                               640
Gly Glu Glu Ser Thr Ala Thr Glu Asn Pro Asn Ser Asn Thr Glu Gly
645                               650                               655
Ser Ser Ala Asn Thr Asn Leu Glu Gly Ser Gln Gly Asp Thr Ala Asp
660                               665                               670
Thr Gly Thr Gly Val Val Asn Asn Glu Ser Gln Asp Thr Ser Asp Thr
675                               680                               685
Gly Asn Ala Glu Ser Gly Glu Gln Leu Gln Asp Ser Thr Gln Ser Asn
690                               695                               700
Glu Glu Asn Thr Leu Pro Asn Ser Ser Ile Asp Gln Ser Asn Glu Asn
705                               710                               715                               720
Thr Asp Glu Ser Ser Asp Ser His Thr Glu Glu Ile Thr Asp Glu Ser
725                               730                               735
Val Ser Ser Ser Ser Lys Ser Gly Ser Ser Thr Pro Gln Asp Gly Gly
740                               745                               750
Ala Ala Ser Ser Gly Ala Pro Ser Gly Asp Gln Ser Ile Ser Ala Asn
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Ser	Leu	Ser	175	Gly	Ile	Thr	Lys	180	Ala	Thr	Phe	Ser	185	Cys	Asn	Ser	Ala
Val	Pro	Ala	195	Pro	Val	Lys	Lys	200	Thr	Glu	Pro	Lys	205	Ala	Gln	Thr	Ala
Ser	Glu	Thr	210	Ser	Gly	Ser	Ser	215	Ser	Ser	Gly	Asn	220	Asp	Ser	Val	Ser
Ser	Pro	Ser	225	Ser	Ser	Arg	Ala	230	Glu	Pro	Ala	Ala	235	Ala	Asn	Leu	Gln
His	Phe	Ile	240	Cys	Ala	Thr	Ala	245	Thr	Pro	Ala	Ala	250	Gln	Thr	Asp	Thr
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 Glu Gln Pro Ala Ala Ser Ala Ala Thr Ser Thr Pro Lys Ser Ala
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 Pro Val Ser Thr Ala Leu Ser Thr Pro Ser Ser Ser Thr Val Ser Ser
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<211> 2466

<212> DNA

<213> Chlamydia

<400> 187

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 <212> DNA
 <213> Chlamydia

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<210> 189
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35 40 45
His Ala Ser Gln Asp Asp Pro Leu Tyr Val Leu Gly Asn Ser Tyr Cys
50 55 60
Trp Phe Val Ser Lys Leu His Ile Thr Asp Phe Arg Phe Leu Ser Phe
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Lys Glu Lys Gly Asp Leu Ser Ile Gln Asn Phe Arg Phe Leu Ser Phe
85 90 95
Thr Asp Cys Ser Ser Lys Glu Ser Ser Pro Ser Ile Ile His Gln Lys
100 105 110
Asn Gly Gln Leu Ser Leu Arg Asn Asn Gly Ser Met Ser Phe Cys Arg
115 120 125
Asn His Ala Glu Gly Ser Gly Gly Ala Ile Ser Ala Asp Ala Phe Ser
130 135 140
Leu Gln His Asn Tyr Leu Phe Thr Ala Phe Glu Glu Asn Ser Ser Lys
145 150 155
Gly Asn Gly Gly Ala Ile Gln Ala Gln Thr Phe Ser Leu Ser Arg Asn
160 165 170 175
Val Ser Pro Ile Ser Phe Ala Arg Asn Arg Ala Asp Leu Asn Gly Gly
180 185 190
Ala Ile Cys Cys Ser Asn Leu Ile Cys Ser Gly Asn Val Asn Pro Leu
195 200 205
Phe Phe Thr Gly Asn Ser Ala Thr Asn Gly Gly Xaa Ile Cys Cys Ile
210 215 220
Ser Asp Leu Asn Thr Ser Glu Lys Gly Ser Leu Ser Leu Ala Cys Asn
225 230 235 240
Gln Xaa Thr Leu Phe Ala Ser Asn Ser Ala Lys Glu Lys Gly Gly Ala
245 250 255
Ile Tyr Ala Lys His Met Val Leu Arg Tyr Asn Gly Pro Val Ser Phe
260 265 270
Ile Asn Asn Ser Ala Lys Ile Gly Gly Ala Ile Ala Ile Gln Ser Gly
275 280 285
Gly Ser Leu Ser Ile Leu Ala Gly Glu Gly Ser Val Leu Phe Gln Asn
290 295 300
Asn Ser Gln Arg Thr Ser Asp Gln Gly Leu Val Arg Asn Ala Ile Tyr
305 310 315 320
Leu Glu Lys Asp Ala Ile Leu Ser Ser Leu Glu Ala Arg Asn Gly Asp
325 330 335
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Phe	Ser	Ser	370	Glu	Arg	Leu	Ser	Glu	375	Glu	Leu	Lys	Thr	Pro	380	Asp	Asn	Leu
Thr	Ser	Gln	385	Leu	Gln	Gln	Pro	Ile	390	Glu	Leu	Lys	Ser	Gly	400	Arg	Leu	Val
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Gln	Ala	Leu	420	Ile	Met	Glu	Ala	Gly	425	Thr	Ser	Leu	Lys	Thr	430	Ser	Xaa	
Asp	Leu	Lys	435	Leu	Xaa	Thr	Xaa	Ser	440	Ile	Pro	Leu	His	Ser	445	Leu	Asp	Thr
Glu	Lys	Ser	450	Val	Thr	Ile	His	Ala	455	Pro	Asn	Leu	Ser	Ile	460	Gln	Lys	Ile
Phe	Leu	Ser	465	Asn	Ser	Gly	Asp	Glu	470	Asn	Phe	Thr	Glu	Asn	475	Val	Glu	Leu
Leu	Ser	Lys	480	Glu	Gln	Asn	Asn	Ile	485	Pro	Leu	Leu	Thr	Leu	490	Pro	Lys	Glu
Gln	Ser	His	495	Leu	His	Leu	Pro	Asp	500	Gly	Asn	Leu	Ser	Ser	505	His	Phe	Gly
Tyr	Gln	Gly	510	Asp	Trp	Thr	Phe	Ser	515	Trp	Lys	Asp	Ser	Asp	520	Glu	Gly	His
Ser	Leu	Ile	525	Ala	Asn	Trp	Thr	Pro	530	Lys	Asn	Tyr	Val	Pro	535	His	Pro	Glu
Arg	Gln	Ser	540	Thr	Leu	Val	Ala	Asn	545	Leu	Thr	Asn	Thr	Tyr	550	Ser	Asp	
Met	Gln	Ala	555	Val	Gln	Ser	Met	Ile	560	Asn	Thr	Thr	Ala	His	565	Gly	Gly	Ala
Tyr	Leu	Phe	570	Gly	Thr	Trp	Gly	Ser	575	Ala	Val	Ser	Asn	Leu	580	Phe	Thr	Val
His	Asp	Ser	585	Ser	Gly	Lys	Pro	Ile	590	Asn	Trp	His	His	Arg	595	Ser	Leu	
Gly	Thr	Leu	600	Phe	Gly	Ile	Ser	Thr	605	Ser	Leu	Asp	Asp	His	610	Ser	Phe	
Cys	Leu	Ala	615	Ala	Gly	Gln	Leu	Leu	620	Lys	Ser	Ser	Ser	Ser	625	Phe	Ile	
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Ser	Gly	Glu	720	Ile	Arg	Ser	Phe	Ser	725	Ala	Ser	Ser	Phe	Arg	730	Asn	Ile	Ser
Leu	Pro	Ile	735	Gly	Ile	Thr	Phe	Glu	740	Lys	Lys	Ser	Gln	Lys	745	Thr	Arg	Thr
Tyr	Thr	Tyr	750	Phe	Leu	Gly	Ala	Tyr	755	Gln	Asp	Leu	Lys	Arg	760	Asp	Val	
Glu	Ser	Gly	765	Pro	Val	Val	Leu	Leu	770	Asn	Ala	Val	Ser	Trp	775	Asp	Ala	
Pro	Met	Ala	780	Asn	Leu	Asp	Ser	Arg	785	Tyr	Met	Phe	Arg	Leu	790	Thr	Asn	

Gln Arg Ala Leu His Arg Leu Gln Thr Leu Leu Asn Val Ser Cys Val
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 Arg Phe
 865

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<211> 1006

<212> PRT

<213> Chlamydia

<400> 190

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 Ser Gly Thr Thr Val Phe Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu
 50 55 60
 Asp Asn Ser Ile Ala Ala Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu
 65 70 75 80
 Gly Ser Phe Thr Val Leu Gly Arg Gly His Ser Leu Thr Phe Glu Asn
 85 90 95
 Ile Arg Thr Ser Thr Asn Gly Ala Ala Leu Ser Asn Ser Ala Ala Asp
 100 105 110
 Gly Leu Phe Thr Ile Glu Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys
 115 120 125
 Asn Ser Leu Leu Ala Val Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser
 130 135 140
 Gln Thr Pro Thr Thr Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser
 145 150 155 160
 Lys Thr Asp Leu Leu Leu Leu Asn Asn Glu Lys Phe Ser Phe Tyr Ser
 165 170 175
 Asn Leu Val Ser Gly Asp Gly Gly Ala Ile Asp Ala Lys Ser Leu Thr
 180 185 190
 Val Gln Gly Ile Ser Lys Leu Cys Val Phe Gln Glu Asn Thr Ala Gln
 195 200 205
 Ala Asp Gly Gly Ala Cys Gln Val Val Thr Ser Phe Ser Ala Met Ala
 210 215 220
 Asn Glu Ala Pro Ile Ala Phe Val Ala Asn Val Ala Gly Val Arg Gly
 225 230 235 240
 Gly Gly Ile Ala Ala Val Gln Asp Gly Gln Gln Gly Val Ser Ser Ser
 245 250 255
 Thr Ser Thr Glu Asp Pro Val Val Ser Phe Ser Arg Asn Thr Ala Val
 260 265 270
 Glu Phe Asp Gly Asn Val Ala Arg Val Gly Gly Gly Ile Tyr Ser Tyr
 275 280 285
 Gly Asn Val Ala Phe Leu Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn
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 Val Ala Ser Pro Val Tyr Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln
 305 310 315 320
 Ala Ser Asn Thr Ser Asn Asn Tyr Gly Asp Gly Gly Ala Ile Phe Cys
 325 330 335
 Lys Asn Gly Ala Gln Ala Gly Ser Asn Asn Ser Gly Ser Val Ser Phe
 340 345 350
 Asp Gly Glu Gly Val Val Phe Phe Ser Ser Asn Val Ala Ala Gly Lys
 355 360 365
 Gly Gly Ala Ile Tyr Ala Lys Lys Leu Ser Val Ala Asn Cys Gly Pro
 370 375 380

Val Gln Phe Leu Arg Asn Ile Ala Asn Asp Gly Gly Ala Ile Tyr Leu
 385 390 400
 Gly Glu Ser Gly Glu Leu Ser Leu Ser Ala Asp Tyr Gly Asp Ile Ile
 405 415
 Phe Asp Gly Asn Leu Lys Arg Thr Ala Lys Glu Asn Ala Ala Asp Val
 420 425 430
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 450 455 460
 Asp Pro Ile Glu Met Ala Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser
 465 470 475
 Lys Leu Leu Lys Ile Asn Asp Gly Glu Gly Tyr Thr Gly Asp Ile Val
 485 490 495
 Phe Ala Asn Gly Ser Ser Thr Leu Tyr Gln Asn Val Thr Ile Glu Gln
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 595 600 605
 Pro Ile Phe Phe Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp
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 625 630 635
 Thr Lys Pro Pro Ala Asn Ala Pro Ser Asp Leu Thr Leu Gly Asn Glu
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 Lys Asp Tyr Val Val Cys Arg Ser Asn His Ala Cys Ile Gly Ser
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 835 840 845
 Cys Leu Ala Gly Glu Ile Gly Ala Gly Leu Pro Ile Val Ile Thr Pro
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 Ser Lys Leu Tyr Leu Asn Glu Leu Arg Pro Phe Val Gln Ala Glu Phe

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Lys	Phe	Asp	Arg	Cys	Ser	Ser	Thr	His	Pro	Asn	Lys	Tyr	Ser	Phe	Met
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Ala	Ala	Tyr	Ile	Cys	Asp	Ala	Tyr	Arg	Thr	Ile	Ser	Gly	Thr	Glu	Thr
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945					950				955					960	
Ala	Arg	His	Gly	Val	Val	Val	Arg	Gly	Ser	Met	Tyr	Ala	Ser	Leu	Thr
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Ser	Asn	Ile	Glu	Val	Tyr	Gly	His	Gly	Arg	Tyr	Glu	Tyr	Arg	Asp	Ala
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<211> 977
<212> PRT
<213> Chlamydia
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Thr	Lys	Glu	Ser	Leu	Ser	Asn	Lys	Ile	Ser	Leu	Thr	Gly	Asp	Thr	His
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Asn	Leu	Thr	Asn	Cys	Tyr	Leu	Asp	Asn	Leu	Arg	Tyr	Ile	Leu	Ala	Ile
65				70						75				80	
Leu	Gln	Lys	Thr	Pro	Asn	Gly	Ala	Ala	Val	Thr	Ile	Thr	Asp	Tyr	
			85					90					95		
Leu	Ser	Phe	Phe	Asp	Thr	Gln	Lys	Glu	Gly	Ile	Tyr	Phe	Ala	Lys	Asn
			100					105					110		
Leu	Thr	Pro	Glu	Ser	Gly	Gly	Ala	Ile	Gly	Tyr	Ala	Ser	Pro	Asn	Ser
			115				120				125				
Pro	Thr	Val	Glu	Ile	Arg	Asp	Thr	Ile	Gly	Pro	Val	Ile	Phe	Glu	Asn
			130			135					140				
Asn	Thr	Cys	Cys	Arg	Leu	Phe	Thr	Trp	Arg	Asn	Pro	Tyr	Ala	Ala	Asp
145					150					155					160
Lys	Ile	Arg	Glu	Gly	Gly	Ala	Ile	His	Ala	Gln	Asn	Leu	Tyr	Ile	Asn
			165					170						175	
His	Asn	His	Asp	Val	Val	Gly	Phe	Met	Lys	Asn	Phe	Ser	Tyr	Val	Gln
			180					185					190		
Gly	Gly	Ala	Ile	Ser	Thr	Ala	Asn	Thr	Phe	Val	Val	Ser	Glu	Asn	Gln
			195				200					205			
Ser	Cys	Phe	Leu	Phe	Met	Asp	Asn	Ile	Cys	Ile	Gln	Thr	Asn	Thr	Ala
			210			215					220				
Gly	Lys	Gly	Gly	Ala	Ile	Tyr	Ala	Gly	Thr	Ser	Asn	Ser	Phe	Glu	Ser
225				230						235				240	
Asn	Asn	Cys	Asp	Leu	Phe	Phe	Ile	Asn	Asn	Ala	Cys	Cys	Ala	Gly	Gly
			245					250					255		
Ala	Ile	Phe	Ser	Pro	Ile	Cys	Ser	Leu	Thr	Gly	Asn	Arg	Gly	Asn	
			260					265					270		
Val	Phe	Tyr	Asn	Asn	Arg	Cys	Phe	Lys	Asn	Val	Glu	Thr	Ala	Ser	Ser
			275				280					285			
Glu	Ala	Ser	Asp	Gly	Gly	Ala	Ile	Lys	Val	Thr	Thr	Arg	Leu	Asp	Val

290		295		300
Thr Gly Asn Arg Gly Arg Ile Phe Phe Ser Asp Asn Ile Thr Lys Asn				
305		310		315
Tyr Gly Gly Ala Ile Tyr Ala Pro Val Val Thr Leu Val Asp Asn Gly				
		325		330
Pro Thr Tyr Phe Ile Asn Asn Ile Ala Asn Asn Lys Gly Gly Ala Ile				
		340		345
Tyr Ile Asp Gly Thr Ser Asn Ser Lys Ile Ser Ala Asp Arg His Ala				
		355		360
Ile Ile Phe Asn Glu Asn Ile Val Thr Asn Val Thr Asn Ala Asn Gly				
		370		375
Thr Ser Thr Ser Ala Asn Pro Pro Arg Arg Asn Ala Ile Thr Val Ala				
385		390		395
Ser Ser Ser Gly Glu Ile Leu Leu Gly Ala Gly Ser Ser Gln Asn Leu				
		405		410
Ile Phe Tyr Asp Pro Ile Glu Val Ser Asn Ala Gly Val Ser Val Ser				
		420		425
Phe Asn Lys Glu Ala Asp Gln Thr Gly Ser Val Val Phe Ser Gly Ala				
		435		440
Thr Val Asn Ser Ala Asp Phe His Gln Arg Asn Leu Gln Thr Lys Thr				
450		455		460
Pro Ala Pro Leu Thr Leu Ser Asn Gly Phe Leu Cys Ile Glu Asp His				
465		470		475
Ala Gln Leu Thr Val Asn Arg Phe Thr Gln Thr Gly Gly Val Val Ser				
		485		490
Leu Gly Asn Gly Ala Val Leu Ser Cys Tyr Lys Asn Gly Thr Gly Asp				
		500		505
Ser Ala Ser Asn Ala Ser Ile Thr Leu Lys His Ile Gly Leu Asn Leu				
		515		520
Ser Ser Ile Leu Lys Ser Gly Ala Glu Ile Pro Leu Leu Trp Val Glu				
530		535		540
Pro Thr Asn Asn Ser Asn Asn Tyr Thr Ala Asp Thr Ala Ala Thr Phe				
545		550		555
Ser Leu Ser Asp Val Lys Leu Ser Leu Ile Asp Asp Tyr Gly Asn Ser				
		565		570
Pro Tyr Glu Ser Thr Asp Leu Thr His Ala Leu Ser Ser Gln Pro Met				
		580		585
Leu Ser Ile Ser Glu Ala Ser Asp Asn Gln Leu Gln Ser Glu Asn Ile				
		595		600
Asp Phe Ser Gly Leu Asn Val Pro His Tyr Gly Trp Gln Gly Leu Trp				
610		615		620
Thr Trp Gly Trp Ala Lys Thr Gln Asp Pro Glu Pro Ala Ser Ser Ala				
625		630		635
Thr Ile Thr Asp Pro Gln Lys Ala Asn Arg Phe His Arg Thr Leu Leu				
		645		650
Leu Thr Trp Leu Pro Ala Gly Tyr Val Pro Ser Pro Lys His Arg Ser				
		660		665
Pro Leu Ile Ala Asn Thr Leu Trp Gly Asn Met Leu Leu Ala Thr Glu				
		675		680
Ser Leu Lys Asn Ser Ala Glu Leu Thr Pro Ser Gly His Pro Phe Trp				
		695		700
Gly Ile Thr Gly Gly Gly Leu Gly Met Met Val Tyr Gln Asp Pro Arg				
705		710		715
Glu Asn His Pro Gly Phe His Met Arg Ser Ser Gly Tyr Ser Ala Gly				
		725		730
Met Ile Ala Gly Gln Thr His Thr Phe Ser Leu Lys Phe Ser Gln Thr				
		740		745
Tyr Thr Lys Leu Asn Glu Arg Tyr Ala Lys Asn Asn Val Ser Ser Lys				
		755		760
Asn Tyr Ser Cys Gln Gly Glu Met Leu Phe Ser Leu Gln Glu Gly Phe				
770		775		780

Leu Leu Thr Lys Leu Val Gly Leu Tyr Ser Tyr Gly Asp His Asn Cys
 785 790 795 800
 His His Phe Tyr Thr Gln Gly Glu Asn Leu Thr Ser Gln Gly Thr Phe
 805 810 815
 Arg Ser Gln Thr Met Gly Gly Ala Val Phe Asp Leu Pro Met Lys
 820 825 830
 Pro Phe Gly Ser Thr His Ile Leu Thr Ala Pro Phe Leu Gly Ala Leu
 835 840 845
 Gly Ile Tyr Ser Ser Leu Ser His Phe Thr Glu Val Gly Ala Tyr Pro
 850 855 860
 Arg Ser Phe Ser Thr Lys Thr Pro Leu Ile Asn Val Leu Val Pro Ile
 865 870 875 880
 Gly Val Lys Gly Ser Phe Met Asn Ala Thr His Arg Pro Gln Ala Trp
 885 890 895
 Thr Val Glu Leu Ala Tyr Gln Pro Val Leu Tyr Arg Gln Glu Pro Gly
 900 905 910
 Ile Ala Thr Gln Leu Leu Ala Ser Lys Gly Ile Trp Phe Gly Ser Gly
 915 920 925
 Ser Pro Ser Ser Arg His Ala Met Ser Tyr Lys Ile Ser Gln Gln Thr
 930 935 940
 Gln Pro Leu Ser Trp Leu Thr Leu His Phe Gln Tyr His Gly Phe Tyr
 945 950 955 960
 Ser Ser Ser Thr Phe Cys Asn Tyr Leu Asn Gly Glu Ile Ala Leu Arg
 965 970 975
 Phe

<210> 192

<211> 848

<212> PRT

<213> Chlamydia

<400> 192

Met Ala Ser His His His His His Gly Ala Ile Ser Cys Leu Arg
 1 5 10 15
 Gly Asp Val Val Ile Ser Gly Asn Lys Gly Arg Val Glu Phe Lys Asp
 20 25 30
 Asn Ile Ala Thr Arg Leu Tyr Val Glu Glu Thr Val Glu Lys Val Glu
 35 40 45
 Glu Val Glu Pro Ala Pro Gln Gln Lys Asp Asn Asn Glu Leu Ser Phe
 50 55 60
 Leu Gly Ser Val Glu Gln Ser Phe Ile Thr Ala Ala Asn Gln Ala Leu
 65 70 75 80
 Phe Ala Ser Glu Asp Gly Asp Leu Ser Pro Glu Ser Ser Ile Ser Ser
 85 90 95
 Glu Glu Leu Ala Lys Arg Arg Glu Cys Ala Gly Gly Ala Ile Phe Ala
 100 105 110
 Lys Arg Val Arg Ile Val Asp Asn Gln Glu Ala Val Val Phe Ser Asn
 115 120 125
 Asn Phe Ser Asp Ile Tyr Gly Gly Ala Ile Phe Thr Gly Ser Leu Arg
 130 135 140
 Glu Glu Asp Lys Leu Asp Gly Gln Ile Pro Glu Val Leu Ile Ser Gly
 145 150 155 160
 Asn Ala Gly Asp Val Val Phe Ser Gly Asn Ser Ser Lys Arg Asp Glu
 165 170 175
 His Leu Pro His Thr Gly Gly Gly Ala Ile Cys Thr Gln Asn Leu Thr
 180 185 190
 Ile Ser Gln Asn Thr Gly Asn Val Leu Phe Tyr Asn Asn Val Ala Cys
 195 200 205
 Ser Gly Gly Ala Val Arg Ile Glu Asp His Gly Asn Val Leu Leu Glu
 210 215 220

Ala Phe Gly Gly Asp Ile Val Phe Lys Gly Asn Ser Ser Phe Arg Ala
 225 230 235 240
 Gln Gly Ser Asp Ala Ile Tyr Phe Ala Gly Lys Glu Ser His Ile Thr
 245 250 255
 Ala Leu Asn Ala Thr Glu Gly His Ala Ile Val Phe His Asp Ala Leu
 260 265 270
 Val Phe Glu Asn Leu Lys Glu Arg Lys Ser Ala Glu Val Leu Leu Ile
 275 280 285
 Asn Ser Arg Glu Asn Pro Gly Tyr Thr Gly Ser Ile Arg Phe Leu Glu
 290 295 300
 Ala Glu Ser Lys Val Pro Gln Cys Ile His Val Gln Gln Gly Ser Leu
 310 315 320
 Glu Leu Leu Asn Gly Ala Thr Leu Cys Ser Tyr Gly Phe Lys Gln Asp
 325 330 335
 Ala Gly Ala Lys Leu Val Leu Ala Ala Gly Ser Lys Leu Lys Ile Leu
 340 345 350
 Asp Ser Gly Thr Pro Val Gln Gly His Ala Ile Ser Lys Pro Glu Ala
 355 360 365
 Glu Ile Glu Ser Ser Ser Glu Pro Glu Gly Ala His Ser Leu Thr Ile
 370 375 380
 Ala Lys Asn Ala Gln Thr Thr Val Pro Met Val Asp Ile His Thr Ile
 385 390 395 400
 Ser Val Asp Leu Ala Ser Phe Ser Ser Ser Gln Gln Glu Gly Thr Val
 405 410 415
 Glu Ala Pro Gln Val Ile Val Pro Gly Gly Ser Tyr Val Arg Ser Gly
 420 425 430
 Glu Leu Asn Leu Glu Leu Val Asn Thr Thr Gly Thr Gly Tyr Glu Asn
 435 440 445
 His Ala Leu Leu Lys Asn Glu Ala Lys Val Pro Leu Met Ser Phe Val
 450 455 460
 Ala Ser Ser Asp Glu Ala Ser Ala Glu Ile Ser Asn Leu Ser Val Ser
 465 470 475 480
 Asp Leu Gln Ile His Val Ala Thr Pro Glu Ile Glu Glu Asp Thr Tyr
 485 490 495
 Gly His Met Gly Asp Trp Ser Glu Ala Lys Ile Gln Asp Gly Thr Leu
 500 505 510
 Val Ile Asn Trp Asn Pro Thr Gly Tyr Arg Leu Asp Pro Gln Lys Ala
 515 520 525
 Gly Ala Leu Val Phe Asn Ala Leu Trp Glu Gly Ala Val Leu Ser
 530 535 540
 Ala Leu Lys Asn Ala Arg Phe Ala His Asn Leu Thr Ala Gln Arg Met
 545 550 555 560
 Glu Phe Asp Tyr Ser Thr Asn Val Trp Gly Phe Ala Phe Gly Gly Phe
 565 570 575
 Arg Thr Leu Ser Ala Glu Asn Leu Val Ala Ile Asp Gly Tyr Lys Gly
 580 585 590
 Ala Tyr Gly Gly Ala Ser Ala Gly Val Asp Ile Gln Leu Met Glu Asp
 595 600 605
 Phe Val Leu Gly Val Ser Gly Ala Ala Phe Leu Gly Lys Met Asp Ser
 610 615 620
 Gln Lys Phe Asp Ala Glu Val Ser Arg Lys Gly Val Val Gly Ser Val
 625 630 635 640
 Tyr Thr Gly Phe Leu Ala Gly Ser Trp Phe Phe Lys Gly Gln Tyr Ser
 645 650 655
 Leu Gly Glu Thr Gln Asn Asp Met Lys Thr Arg Tyr Gly Val Leu Gly
 660 665 670
 Glu Ser Ser Ala Ser Trp Thr Ser Arg Gly Val Leu Ala Asp Ala Leu
 675 680 685
 Val Glu Tyr Arg Ser Leu Val Gly Pro Val Arg Pro Thr Phe Tyr Ala
 690 695 700
 Leu His Phe Asn Pro Tyr Val Glu Val Ser Tyr Ala Ser Met Lys Phe

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705          710          715          720
Pro Gly Phe Thr Glu Gln Gly Arg Glu Ala Arg Ser Phe Glu Asp Ala
      725          730          735
Ser Leu Thr Asn Ile Thr Ile Pro Leu Gly Met Lys Phe Glu Leu Ala
      740          745          750
Phe Ile Lys Gly Gln Phe Ser Glu Val Asn Ser Leu Gly Ile Ser Tyr
      755          760          765
Ala Trp Glu Ala Tyr Arg Lys Val Glu Gly Gly Ala Val Gln Leu Leu
      770          775          780
Glu Ala Gly Phe Asp Trp Glu Gly Ala Pro Met Asp Leu Pro Arg Gln
      785          790          795
Glu Leu Arg Val Ala Leu Glu Asn Asn Thr Glu Trp Ser Ser Tyr Phe
      800          805          810
Ser Thr Val Leu Gly Leu Thr Ala Phe Cys Gly Gly Phe Thr Ser Thr
      815          820          825
Asp Ser Lys Leu Gly Tyr Glu Ala Asn Thr Gly Leu Arg Leu Ile Phe
      830          835          840

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<210> 193

<211> 778

<212> PRT

<213> Chlamydia

<400> 193

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Met His His His His His His Gly Leu Ala Ser Cys Val Asp Leu His
  1          5          10          15
Ala Gly Gly Gln Ser Val Asn Glu Leu Val Tyr Val Gly Pro Gln Ala
      20          25          30
Val Leu Leu Leu Asp Gln Ile Arg Asp Leu Phe Val Gly Ser Lys Asp
      35          40          45
Ser Gln Ala Glu Gly Gln Tyr Arg Leu Ile Val Gly Asp Pro Ser Ser
      50          55          60
Phe Gln Glu Lys Asp Ala Asp Thr Leu Pro Gly Lys Val Glu Gln Ser
      65          70          75
Thr Leu Phe Ser Val Thr Asn Pro Val Val Phe Gln Gly Val Asp Gln
      80          85          90
Gln Asp Gln Val Ser Ser Gln Gly Leu Ile Cys Ser Phe Thr Ser Ser
      95          100          105
Asn Leu Asp Ser Pro Arg Asp Gly Glu Ser Phe Leu Gly Ile Ala Phe
      110          115          120
Val Gly Asp Ser Ser Lys Ala Gly Ile Thr Leu Thr Asp Val Lys Ala
      125          130          135
Ser Leu Ser Gly Ala Ala Leu Tyr Ser Thr Glu Asp Leu Ile Phe Glu
      140          145          150
Lys Ile Lys Gly Gly Leu Glu Phe Ala Ser Cys Ser Ser Leu Glu Gln
      155          160          165
Gly Gly Ala Cys Ala Ala Gln Ser Ile Leu Ile His Asp Cys Gln Gly
      170          175          180
Leu Gln Val Lys His Cys Thr Thr Ala Val Asn Ala Glu Gly Ser Ser
      185          190          195
Ala Asn Asp His Leu Gly Phe Gly Gly Gly Ala Phe Phe Val Thr Gly
      200          205          210
Ser Leu Ser Gly Glu Lys Ser Leu Tyr Met Pro Ala Gly Asp Met Val
      215          220          225
Val Ala Asn Cys Asp Gly Ala Ile Ser Phe Glu Gly Asn Ser Ala Asn
      230          235          240
Phe Ala Asn Gly Gly Ala Ile Ala Ala Ser Gly Lys Val Leu Phe Val
      245          250          255
Ala Asn Asp Lys Lys Thr Ser Phe Ile Glu Asn Arg Ala Leu Ser Gly
      260          265          270
Gly Ala Ile Ala Ala Ser Ser Asp Ile Ala Phe Gln Asn Cys Ala Glu
      275          280          285

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290
 Leu Val Phe Lys Gly 295 Asn Cys Ala Ile Gly 300 Thr Glu Asp Lys Gly Ser
 305 310 315 320
 Leu Gly Gly Gly Ala Ile Ser Ser Leu Gly Thr Val Leu Leu Gln Gly
 325 330 335
 Asn His Gly Ile Thr Cys Asp Lys Asn Glu Ser Ala Ser Gln Gly Gly
 340 345 350
 Ala Ile Phe Gly Lys Asn Cys Gln Ile Ser Asp Asn Glu Gly Pro Val
 355 360 365
 Val Phe Arg Asp Ser Thr Ala Cys Leu Gly Gly Gly Ala Ile Ala Ala
 370 375 380
 Gln Glu Ile Val Ser Ile Gln Asn Asn Gln Ala Gly Ile Ser Phe Glu
 385 390 395 400
 Gly Gly Lys Ala Ser Phe Gly Gly Gly Ile Ala Cys Gly Ser Phe Ser
 405 410 415
 Ser Ala Gly Gly Ala Ser Val Leu Gly Thr Ile Asp Ile Ser Lys Asn
 420 425 430
 Leu Gly Ala Ile Ser Phe Ser Arg Thr Leu Cys Thr Thr Ser Asp Leu
 435 440 445
 Gly Gln Met Glu Tyr Gln Gly Gly Gly Ala Leu Phe Gly Glu Asn Ile
 450 455 460
 Ser Leu Ser Glu Asn Ala Gly Val Leu Thr Phe Lys Asp Asn Ile Val
 465 470 475 480
 Lys Thr Phe Ala Ser Asn Gly Lys Ile Leu Gly Gly Gly Ala Ile Leu
 485 490 495
 Ala Thr Gly Lys Val Glu Ile Thr Asn Asn Ser Gly Gly Ile Ser Phe
 500 505 510
 Thr Gly Asn Ala Arg Ala Pro Gln Ala Leu Pro Thr Gln Glu Glu Phe
 515 520 525
 Pro Leu Phe Ser Lys Lys Glu Gly Arg Pro Leu Ser Ser Gly Tyr Ser
 530 535 540
 Gly Gly Gly Ala Ile Leu Gly Arg Glu Val Ala Ile Leu His Asn Ala
 545 550 555 560
 Ala Val Val Phe Glu Gln Asn Arg Leu Gln Cys Ser Glu Glu Glu Ala
 565 570 575
 Thr Leu Leu Gly Cys Cys Gly Gly Gly Ala Val His Gly Met Asp Ser
 580 585 590
 Thr Ser Ile Val Gly Asn Ser Ser Val Arg Phe Gly Asn Asn Tyr Ala
 595 600 605
 Met Gly Gln Gly Val Ser Gly Gly Ala Leu Leu Ser Lys Thr Val Gln
 610 615 620
 Leu Ala Gly Asn Gly Ser Val Asp Phe Ser Arg Asn Ile Ala Ser Leu
 625 630 635 640
 Gly Gly Gly Ala Leu Gln Ala Ser Glu Gly Asn Cys Glu Leu Val Asp
 645 650 655
 Asn Gly Tyr Val Leu Phe Arg Asp Asn Arg Gly Arg Val Tyr Gly Gly
 660 665 670
 Ala Ile Ser Cys Leu Arg Gly Asp Val Val Ile Ser Gly Asn Lys Gly
 675 680 685
 Arg Val Glu Phe Lys Asp Asn Ile Ala Thr Arg Leu Tyr Val Glu Glu
 690 695 700
 Thr Val Glu Lys Val Glu Glu Val Glu Pro Ala Pro Glu Gln Lys Asp
 705 710 715 720
 Asn Asn Glu Leu Ser Phe Leu Gly Ser Val Glu Gln Ser Phe Ile Thr
 725 730 735
 Ala Ala Asn Gln Ala Leu Phe Ala Ser Glu Asp Gly Asp Leu Ser Pro
 740 745 750
 Glu Ser Ser Ile Ser Ser Glu Glu Leu Ala Lys Arg Arg Glu Cys Ala
 755 760 765
 Gly Gly Ala Asp Ser Ser Arg Ser Gly Cys
 770 775

<210> 194
 <211> 948
 <212> PRT
 <213> Chlamydia

<400> 194
 Met Ala Ser Met His His His His His Val Lys Ile Glu Asn Phe
 1 5 10 15
 Ser Gly Gln Gly Ile Phe Ser Gly Asn Lys Ala Ile Asp Asn Thr Thr
 20 25 30
 Glu Gly Ser Ser Ser Lys Ser Asn Val Leu Gly Gly Ala Val Tyr Ala
 35 40 45
 Lys Thr Leu Phe Asn Leu Asp Ser Gly Ser Ser Arg Arg Thr Val Thr
 50 55 60
 Phe Ser Gly Asn Thr Val Ser Ser Gln Ser Thr Thr Gly Gln Val Ala
 65 70 75 80
 Gly Gly Ala Ile Tyr Ser Pro Thr Val Thr Ile Ala Thr Pro Val Val
 85 90 95
 Phe Ser Lys Asn Ser Ala Thr Asn Asn Ala Asn Asn Ala Thr Asp Thr
 100 105 110
 Gln Arg Lys Asp Thr Phe Gly Gly Ala Ile Gly Ala Thr Ser Ala Val
 115 120 125
 Ser Leu Ser Gly Gly Ala His Phe Leu Glu Asn Val Ala Asp Leu Gly
 130 135 140
 Ser Ala Ile Gly Leu Val Pro Asp Thr Gln Asn Thr Glu Thr Val Lys
 145 150 155 160
 Leu Glu Ser Gly Ser Tyr Tyr Phe Glu Lys Asn Lys Ala Leu Lys Arg
 165 170 175
 Ala Thr Ile Tyr Ala Pro Val Val Ser Ile Lys Ala Tyr Thr Ala Thr
 180 185 190
 Phe Asn Gln Asn Arg Ser Leu Glu Glu Gly Ser Ala Ile Tyr Phe Thr
 195 200 205
 Lys Glu Ala Ser Ile Glu Ser Leu Gly Ser Val Leu Phe Thr Gly Asn
 210 215 220
 Leu Val Thr Pro Thr Ser Thr Thr Thr Glu Gly Thr Pro Ala Thr
 225 230 235 240
 Thr Ser Gly Asp Val Thr Lys Tyr Gly Ala Ala Ile Phe Gly Gln Ile
 245 250 255
 Ala Ser Ser Asn Gly Ser Gln Thr Asp Asn Leu Pro Leu Lys Leu Ile
 260 265 270
 Ala Ser Gly Gly Asn Ile Cys Phe Arg Asn Asn Glu Tyr Arg Pro Thr
 275 280 285
 Ser Ser Asp Thr Gly Thr Ser Thr Phe Cys Ser Ile Ala Gly Asp Val
 290 295 300
 Lys Leu Thr Met Gln Ala Ala Lys Gly Lys Thr Ile Ser Phe Phe Asp
 305 310 315 320
 Ala Ile Arg Thr Ser Thr Lys Lys Thr Gly Thr Gln Ala Thr Ala Tyr
 325 330 335
 Asp Thr Leu Asp Ile Asn Lys Ser Glu Asp Ser Glu Thr Val Asn Ser
 340 345 350
 Ala Phe Thr Gly Thr Ile Leu Phe Ser Ser Glu Leu His Glu Asn Lys
 355 360 365
 Ser Tyr Ile Pro Gln Asn Val Val Leu His Ser Gly Ser Leu Val Leu
 370 375 380
 Lys Pro Asn Thr Glu Leu His Val Ile Ser Phe Glu Gln Lys Glu Gly
 385 390 395 400
 Ser Ser Leu Val Met Thr Pro Gly Ser Val Leu Ser Asn Gln Thr Val
 405 410 415
 Ala Asp Gly Ala Leu Val Ile Asn Asn Met Thr Ile Asp Leu Ser Ser
 420 425 430

Val Glu Lys Asn Gly Ile Ala Glu Gly Asn Ile Phe Thr Pro Pro Glu
 435 440
 Leu Arg Ile Ile Asp Thr Thr Thr Ser Gly Ser Gly Gly Thr Pro Ser
 450 455
 Thr Asp Ser Glu Ser Asn Gln Asn Ser Asp Asp Thr Lys Glu Gln Asn
 465 470
 Asn Asn Asp Ala Ser Asn Gln Gly Glu Ser Ala Asn Gly Ser Ser Ser
 485 490
 Pro Ala Val Ala Ala Ala His Thr Ser Arg Thr Arg Asn Phe Ala Ala
 500 505
 Ala Ala Thr Ala Thr Pro Thr Thr Thr Pro Thr Ala Thr Thr Thr
 515 520
 Ser Asn Gln Val Ile Leu Gly Gly Glu Ile Lys Leu Ile Asp Pro Asn
 530 535
 Gly Thr Phe Phe Gln Asn Pro Ala Leu Arg Ser Asp Gln Gln Ile Ser
 545 550
 Leu Leu Val Leu Pro Thr Asp Ser Ser Lys Met Gln Ala Gln Lys Ile
 565 570
 Val Leu Thr Gly Asp Ile Ala Pro Gln Lys Gly Tyr Thr Gly Thr Leu
 580 585
 Thr Leu Asp Pro Asp Gln Leu Gln Asn Gly Thr Ile Ser Ala Leu Trp
 595 600
 Lys Phe Asp Ser Tyr Arg Gln Trp Ala Tyr Val Pro Arg Asp Asn His
 610 615
 Phe Tyr Ala Asn Ser Ile Leu Gly Ser Gln Met Ser Met Val Thr Val
 625 630
 Lys Gln Gly Leu Leu Asn Asp Lys Met Asn Leu Ala Arg Phe Asp Glu
 645 650
 Val Ser Tyr Asn Asn Leu Trp Ile Ser Gly Leu Gly Thr Met Leu Ser
 660 665
 Gln Val Gly Thr Pro Thr Ser Glu Glu Phe Thr Tyr Tyr Ser Arg Gly
 675 680
 Ala Ser Val Ala Leu Asp Ala Lys Pro Ala His Asp Val Ile Val Gly
 690 695
 Ala Ala Phe Ser Lys Met Ile Gly Lys Thr Lys Ser Leu Lys Arg Glu
 705 710
 Asn Asn Tyr Thr His Lys Gly Ser Glu Tyr Ser Tyr Gln Ala Ser Val
 725 730
 Tyr Gly Gly Lys Pro Phe His Phe Val Ile Asn Lys Lys Thr Glu Lys
 740 745
 Ser Leu Pro Leu Leu Leu Gln Gly Val Ile Ser Tyr Gly Tyr Ile Lys
 755 760
 His Asp Thr Val Thr His Tyr Pro Thr Ile Arg Glu Arg Asn Gln Gly
 770 775
 Glu Trp Glu Asp Leu Gly Trp Leu Thr Ala Leu Arg Val Ser Ser Val
 785 790
 Leu Arg Thr Pro Ala Gln Gly Asp Thr Lys Arg Ile Thr Val Tyr Gly
 805 810
 Glu Leu Glu Tyr Ser Ser Ile Arg Gln Lys Gln Phe Thr Glu Thr Glu
 820 825
 Tyr Asp Pro Arg Tyr Phe Asp Asn Cys Thr Tyr Arg Asn Leu Ala Ile
 835 840
 Pro Met Gly Leu Ala Phe Glu Gly Glu Leu Ser Gly Asn Asp Ile Leu
 850 855
 Met Tyr Asn Arg Phe Ser Val Ala Tyr Met Pro Ser Ile Tyr Arg Asn
 865 870
 Ser Pro Thr Cys Lys Tyr Gln Val Leu Ser Ser Gly Glu Gly Gly Glu
 885 890
 Ile Ile Cys Gly Val Pro Thr Arg Asn Ser Ala Arg Gly Glu Tyr Ser
 900 905
 Thr Gln Leu Tyr Pro Gly Pro Leu Trp Thr Leu Tyr Gly Ser Tyr Thr

915
 Ile Glu Ala Asp Ala His Thr 935
 Arg Met Thr Phe
 945

<210> 195
 <211> 621
 <212> PRT
 <213> Chlamydia

<400> 195
 Met His His His His His His Glu Ala Ser Ser Ile Gln Asp Gln Ile
 1 5 10 15
 Lys Asn Thr Asp Cys Asn Val Ser Lys Val Gly Tyr Ser Thr Ser Gln
 20 25 30
 Ala Phe Thr Asp Met Met Leu Ala Asp Asn Thr Glu Tyr Arg Ala Ala
 35 40 45
 Asp Ser Val Ser Phe Tyr Asp Phe Ser Thr Ser Ser Gly Leu Pro Arg
 50 55 60
 Lys His Leu Ser Ser Ser Ser Glu Ala Ser Pro Thr Thr Glu Gly Val
 65 70 75 80
 Ser Ser Ser Ser Ser Gly Glu Asn Thr Glu Asn Ser Gln Asp Ser Ala
 85 90 95
 Pro Ser Ser Gly Glu Thr Asp Lys Lys Thr Glu Glu Glu Leu Asp Asn
 100 105 110
 Gly Gly Ile Ile Tyr Ala Arg Glu Lys Leu Thr Ile Ser Glu Ser Gln
 115 120 125
 Asp Ser Leu Ser Asn Pro Ser Ile Glu Leu His Asp Asn Ser Phe Phe
 130 135 140
 Phe Gly Glu Gly Glu Val Ile Phe Asp His Arg Val Ala Leu Lys Asn
 145 150 155 160
 Gly Gly Ala Ile Tyr Gly Glu Lys Glu Val Val Phe Glu Asn Ile Lys
 165 170 175
 Ser Leu Leu Val Glu Val Asn Ile Ser Val Glu Lys Gly Gly Ser Val
 180 185 190
 Tyr Ala Lys Glu Arg Val Ser Leu Glu Asn Val Thr Glu Ala Thr Phe
 195 200 205
 Ser Ser Asn Gly Gly Glu Gln Gly Gly Gly Gly Ile Tyr Ser Glu Gln
 210 215 220
 Asp Met Leu Ile Ser Asp Cys Asn Asn Val His Phe Gln Gly Asn Ala
 225 230 235 240
 Ala Gly Ala Thr Ala Val Lys Gln Cys Leu Asp Glu Glu Met Ile Val
 245 250 255
 Leu Leu Thr Glu Cys Val Asp Ser Leu Ser Glu Asp Thr Leu Asp Ser
 260 265 270
 Thr Pro Glu Thr Glu Gln Thr Lys Ser Asn Gly Asn Gln Asp Gly Ser
 275 280 285
 Ser Glu Thr Lys Asp Thr Gln Val Ser Glu Ser Pro Glu Ser Thr Pro
 290 295 300
 Ser Pro Asp Asp Val Leu Gly Lys Gly Gly Gly Ile Tyr Thr Glu Lys
 305 310 315 320
 Ser Leu Thr Ile Thr Gly Ile Thr Gly Thr Ile Asp Phe Val Ser Asn
 325 330 335
 Ile Ala Thr Asp Ser Gly Ala Gly Val Phe Thr Lys Glu Asn Leu Ser
 340 345 350
 Cys Thr Asn Thr Asn Ser Leu Gln Phe Leu Lys Asn Ser Ala Gly Gln
 355 360 365
 His Gly Gly Gly Ala Tyr Val Thr Gln Thr Met Ser Val Thr Asn Thr
 370 375 380
 Thr Ser Glu Ser Ile Thr Thr Pro Pro Leu Val Gly Glu Val Ile Phe

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385          390          395          400
Ser Glu Asn Thr Ala Lys Gly His Gly Gly Ile Cys Thr Asn Lys
              405              410              415
Leu Ser Leu Ser Asn Leu Lys Thr Val Thr Leu Thr Lys Asn Ser Ala
              420              425              430
Lys Glu Ser Gly Gly Ala Ile Phe Thr Asp Leu Ala Ser Ile Pro Thr
              435              440              445
Thr Asp Thr Pro Glu Ser Ser Thr Pro Ser Ser Ser Pro Ala Ser
              450              455              460
Thr Pro Glu Val Val Ala Ser Ala Lys Ile Asn Arg Phe Phe Ala Ser
465              470              475              480
Thr Ala Glu Pro Ala Ala Pro Ser Leu Thr Glu Ala Glu Ser Asp Gln
              485              490              495
Thr Asp Gln Thr Glu Thr Ser Asp Thr Asn Ser Asp Ile Asp Val Ser
              500              505              510
Ile Glu Asn Ile Leu Asn Val Ala Ile Asn Gln Asn Thr Ser Ala Lys
              515              520              525
Lys Gly Gly Ala Ile Tyr Gly Lys Lys Ala Lys Leu Ser Arg Ile Asn
530              535              540
Asn Leu Glu Leu Ser Gly Asn Ser Ser Gln Asp Val Gly Gly Gly Leu
545              550              555              560
Cys Leu Thr Glu Ser Val Glu Phe Asp Ala Ile Gly Ser Leu Leu Ser
              565              570              575
His Tyr Asn Ser Ala Ala Lys Glu Gly Gly Val Ile His Ser Lys Thr
              580              585              590
Val Thr Leu Ser Asn Leu Lys Ser Thr Phe Thr Phe Ala Asp Asn Thr
              595              600              605
Val Lys Ala Ile Val Glu Ser Thr Pro Glu Ala Pro Glu Glu Ile Pro
610              615              620
Pro Val Glu Gly Glu Ser Thr Ala Thr Glu Asn Pro Asn Ser Asn
625              630              635              640
Thr Glu Gly Ser Ser Ala Asn Thr Asn Leu Glu Gly Ser Gln Gly Asp
              645              650              655
Thr Ala Asp Thr Gly Thr Gly Val Val Asn Asn Glu Ser Gln Asp Thr
              660              665              670
Ser Asp Thr Gly Asn Ala Glu Ser Gly Glu Gln Leu Gln Asp Ser Thr
              675              680              685
Gln Ser Asn Glu Glu Asn Thr Leu Pro Asn Ser Ser Ile Asp Gln Ser
              690              695              700
Asn Glu Asn Thr Asp Glu Ser Ser Asp Ser His Thr Glu Glu Ile Thr
705              710              715              720
Asp Glu Ser Val Ser Ser Ser Lys Ser Gly Ser Ser Thr Pro Gln
              725              730              735
Asp Gly Gly Ala Ala Ser Ser Gly Ala Pro Ser Gly Asp Gln Ser Ile
              740              745              750
Ser Ala Asn Ala Cys Leu Ala Lys Ser Tyr Ala Ala Ser Thr Asp Ser
              755              760              765
Ser Pro Val Ser Asn Ser Ser Gly Ser Asp Val Thr Ala Ser Ser Asp
770              775              780
Asn Pro Asp Ser Ser Ser Ser Gly Asp Ser Ala Gly Asp Ser Glu Gly
785              790              795              800
Pro Thr Glu Pro Glu Ala Gly Ser Thr Thr Glu Thr Pro Thr Leu Ile
              805              810              815
Gly Gly Gly Ala Ile
              820

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<210> 196

<211> 525

<212> PRT

<213> Chlamydia

<400> 196

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Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1      5      10      15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
20      25      30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
35      40      45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
50      55      60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65      70      75      80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
85      90      95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
100     105
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
115     120     125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Pro Leu Val Pro Arg Gly Ser
130     135     140
Pro Leu Pro Val Gly Asn Pro Ala Glu Pro Ser Leu Leu Ile Asp Gly
145     150     155     160
Thr Met Trp Glu Gly Ala Ser Gly Asp Pro Cys Asp Pro Cys Ala Thr
165     170     175
Trp Cys Asp Ala Ile Ser Ile Arg Ala Gly Tyr Tyr Gly Asp Tyr Val
180     185
Phe Asp Arg Val Leu Lys Val Asp Val Asn Lys Thr Phe Ser Gly Met
195     200
Ala Ala Thr Pro Thr Gln Ala Ile Gly Asn Ala Ser Asn Thr Asn Gln
210     215
Pro Glu Ala Asn Gly Arg Pro Asn Ile Ala Tyr Gly Arg His Met Gln
225     230     235     240
Asp Ala Glu Trp Phe Ser Asn Ala Ala Phe Leu Ala Leu Asn Ile Trp
245     250     255
Asp Arg Phe Asp Ile Phe Cys Thr Leu Gly Ala Ser Asn Gly Tyr Phe
260     265     270
Lys Ala Ser Ser Ala Ala Phe Asn Leu Val Gly Leu Ile Gly Phe Ser
275     280     285
Ala Ala Ser Ser Ile Ser Thr Asp Leu Pro Met Gln Leu Pro Asn Val
290     295     300
Gly Ile Thr Gln Gly Val Val Glu Phe Tyr Thr Asp Thr Ser Phe Ser
305     310     315     320
Trp Ser Val Gly Ala Arg Gly Ala Leu Trp Glu Cys Gly Cys Ala Thr
325     330     335
Leu Gly Ala Glu Phe Gln Tyr Ala Gln Ser Asn Pro Lys Ile Glu Met
340     345     350
Leu Asn Val Thr Ser Ser Pro Ala Gln Phe Val Ile His Lys Pro Arg
355     360     365
Gly Tyr Lys Gly Ala Ser Ser Asn Phe Pro Leu Pro Ile Thr Ala Gly
370     375     380
Thr Thr Glu Ala Thr Asp Thr Lys Ser Ala Thr Ile Lys Tyr His Glu
385     390     395     400
Trp Gln Val Gly Leu Ala Leu Ser Tyr Arg Leu Asn Met Leu Val Pro
405     410     415
Tyr Ile Gly Val Asn Trp Ser Arg Ala Thr Phe Asp Ala Asp Thr Ile
420     425     430
Arg Ile Ala Gln Pro Lys Leu Lys Ser Glu Ile Leu Asn Ile Thr Thr
435     440     445
Trp Asn Pro Ser Leu Ile Gly Ser Thr Thr Ala Leu Pro Asn Asn Ser
450     455     460
Gly Lys Asp Val Leu Ser Asp Val Leu Gln Ile Ala Ser Ile Gln Ile
465     470     475     480

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Asn	Lys	Met	Lys	Ser	Arg	Lys	Ala	Cys	Gly	Val	Ala	Val	Gly	Ala	Thr
			485						490					495	
Leu	Ile	Asp	Ala	Asp	Lys	Trp	Ser	Ile	Thr	Gly	Glu	Ala	Arg	Leu	Ile
		500					505						510		
Asn	Glu	Arg	Ala	Ala	His	Met	Asn	Ala	Gln	Phe	Arg	Phe			
		515				520						525			

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<211> 43

<212> DNA

<213> Chlamydia

<400> 197

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43

<210> 198

<211> 34

<212> DNA

<213> Chlamydia

<400> 198

cagaacgcgt ttagaatgtc atacgagcac cgca

34

<210> 199

<211> 6

<212> DNA

<213> Chlamydia

<400> 199

gcaatc

6

<210> 200

<211> 34

<212> DNA

<213> Chlamydia

<400> 200

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34

<210> 201

<211> 38

<212> DNA

<213> Chlamydia

<400> 201

cagagctagc ttaaaagatc aatcgcaatc cagtattc

38

<210> 202

<211> 5

<212> DNA

<213> Chlamydia

<400> 202

caatc

5

<210> 203

<211> 31

<212> DNA

<213> Chlamydia

<400> 203

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<210> 204
 <211> 31
 <212> DNA
 <213> Chlamydia

<400> 204
 cagaacgcgt ctagaatcgc agagcaattt c 31

<210> 205
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<400> 205
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<210> 206
 <211> 31
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<400> 206
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<210> 207
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<210> 208
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 <212> DNA
 <213> Chlamydia

<400> 208
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<210> 209
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 <212> DNA
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<210> 210
 <211> 35
 <212> DNA
 <213> Chlamydia

<400> 210
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<210> 211
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<213> Chlamydia
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 <213> Chlamydia
 <400> 212
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 <210> 214
 <211> 38
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 1 5 10 15

Val Pro Ser Ser Asp Pro
20

<210> 219
<211> 51
<212> DNA
<213> Chlamydia

<400> 219
cagaggtacc gcatcaccat caccatcaca tgattcctca aggaatttac g 51

<210> 220
<211> 33
<212> DNA
<213> Chlamydia

<400> 220
cagagcggcc gcttagaacc ggactttact tcc 33

<210> 221
<211> 24
<212> FRT
<213> Chlamydia

<400> 221
Met Ala Ser Met Thr Gly Gly Gln Gln Asn Gly Arg Asp Ser Ser Leu
1 5 10 15
Val Pro His His His His His His
20

<210> 222
<211> 46
<212> DNA
<213> Chlamydia

<400> 222
cagagctagc catcaccatc accatcacct ctttgccag gatccc 46

<210> 223
<211> 30
<212> DNA
<213> Chlamydia

<400> 223
cagaactagt ctagaacctg taagtgggcc 30

<210> 224
<211> 20
<212> FRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 224
Met Ser Gln Lys Asn Lys Asn Ser Ala Phe Met His Pro Val Asn Ile
1 5 10 15
Ser Thr Asp Leu
20

<210> 225

<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 225
Lys Asn Ser Ala Phe Met His Pro Val Asn Ile Ser Thr Asp Leu Ala
1 5 10 15
Val Ile Val Gly
20

<210> 226
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 226
His Pro Val Asn Ile Ser Thr Asp Leu Ala Val Ile Val Gly Lys Gly
1 5 10 15
Pro Met Pro Arg
20

<210> 227
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 227
Ser Thr Asp Leu Ala Val Ile Val Gly Lys Gly Pro Met Pro Arg Thr
1 5 10 15
Glu Ile Val Lys
20

<210> 228
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 228
Val Ile Val Gly Lys Gly Pro Met Pro Arg Thr Glu Ile Val Lys Lys
1 5 10 15
Val Trp Glu Tyr
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<210> 229
<211> 20
<212> PRT
<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 229

Gly Pro Met Pro Arg Thr Glu Ile Val Lys Lys Val Trp Glu Tyr Ile
 1 5 10 15
 Lys Lys His Asn
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<210> 230

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 230

Ile Lys Lys His Asn Cys Gln Asp Gln Lys Asn Lys Arg Asn Ile Leu
 1 5 10 15
 Pro Asp Ala Asn
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<210> 231

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 231

Asn Cys Gln Asp Gln Lys Asn Lys Arg Asn Ile Leu Pro Asp Ala Asn
 1 5 10 15
 Leu Ala Lys Val
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<210> 232

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 232

Lys Asn Lys Arg Asn Ile Leu Pro Asp Ala Asn Leu Ala Lys Val Phe
 1 5 10 15
 Gly Ser Ser Asp
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<210> 233

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 233

Ile Leu Pro Asp Ala Asn Leu Ala Lys Val Phe Gly Ser Ser Asp Pro
 1 5 10 15

Ile Asp Met Phe
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<210> 234
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 234
Asn Leu Ala Lys Val Phe Gly Ser Ser Asp Pro Ile Asp Met Phe Gln
1 5 10 15
Met Thr Lys Ala
20

<210> 235
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 235
Phe Gly Ser Ser Asp Pro Ile Asp Met Phe Gln Met Thr Lys Ala Leu
1 5 10 15
Ser Lys His Ile Val Lys
20

<210> 236
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 236
Val Glu Ile Thr Gln Ala Val Pro Lys Tyr Ala Thr Val Gly Ser Pro
1 5 10 15
Tyr Pro Val Glu
20

<210> 237
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 237
Ala Val Pro Lys Tyr Ala Thr Val Gly Ser Pro Tyr Pro Val Glu Ile
1 5 10 15
Thr Ala Thr Gly
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<210> 238
<211> 20

<212> FRT
 <213> Artificial Sequence

 <220>
 <223> Made in a lab

 <400> 238
 Ala Thr Val Gly Ser Pro Tyr Pro Val Glu Ile Thr Ala Thr Gly Lys
 1 5 10 15
 Arg Asp Cys Val
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 <210> 239
 <211> 20
 <212> FRT
 <213> Artificial Sequence

 <220>
 <223> Made in a lab

 <400> 239
 Pro Tyr Pro Val Glu Ile Thr Ala Thr Gly Lys Arg Asp Cys Val Asp
 1 5 10 15
 Val Ile Ile Thr
 20

 <210> 240
 <211> 21
 <212> FRT
 <213> Artificial Sequence

 <220>
 <223> Made in a lab

 <400> 240
 Ile Thr Ala Thr Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln
 1 5 10 15
 Gln Leu Pro Cys Glu
 20

 <210> 241
 <211> 20
 <212> FRT
 <213> Artificial Sequence

 <220>
 <223> Made in a lab

 <400> 241
 Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln Gln Leu Pro Cys Glu
 1 5 10 15
 Ala Glu Phe Val
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 <210> 242
 <211> 20
 <212> FRT
 <213> Artificial Sequence

 <220>
 <223> Made in a lab

<400> 242
 Asp Val Ile Ile Thr Gln Gln Leu Pro Cys Glu Ala Glu Phe Val Arg
 1 5 10 15
 Ser Asp Pro Ala
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<210> 243
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 243
 Thr Gln Gln Leu Pro Cys Glu Ala Glu Phe Val Arg Ser Asp Pro Ala
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 Thr Thr Pro Thr
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<210> 244
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 244
 Cys Glu Ala Glu Phe Val Arg Ser Asp Pro Ala Thr Thr Pro Thr Ala
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 Asp Gly Lys Leu
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<210> 245
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 245
 Val Arg Ser Asp Pro Ala Thr Thr Pro Thr Ala Asp Gly Lys Leu Val
 1 5 10 15
 Trp Lys Ile Asp
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<210> 246
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 246
 Ala Thr Thr Pro Thr Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg
 1 5 10 15
 Leu Gly Gln Gly

20

<210> 247
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 247
Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln Gly Glu
1 5 10 15
Lys Ser Lys Ile
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<210> 248
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 248
Val Trp Lys Ile Asp Arg Leu Gly Gln Gly Glu Lys Ser Lys Ile Thr
1 5 10 15
Val Trp Val Lys
20

<210> 249
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 249
Arg Leu Gly Gln Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro
1 5 10 15
Leu Lys Glu Gly
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<210> 250
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<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 250
Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly
1 5 10 15
Cys Cys Phe Thr
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<210> 251
<211> 16
<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 251

Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly
1 5 10 15

<210> 252

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 252

Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly
1 5 10

<210> 253

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 253

Gly Asp Lys Cys Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly
1 5 10 15

<210> 254

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 254

Thr Glu Tyr Pro Leu Leu Ala Asp Pro Ser Phe Lys Ile Ser Glu Ala
1 5 10 15
Phe Gly Val Leu
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<210> 255

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 255

Leu Ala Asp Pro Ser Phe Lys Ile Ser Glu Ala Phe Gly Val Leu Asn
1 5 10 15
Pro Glu Gly Ser
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<210> 256
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 256
Phe Lys Ile Ser Glu Ala Phe Gly Val Leu Asn Pro Glu Gly Ser Leu
1 5 10 15
Ala Leu Arg Ala
20

<210> 257
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 257
Ala Phe Gly Val Leu Asn Pro Glu Gly Ser Leu Ala Leu Arg Ala Thr
1 5 10 15
Phe Leu Ile Asp
20

<210> 258
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 258
Asn Pro Glu Gly Ser Leu Ala Leu Arg Ala Thr Phe Leu Ile Asp Lys
1 5 10 15
His Gly Val Ile
20

<210> 259
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 259
Leu Ala Leu Arg Ala Thr Phe Leu Ile Asp Lys His Gly Val Ile Arg
1 5 10 15
His Ala Val Ile
20

<210> 260
<211> 20
<212> PRT
<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 260

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Thr Phe Leu Ile Asp Lys His Gly Val Ile Arg His Ala Val Ile Asn
 1             5             10             15
Asp Leu Pro Leu
 20

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<210> 261

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 261

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Lys His Gly Val Ile Arg His Ala Val Ile Asn Asp Leu Pro Leu Gly
 1             5             10             15
Arg Ser Ile Asp
 20

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<210> 262

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 262

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Arg His Ala Val Ile Asn Asp Leu Pro Leu Gly Arg Ser Ile Asp Glu
 1             5             10             15
Glu Leu Arg Ile
 20

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<210> 263

<211> 897

<212> DNA

<213> Chlamydia

<220>

<221> misc_feature

<222> 604

<223> n = A,T,C or G

<400> 263

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acacagcccca	acaataaaaat	ggcaagggta	gtaaataaga	cgaagggaagt	ggataaagact	120
attaagggttg	ccaagtctgc	tgccgaattg	accgcaataa	ttttggaaca	agctggagggc	180
gcgggtctctt	cgcacacacat	tacagcttcc	caagtgtcca	aaggattagg	ggatgcgaga	240
actgtgttcg	ctttagggaa	tgcccttaac	ggagcgttgc	caggaaacagt	tcaaatgtgcg	300
caaagcttct	tctctcacat	gaaagctgct	agtcaaaaaa	cgcaagaagg	ggatgagggg	360
ctcacagcag	atcttttgtt	gtctcataag	cgcagagcgg	ctgcggctgt	ctgtagcattc	420
atcggaggaa	ttacctacct	cgcgacattc	ggagctatcc	gtccgattct	gtttgtcaac	480
aaaatgctgg	caaaaaccgtt	tctttcttcc	caaaactaaag	caaatatggg	atcttctgtt	540
agctatatta	tggcggctaa	ccatgcagcg	tctgtggtgg	gtgctggact	cgctatcagt	600
cgnaaagag	cagattgcga	agcccgctgc	gctcgtattg	cgagagaaga	gtcgttactc	660
gaagtgccgg	gagaggaaaa	tgcttgcgag	aagaaaagtcg	ctggagagaa	agccaagacg	720
ttcacgcgca	tcaagtatgc	actcctcact	atgctcgaga	agtttttggg	atgcgttgcc	780

gacgttttca aattggtgcc gctgcctatt acaatgggta ttcgtgcgat tgtggctgct 840
 ggatgtacgt tcacttctgc aattattgga ttgtgcactt tctgcgccag agcataa 897

<210> 264

<211> 298

<212> PRT

<213> Chlamydia

<220>

<221> VARIANT

<222> 202

<223> Xaa = Any Amino Acid

<400> 264

Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
 1 5 10 15
 Lys Ala Phe Phe Thr Gln Pro Asn Asn Lys Met Ala Arg Val Val Asn
 20 25 30
 Lys Thr Lys Gly Val Asp Lys Thr Ile Lys Val Ala Lys Ser Ala Ala
 35 40 45
 Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
 50 55 60
 Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
 65 70 75 80
 Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
 85 90 95
 Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
 100 105 110
 Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser
 115 120 125
 His Lys Arg Arg Ala Ala Ala Val Cys Ser Ile Ile Gly Gly Ile
 130 135 140
 Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
 145 150 155 160
 Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
 165 170 175
 Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
 180 185 190
 Val Gly Ala Gly Leu Ala Ile Ser Ala Xaa Arg Ala Asp Cys Glu Ala
 195 200 205
 Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Pro Gly
 210 215 220
 Glu Glu Asn Ala Cys Glu Lys Lys Val Ala Gly Glu Lys Ala Lys Thr
 225 230 235 240
 Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
 245 250 255
 Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
 260 265 270
 Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
 275 280 285
 Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
 290 295

<210> 265

<211> 897

<212> DNA

<213> Chlamydia

<220>

<221> misc_feature

<222> 604

<223> n = A, T, C or G

<400> 265

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attaaggttg	ccaagtctgc	tgccgaattg	accgcaataa	ttttggaaca	agctggaggg	180
gcgggctctt	ccgcacacat	tacagcttcc	caagtgtcca	aaggattagg	ggatgcggaga	240
acgtgtgtcg	cttttagggaa	tgcccttaac	ggagcgttgc	caggaacagt	tcaaatgtcg	300
caagactctt	tctctcacat	gaaagctgct	agtcagaaaa	cgcgaagaag	ggatgagggg	360
ctccacagcag	atcttttgtgt	gtctcataag	cgcagagcgg	ctgcggctgt	ctgtagcatc	420
atcggaggaa	ttacctacct	cgcgacattc	ggagctatcc	gtccgattct	gtttgtcaac	480
aaaaatgctgg	caaaaccgttt	tctttcttcc	caaaactaaag	caaatatggg	atcttctggt	540
agctatatatta	tggcgggctaa	ccatgcagcg	tctgtggttg	gtgctggact	cgctatcagt	600
gcgnaaagag	cagattgcca	agcccgctgc	gctcgtattg	cagagaaga	gtcgttactc	660
gaagtgcggg	gagaggaaaa	tgcttgcgag	aagaaagtgc	ctggagagaa	agccaagacg	720
ttcacgcgca	tcaagtatgc	actcctcact	atgctcgaga	agtttttgga	atcggtgtcc	780
gacgttttca	aatttggtgcc	gctgcctatt	acaatgggta	ttcgtgcgat	tgtggctgct	840
ggatgtacgt	tcacttctgc	aattattgga	ttgtgcactt	tctgcgccag	agcataa	897

<210> 266

<211> 298

<212> PRT

<213> Chlamydia

<220>

<221> VARIANT

<222> 202

<223> Xaa = Any Amino Acid

<400> 266

Met	Ala	Ser	Ile	Cys	Gly	Arg	Leu	Gly	Ser	Gly	Thr	Gly	Asn	Ala	Leu
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Lys	Ala	Phe	Phe	Thr	Gln	Pro	Asn	Asn	Lys	Met	Ala	Arg	Val	Val	Asn
			20					25					30		
Lys	Thr	Lys	Gly	Met	Asp	Lys	Thr	Ile	Lys	Val	Ala	Lys	Ser	Ala	Ala
			35				40					45			
Glu	Leu	Thr	Ala	Asn	Ile	Leu	Glu	Gln	Ala	Gly	Gly	Ala	Gly	Ser	Ser
	50				55						60				
Ala	His	Ile	Thr	Ala	Ser	Gln	Val	Ser	Lys	Gly	Leu	Gly	Asp	Ala	Arg
65					70				75					80	
Thr	Val	Val	Ala	Leu	Gly	Asn	Ala	Phe	Asn	Gly	Ala	Leu	Pro	Gly	Thr
			85						90				95		
Val	Gln	Ser	Ala	Gln	Ser	Phe	Phe	Ser	His	Met	Lys	Ala	Ala	Ser	Gln
			100					105					110		
Lys	Thr	Gln	Glu	Gly	Asp	Glu	Gly	Leu	Thr	Ala	Asp	Leu	Cys	Val	Ser
		115				120						125			
His	Lys	Arg	Arg	Ala	Ala	Ala	Ala	Val	Cys	Ser	Ile	Ile	Gly	Gly	Ile
	130					135					140				
Thr	Tyr	Leu	Ala	Thr	Phe	Gly	Ala	Ile	Arg	Pro	Ile	Leu	Phe	Val	Asn
145					150				155					160	
Lys	Met	Leu	Ala	Lys	Pro	Phe	Leu	Ser	Ser	Gln	Thr	Lys	Ala	Asn	Met
				165					170				175		
Gly	Ser	Ser	Val	Ser	Tyr	Ile	Met	Ala	Ala	Asn	His	Ala	Ala	Ser	Val
			180					185					190		
Val	Gly	Ala	Gly	Leu	Ala	Ile	Ser	Ala	Xaa	Arg	Ala	Asp	Cys	Glu	Ala
		195				200						205			
Arg	Cys	Ala	Arg	Ile	Ala	Arg	Glu	Ser	Leu	Leu	Glu	Val	Pro	Gly	
	210					215				220					
Glu	Glu	Asn	Ala	Cys	Glu	Lys	Lys	Val	Ala	Gly	Glu	Lys	Ala	Lys	Thr
225					230					235				240	

Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
 245 250
 Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
 260 265
 Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
 275 280 285
 Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
 290 295

<210> 267
 <211> 680
 <212> DNA
 <213> Chlamydia

<400> 267
 tctatatcca tattgatagg aaaaaacgtc gcagaaagat tttagctatg acgtttatcc 60
 gagcttttagg atattcaaca gatcgagata ttattgaaga gtltcttttct glagaggagc 120
 gtctcttagc ttcagagaag gattttctcg cgttagttgg taaagtttta gctgataaac 180
 tagttgatcg ggattcttca ttagtttacg ggaagctgg agagaagcta agtactcgta 240
 gtctaaaaag catcttagat acgggagtc aatctttgaa gattgctgtt ggccgagatg 300
 aaaaacacc aattattaag atgctcgcaa aagatcctac ggattcttac gaagctgctc 360
 ttaaagattt ttatcgaga ttacgaccag gagagcctgc aacttttagt aatgctcgat 420
 cacaatttat gcgttttatt ttogatgcta aacgtttataa tttaggccgc gttggacgtt 480
 ataatataaa taaaaaatta ggcttcccat tagacgcaga aacattatct caagtgactt 540
 tgagaaaaag agatgttatc ggcgcgttga aatatttgat tctgtttcga atggcgatg 600
 agaagacatc tatcgatgat attgaccatt tggcaaacgc acgagttcgc tctgttgagg 660
 aactaattca gaatactgtg 680

<210> 268
 <211> 359
 <212> DNA
 <213> Chlamydia

<400> 268
 cttatgttct ggagaatgtt gcaacaacat attaatcgaa ccagctcctc ctagtaacat 60
 agaaaccaag cctcttttag aaaaaacctg tacttcgcat ccttttagcca ttgtgtgaat 120
 agctcctaac aaagagctaa ttittttcct ttccttgttt ttctgaggcg ctgtggactc 180
 taaatatagc aagtgcctct ggaacacctc atcaacaatc gcttgcctca gattaggtat 240
 agagaactgc tctccatcaa ttaaatggag ttcaaaagta atatccctt ccgtccctcc 300
 atcacaagac tctatgaaag ctatctgatt ccactcgaca gaaatgtatg gggaaatac 359

<210> 269
 <211> 124
 <212> DNA
 <213> Chlamydia

<400> 269
 gatcgaatca attgagggag ctcatataca agaataagctg cagttttcttt gcgttcttct 60
 ggaataacaa gaaatagcta atcggtagca ttgatagaac gaacacgaca aatcgagaa 120
 ggtt 124

<210> 270
 <211> 219
 <212> DNA
 <213> Chlamydia

<400> 270
 gatcctgttg ggcctagtaa taatacgttg gatttcccat aactcacttg tttatcctgc 60
 ataagagcac ggatacgctt atagtgttta tagacggcaa ccgaaactgt tttttctgcg 120
 cgctcttgtc caatgacata agatcgatg tggcgtttga tttcttttag gggttaacct 180
 ctcgactctg ttggagagct tgtggaagat gttgcgatc 219

<210> 271
 <211> 511
 <212> DNA
 <213> Chlamydia

<220>
 <221> misc_feature
 <222> 447
 <223> n = A,T,C or G

<400> 271							
ggatccgaat	toggcagcag	gagaaaatat	aggagggttcc	akcatcgga	gatctaatag		60
acaaagaggt	tttggcatag	atggctcctc	cttgtacgtt	caacgatgat	tgggagggat		120
tgttatcgat	agcttgggttc	ccagagaact	gacaaagccc	gctacattga	gagaatgtaa		180
ccgtttctcc	atagatagct	cctcctaact	caactgaata	agttgggtgtt	gctggagatg		240
atgggtggcg	tgctggcgct	gctttagagg	aagcagcagc	tgacagcaggt	gctgaagctg		300
ttgttggcag	tctctgggag	gaggagtttg	ctttgttgtt	cgagaaagag	aagcctgatt		360
tcagatctaga	aattattaca	gttttagcat	gtaagccctc	accttctcttc	ccaacaaggat		420
tctctgttac	agataaggag	actagangca	tctagtttta	aagatttttt	acagcagata		480
cctccacctc	tctctgtagc	ggagtcttca	g				511

<210> 272
 <211> 598
 <212> DNA
 <213> Chlamydia

<400> 272							
ctctctctct	cctcaatcta	gttctggagc	aactacagtc	tcgactcag	gagactctag		60
ctctggctca	aactcggata	cctcaaaaac	agttccagtc	acagctaag	gcggtgggct		120
ttatactgat	aagaatcttt	cgattactaa	catcacagga	attatcgaaa	ttgcaaataa		180
caaaagcgaca	gatgttggag	gtgggtctta	cgtaaaagga	acccttactt	gtaaaaactc		240
tcacgctcta	caatttttga	aaaactcttc	cgataaacaa	gggtggaggaa	tctacggaga		300
agacaacatc	accctatcta	atttgacagg	gaagactcta	ttccaagaga	atactgccaa		360
aaaagaggcg	gggtgactct	tcataaaaagg	tacagataaa	gctcttacaa	tgacaggact		420
ggatagtttc	tgttttaatta	ataacacatc	agaaaaacat	gggtggggga	gcctttgtta		480
ccaaagaaat	ctctcagact	tacccctctt	gatgtggaag	caattccagg	aatcacgcct		540
gtacatgggtg	aaacagtcac	tactggcaat	aaatctacag	gaggtaatgg	tgaggggc		598

<210> 273
 <211> 126
 <212> DNA
 <213> Chlamydia

<400> 273							
ggatccgaat	toggcagcag	atgagcotta	tagtttaaca	aaagcttctc	acattccttc		60
gatagctttt	tattagcgtt	ttttagcctc	ctaagagat	ctctctgttc	gtaacaataa		120
cgagag							126

<210> 274
 <211> 264
 <212> DNA
 <213> Chlamydia

<400> 274							
ggatccgaat	toggcagcag	ctctttttaa	tcttaattac	aaaagacaa	attaattcaa		60
tttttcaaaa	aagaatttaa	acattaatgt	ttgtaaaaaa	acaattatta	ttctaaaaata		120
ataaccatag	ttacggggga	atctctttca	tggtttattt	tagagctcat	caacctaggc		180
atacgctcaa	aacatctctc	ttgaaggttc	accattctgt	ctccgataag	cactctcaaa		240
ttgctaaagc	tatgtggatt	acgg					264

<210> 275
 <211> 359
 <212> DNA
 <213> Chlamydia

<400> 275
 ggatccgaat tcggcacgag ataaaacctg aaccacaaca aagatctaaa actctctgat 60
 ttccagctgc aaattctttt agataaaat caaccatttc ttcagtttca tatcttggaa 120
 ttaaaacttg ttctctttaa ttaattctag tatllaaagta ttcaacatag cccattatta 180
 attgaatttg ataattttgc cttaataatt cacattcttt ttcagtaatt ttagggtcta 240
 aacgtaacg ctttttttct aaaattaatg ttctctcatt attcatttta taagccactt 300
 tcttttattt ttgtattttg ttcttctgtt agtaatgctt caataatagt taataattt 359

<210> 276
 <211> 357
 <212> DNA
 <213> Chlamydia

<400> 276
 aaaaacttg atataattt ttttttcata acttcacagc tcttttctag aaaagcttt 60
 atgggtagta gtgactctaa cgttttttat tattaagacg atccccggag atccttttaa 120
 tgaatgaana ggaacatcc ttccgcaga aacttttagca ctatataaga atcggttacgg 180
 gttagataag cctttattca cccagatctc tatctatttg aaatgtctgc taacacatga 240
 ttccgggaaa tctcttatct acaagatcgc aaatctcagc attattgtcg ccgctctccc 300
 atcttccgct attcttgagc ttgaaagctt gtgtttactc gtgccgaatt cggatcc 357

<210> 277
 <211> 505
 <212> DNA
 <213> Chlamydia

<400> 277
 ggatccgaat tcggcacgag ctcggtccga ttgcttgctt cagtcacccc atcggtatag 60
 agcactaaaa gagactcttc ttcaagaacg agagtgttag cagggtgagg aggaacttca 120
 ggtaaaaaat ctaaggccat accaggatgc gacaggaaag agatatctcc attaggagct 180
 cggagacacg ctgggtttgt gccacaagaa tagtattcta gtctctgttg tgcgtaatga 240
 taacaataaa tgcataagtg tacaacatc ccagattcag ctgtctgttg atagaagaga 300
 cgagctgttt gttgaacggc ttcttgtaata gaggagagct cactcaaaaa ggtatgtaac 360
 atgtttttca ggaataaagg gtatggcgac ctatttgact ctttcccgga agcatcagca 420
 acgattagaa agagttagc ttggggacct tcgcctataa caaagatctc aaagaaatct 480
 cctctacgg taactgcagg aatat 505

<210> 278
 <211> 407
 <212> DNA
 <213> Chlamydia

<400> 278
 ggatccgaat tcggcacgag aactactgag caaattgggt atccaacttc ctctttaoga 60
 aagaaaaaca gaagccattc tccataccaa gatttgttgc atcgacaata aaactccaat 120
 ctttggctct gctaactgga gcggtgctgg tatgattaaa aactttgaag acctattcat 180
 ctctggccca attacagaga cacagcttca ggcctttatg gacgtctggt ctcttclaga 240
 aacaaatagc tctctatctg cccagagagc cgtgcttacg gccctactc ctccaagtag 300
 acctactcaa caagatacag attctgatga cgaacaacgc agtaccagg agcaagctat 360
 cgtatgaga aaataggatt agggaaacaa aacgacagca aaccaca 407

<210> 279
 <211> 351
 <212> DNA
 <213> Chlamydia

```

<400> 279
ctcgtgcccgc ttacaggagg cttgtatcct ttaaaataga gtttttctta tgaccccacg 60
tggcgatagg ccgggtctag cgcgcgatag agaaatalcg gtlgggtttt glccttgagg 120
ggatcgtata ctttttcaaa gtatgtgtccc cgtatcgatt atctggagge tcttatgtct 180
ttttttcata ctagaaaata taagcttctc ctcaggaggc tcttgtgttt agcaggctgt 240
ttcttaataa acagctgttc cttctagtca ggaatacaac ccgctgatga gacgatctat 300
gtcttgtcta tgaatcgcat gatttgtgat tctcgtgcgc aattcggatc c 351

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```

<210> 280
<211> 522
<212> DNA
<213> Chlamydia

```

```

<400> 280
ggatccgaat tcggcacgag cagaggaaaa aggcgatact cctcttgaag atcgtttcac 60
agaagatctt tcggaagtct ctggagaaga ttttcgagga ttgaaaaatt cgttcgatga 120
tgattcttct tctgacgaaa ttctcgatgc gctcacaaat aaattttctg atccccaat 180
aaagatctta gctcttgatt atctaattca aatagctccc tctgatggga aacttaagtc 240
cgctctcatt caggcaaaag atcaactgat gagccagaat cctcaggcga ttgttggagg 300
acgcaatggt ctgttagctt cagaaaacct tgcttcacga gcaaatatcat ctcttctatc 360
gottcgctcc ttatatctcc aagtaacctc atccccctct aattgcgcta atttcatatc 420
aatgcttgct tcttactcgc catcagagaa aaccgctggt atggagtctt tagtgaatgg 480
catggtagca gattttaaat cggaggggccc ttccattcct cc 522

```

```

<210> 281
<211> 577
<212> DNA
<213> Chlamydia

```

```

<400> 281
ggatccgaat tcggcacgag atgcttctat tacaatttgt ttggatgcgg aaaaagctta 60
ccagcttat: ctgaaaaggt tgggagatca aattcttgtt ggaattgctg atactattgt 120
tgatagtaca gtccaagata ttttagacaa aatcacacaa gacccttctc taggtttgtt 180
gaaagctttt aacaactttc caatcactaa taaaattcaa tgcaacgggt tatttacttc 240
caggaaacatt gaaaactttat taggaggaac tgaataggaa aaattcacag tcacacccaa 300
aagctctggg agcatgttct tagtctcagc agatattatt gcatcaagaa ttggaaggcgg 360
cgtttgtcta cgtttgttac gagaagtgta ttctaagccc tacgcgatta gttatggata 420
ctcatcaggg gtttcctaat tatgtagtct aagaaccaga atlatataa caggattgac 480
tcgacaacag tattcattac gtgtaggcgg tttagaaaag ggtgtggtat ggggttaatgc 540
cctttctaat ggcaatgata ttttaggaat aacaaat 577

```

```

<210> 282
<211> 607
<212> DNA
<213> Chlamydia

```

```

<400> 282
actmatcttc cccgggctcg agtgcggcgg caagcttgct gacggagctc gatacaaaaa 60
tgtgtgcgtg tgaacogctt ctcaaaaaag tigtcttaaa agatattgtc tgcgttcogg 120
atlagttaca tgttttaaaa ttgctagaac aatattattc ccaaccaagc tctctgoggf 180
gctgaaaaaa cctaaattca aaagaatgac tgcgcgctca tcttcagaaa gacgatccga 240
cttccataat tgcagtgtct tcccactggg gatctctgta gggagccagt tatitggcga 300
gccattcaaa taatgttccc aagccacttt gtacttaata ggaacaagtt ggttgacatc 360
gacctggttg cagltcacta gacgcttgct attlagat ta acgctgttct glltccatc 420
taaaatattc gcttgcataa gaaccgttaa ttttattggt aatttatatg attaataact 480
gacatgcttc acaccttct tcacaagaac agacagggtc ttctctgct ctttcaacaa 540
taattcctgc cgaagcagac ttattcttca tccaacgagg ctgaattcct ctcttaltaa 600
tatctac 607

```

```

<210> 283
<211> 1077

```


<212> DNA

<213> Chlamydia

<400> 283

ggatcogaat	toggcagcag	aagttaacga	tgaacgattg	ttcctttggt	agagaaggag	60
caatcgaaac	taaaagtgcg	agagcatgtg	aagactccaa	tgcagggaata	atccccat	120
ttctagtaag	caggaaaaaa	gctcgltaacg	ccctcttcac	ggtggctaata	gtataaaaag	180
ctcgctctga	ctcatgcatt	tggcgaatgat	ctggcccaac	tgaaggataa	tctaataccag	240
cggaaatgga	gtgagtttgt	aataactgtc	catcgctcat	tgaagaaga	tacgaataaa	300
atccgtggaa	tactccaggt	cgccctgttg	caaaaactgc	tgcattgttt	ccctgaagaaa	360
tgccagcttc	tcccccttc	actccaatta	attggacttt	tggattcggt	ataaaaatgat	420
ggaaaaatcc	aataagcgtg	gagccacctc	cgatacatgc	aatacagaata	tcaggatctc	480
ttcctgcaac	tgcattggatt	tgtcttttca	cttcagcgct	tataacagac	tgaaaaaatc	540
gaacgatata	gggataaagg	aaaggtccta	aggccgatcc	taagcaaatg	tgagtaaatg	600
agtggtgtgt	tgcccaatct	tgtagagctt	gattaaactgc	atcttttgat	ccacaagatc	660
cttttgtttac	agaaaacgact	tcagcaccta	aaaagcgcat	tttctctaca	tttggtttct	720
gtcgcttccac	atcttttgtct	cccatgtata	ctacacaaac	taactctaga	taagcacacg	780
ctgtgtgtgt	tgctactcca	tgtgtcccg	caactgtttc	agctacaaca	cgtgttttcc	840
caagataatt	agcaagcaaaa	cactgaccaa	gagcattatt	cagtttatgt	gctcctgtat	900
gcaaaagatc	ttcgcgttta	agaaatactc	tagggccatc	aatagctcga	gcaaaattct	960
taacttcagt	cagaggagtt	tgtctcccg	catagttttt	caaaatacaa	tctagtccag	1020
ataaaaaact	ttgctgagtt	ttgagaactc	cccatccgcg	tttttagattc	tgtatag	1077

<210> 284

<211> 407

<212> DNA

<213> Chlamydia

<400> 284

ggatcogaat	toggcagcag	aactactgag	caaattgggt	atccaacttc	ctctttacga	60
aagaaaaaca	gaaggcattc	tcoataccaa	gattttgttc	atcgacaata	aaactccaat	120
cttttggctct	gctaactgga	ggggtgctgg	tatgattaaa	aactttgaag	acctattcat	180
cccttgcgcc	attacagaga	cacagcttca	ggcctttatg	gacgtctggg	ctcttctaga	240
aaacaaatag	tcttatctgt	ccccagagag	cgtgotttacg	gccccactc	cttcaagtag	300
acctaactca	caagatcacg	attctgatga	cgaaacaaccg	agtaaccagc	agcaagctat	360
cogtatgaga	aaataggatt	agggaaacaa	aacgacagca	aaccaca		407

<210> 285

<211> 802

<212> DNA

<213> Chlamydia

<400> 285

ggatcogaat	toggcagcag	ttagcttaaat	gtctttgtca	tctctaccta	cattttgcagc	60
taattctaca	ggcacaattg	gaatcgtaa	gaatcgtcgc	tgccatagaag	agttctgctct	120
tgggaaaaaa	gaatctgctg	aattcgaaaa	gatgaaaaac	caattctcta	acagcatggg	180
gaagtaggag	gaagaactgt	ctttctatcta	ttccaaaggtc	caagaagcag	attacatgga	240
gaggtctatcc	gagacgcgag	ctggccgaatt	aagaaaaaaa	ttcgaagact	tatctgcaga	300
atacaacaca	gtccaagggc	agtatacca	aattataaac	caaagtaact	tcaagcgcat	360
gcaaaagatt	atggaagaa	tgaaaaaagc	ttctgaact	gtgcgtatc	ataaaggctt	420
ctcagctcct	cttaacgaag	atattgtctt	atctatcgat	agttcggcag	ataaaaacga	480
tgtctgtatt	aaagtctctg	atgattcttt	tcaaaaatct	taacatcgga	agcaagcaga	540
ggagtgccgt	atgtctcaat	ccacttatc	tcttggaaca	tttagctgatt	ttttgaaagt	600
cgaatttcaa	ggaaatggag	ctactctctc	ttccggaggt	gaagagatcg	aggaagcaat	660
aacggcacac	atcacattct	tagataatga	aaaaatagct	aaacatttaa	aatcatcgga	720
agctggcgct	atcatcatat	ctcgaacaca	gtttcaaaaa	tatcgagact	tgaataaaaa	780
ctttctctatc	actctcgagt	ct				802

<210> 286

<211> 588

<212> DNA

<213> Chlamydia

```

<400> 286
ggatccgaat tcggcacgag gcaatattta cccccaacat tacggttcca aataagcgat 60
aaggtcttct aataaggaag ttaatgtaag aggtcttttt attgcttttc gtaaggtagt 120
attgcaacgc caogcgattg aatgatacgc aagccatttc catcatggaa aagaaccottt 180
ggacaaaat acaaaggagg ttccactccta accagaaaaa gggagagtta gtttccatgg 240
gttttctcta tatcacccgc ttccacacaa ttaggagccg cgtctagtat ttggaataca 300
aattgtcccc aagcgaattt tgttctcgtt tcaggggattt ctctaatgt tctgtcagc 360
catccgccta tggtaaacga attagctgta gtaggaaagt caactccaaa caggtcatag 420
aaatcagaaa gcctcatagg gctcgcagca ataacaacat tcttgtctga gtagcgcaat 480
tgtttaaaag atggcgcatg atgagctacc tcatcagaga ctatttttaa tagatcattt 540
tgggtaatca atccttctat agaccatat tcatcaatga taatctcg 588

```

<210> 287

<211> 489

<212> DNA

<213> Chlamydia

<220>

<221> misc_feature

<222> 488

<223> n = A,T,C or G

```

<400> 287
agtgccattt gttttgcagg ctttgtctga tgatagcgat accgtacgtg agattgctgt 60
acaagtagct gttatgtatg gttctagtgt cttactgcgc gccgtggcgc atttagcgaa 120
aaatgattct totattcaag tacgcatacgc tgcattatcgt gctgcagccg tgttggagat 180
acaagattct gtgcctcatt tacgagttgt agtccaaaat acacaattag atggaaocgga 240
aagaagagaa gcttggagat ctttatgtgt tcttactcgg cctcatagtg gtgtattaac 300
tgccatagat caagctttaa tgacctgtga gatgttaaa gaaatcctg aaaagtgtac 360
ggaagaacag attogtcat tattggctcg agatcatcca gaagtgcagg tagctacttt 420
acagatcatt ctgagaggag gtagagtatt ccggtcatct tctataatgg aatcggttct 480
cgtgccgnt 489

```

<210> 288

<211> 191

<212> DNA

<213> Chlamydia

```

<400> 288
ggatccgaat tcaggatagt ctgttggggt atcaataaaa aggggttttg cattttttaa 60
gacgactttg tagataacgc taggagctgt agcaataata tcgagatcaa attctctaga 120
gattctctca aagatgattt ctaagtgcag cagtctctaa aatccacagc ggaacccaaa 180
tcggagagag t 191

```

<210> 289

<211> 515

<212> DNA

<213> Chlamydia

```

<400> 289
ggatccgaat tcggcacgag gagcgaogtg aaatagtgga atcttccocgt attcttatta 60
cttctcgtt gcctttacga aatggctcct tgcattttgg acatattacc ggtgcctatt 120
tgcttcgaga tgtttatcgc cgttttcaga gactacaagg caaagaggtt ttgtatattt 180
gtggttctga tgaatacggga atcgcaatta ccttaaatgc agagttggca ggcattgggt 240
atcaagaata tgtcgacatg tatcataaag ttcataaaga taccttcaag aaattgggaa 300
tttctgtaga tttcttttcc agaactacga acgcttatca tctctgtatt gtccaagatt 360
tctatcgaaa cttgcagaaa ccgggactcg tagagaatca ggtgaoccaa cagctgtatt 420
ctgaggaaag agggaaagtt tttagcgacc gttatgtgt aggtacttgt cccaagtgtg 480
gttttgatcg agctcgagga gatgagtgct agcag 515

```

<210> 290
 <211> 522
 <212> DNA
 <213> Chlamydia

<400> 290
 ggatccgaat toggcacgag ggaggaatgg aaggggccctc cgattktama tctgtaccaa 60
 tgccattcac tagaaaactcc ataacagcgg tttctctcga tggcgagtaa gaagcaagca 120
 ttgtgatgtaa attagcgcaa tttagaggggg atgaggttac ttggaaataa aaggagcgaa 180
 gcgatgaagg agatgtattt gctctggaag caaagggttc tgaagctaac agaactatgc 240
 gtccctcaac aatcgactga ggattctggc tcatcagttg atgctttggc tgaatgagag 300
 cggacttaag ttcccatca gagggagcta ttggaattag ataactaaga gctagatcct 360
 ttatttgtggg atcagaaaaa ttactttgtga ggcgcatcgaa aatttcgtca gaagaagaat 420
 catcatcgaa cgaatttttc aatcctcgaa aatcttctcc agagactctg gaaagatctt 480
 ctgtgaaagc atcttcaaga ggagtatcgc ctttttcocyc tg 522

<210> 291
 <211> 1002
 <212> DNA
 <213> Chlamydia

<400> 291
 atggcgacta acgcaattag atcggcagga agtgcagcaa gtaagatgct gctgccagtt 60
 gccaaaagaac cagcggtgtt cagctccttt gctcagaaga ggattttattg tattcaacaa 120
 ttttttacaa accctgggaa taagttagca aagttttagt gggcaacaaa aagtttagat 180
 aaatgcttta agctaagttaa ggcgttttct gactgtgtcg taggatcgct ggaagagcgc 240
 gggatgcacag gggacgcatt gacctcgcgc agaaccgccc agggtagttt aaaaacaact 300
 cgagaagtgt ttgccttagc taatgtgctc aatggagctg ttccatctat cgttaactcg 360
 actcagaggt gttaccaata cacacgtcaa gctctcaggt taggaagcaa gacaaaagaa 420
 agaaaaaacg ctggggagta tagtaaaaat ctattaactc gagtgatta cctattggca 480
 gctccacagg aagctgttac ggcagtcgtt gcaacgactt actcagcgac attcgggtgt 540
 ttacgtccgt taatgttaat caataaaact acagcaaaac cattcttaga caaagcgact 600
 gttagcaatt ttggcgcggc tgttgctgga attatgacca ttaatcataa ggcaggagtt 660
 gctggtgctg ttggcgggaat cgcattagaa caaaagctgt tcaaacgtgc gaaggaatcc 720
 ctatacaatg agagatgtgc cttagaaaaa caacaatctc agttgagtggt ggacgtgatt 780
 ctaagcgcgg aaaggcatt acgtaaaaga cagcttgcta ctctaaaaag aaatgtttta 840
 actcttcttg aaaaagcttt agagtttgta gtgtagtgag tcaaaactat tcctttaccg 900
 attacagtggt cttgctccgc tgcaatttct ggagccttga cggcagcatc cgacgaat 960
 ggcttatata gcatatggca gaaaacaaag tctggcaaat aa 1002

<210> 292
 <211> 333
 <212> PRT
 <213> Chlamydia

<400> 292
 Met Ala Thr Asn Ala Ile Arg Ser Ala Gly Ser Ala Ala Ser Lys Met
 1 5 10 15
 Leu Leu Pro Val Ala Lys Glu Pro Ala Ala Val Ser Ser Phe Ala Gln
 20 25 30
 Lys Gly Ile Tyr Cys Ile Gln Phe Phe Thr Asn Pro Gly Asn Lys
 35 40 45
 Leu Ala Lys Phe Val Gly Ala Thr Lys Ser Leu Asp Lys Cys Phe Lys
 50 55 60
 Leu Ser Lys Ala Val Ser Asp Cys Val Val Gly Ser Leu Glu Glu Ala
 65 70 75 80
 Gly Cys Thr Gly Asp Ala Leu Thr Ser Ala Arg Asn Ala Gln Gly Met
 85 90 95
 Leu Lys Thr Thr Arg Glu Val Val Ala Leu Ala Asn Val Leu Asn Gly
 100 105 110

Ala Val Pro Ser Ile Val Asn Ser Thr Gln Arg Cys Tyr Gln Tyr Thr
 115 120 125
 Arg Gln Ala Phe Glu Leu Gly Ser Lys Thr Lys Glu Arg Lys Thr Pro
 130 135 140
 Gly Glu Tyr Ser Lys Met Leu Leu Thr Arg Gly Asp Tyr Leu Leu Ala
 145 150 155 160
 Ala Ser Arg Glu Ala Cys Thr Ala Val Gly Ala Thr Thr Tyr Ser Ala
 165 170 175
 Thr Phe Gly Val Leu Arg Pro Leu Met Leu Ile Asn Lys Leu Thr Ala
 180 185 190
 Lys Pro Phe Leu Asp Lys Ala Thr Val Gly Asn Phe Gly Thr Ala Val
 195 200 205
 Ala Gly Ile Met Thr Ile Asn His Met Ala Gly Val Ala Gly Ala Val
 210 215 220
 Gly Gly Ile Ala Leu Glu Gln Lys Leu Phe Lys Arg Ala Lys Glu Ser
 225 230 235 240
 Leu Tyr Asn Glu Arg Cys Ala Leu Glu Asn Gln Gln Ser Gln Leu Ser
 245 250 255
 Gly Asp Val Ile Leu Ser Ala Glu Arg Ala Leu Arg Lys Glu His Val
 260 265 270
 Ala Thr Leu Lys Arg Asn Val Leu Thr Leu Leu Glu Lys Ala Leu Glu
 275 280 285
 Leu Val Val Asp Gly Val Lys Leu Ile Pro Leu Pro Ile Thr Val Ala
 290 295 300
 Cys Ser Ala Ala Ile Ser Gly Ala Leu Thr Ala Ala Ser Ala Gly Ile
 305 310 315 320
 Gly Leu Tyr Ser Ile Trp Gln Lys Thr Lys Ser Gly Lys
 325 330

<210> 293

<211> 7

<212> DNA

<213> Chlamydia

<400> 293

tgcaatc

<210> 294

<211> 196

<212> PRT

<213> Chlamydia

<400> 294

Thr Met Gly Ser Leu Val Gly Arg Gln Ala Pro Asp Phe Ser Gly Lys
 5 10 15

Ala Val Val Cys Gly Glu Glu Lys Glu Ile Ser Leu Ala Asp Phe Arg
 20 25 30

Gly Lys Tyr Val Val Leu Phe Phe Tyr Pro Lys Asp Phe Thr Tyr Val
 35 40 45

Cys Pro Thr Glu Leu His Ala Phe Gln Asp Arg Leu Val Asp Phe Glu
 50 55 60

Glu His Gly Ala Val Val Leu Gly Cys Ser Val Asp Asp Ile Glu Thr
 65 70 75 80

His Ser Arg Trp Leu Thr Val Ala Arg Asp Ala Gly Gly Ile Glu Gly
 85 90 95

Thr Glu Tyr Pro Leu Leu Ala Asp Pro Ser Phe Lys Ile Ser Glu Ala
 100 105 110
 Phe Gly Val Leu Asn Pro Glu Gly Ser Leu Ala Leu Arg Ala Thr Phe
 115 120 125
 Leu Ile Asp Lys His Gly Val Ile Arg His Ala Val Ile Asn Asp Leu
 130 135 140
 Pro Leu Gly Arg Ser Ile Asp Glu Glu Leu Arg Ile Leu Asp Ser Leu
 145 150 155 160
 Ile Phe Phe Glu Asn His Gly Met Val Cys Pro Ala Asn Trp Arg Ser
 165 170 175
 Gly Glu Arg Gly Met Val Pro Ser Glu Glu Lys Leu Tyr Phe
 180 185 190
 Gln Thr Met Asp
 195

<210> 295
 <211> 181
 <212> FRT
 <213> Chlamydia

<400> 295
 Lys Gly Gly Lys Met Ser Thr Thr Ile Ser Gly Asp Ala Ser Ser Leu
 5 10 15
 Pro Leu Pro Thr Ala Ser Cys Val Glu Thr Lys Ser Thr Ser Ser Ser
 20 25 30
 Thr Lys Gly Asn Thr Cys Ser Lys Ile Leu Asp Ile Ala Leu Ala Ile
 35 40 45
 Val Gly Ala Leu Val Val Val Ala Gly Val Leu Ala Leu Val Leu Cys
 50 55 60
 Ala Ser Asn Val Ile Phe Thr Val Ile Gly Ile Pro Ala Leu Ile Ile
 65 70 75 80
 Gly Ser Ala Cys Val Gly Ala Gly Ile Ser Arg Leu Met Tyr Arg Ser
 85 90 95
 Ser Tyr Ala Ser Leu Glu Ala Lys Asn Val Leu Ala Glu Gln Arg Leu
 100 105 110
 Arg Asn Leu Ser Glu Glu Lys Asp Ala Leu Ala Ser Val Ser Phe Ile
 115 120 125
 Asn Lys Met Phe Leu Arg Gly Leu Thr Asp Asp Leu Gln Ala Leu Glu
 130 135 140
 Ala Lys Val Met Glu Phe Glu Ile Asp Cys Leu Asp Arg Leu Glu Lys
 145 150 155 160
 Asn Glu Gln Ala Leu Leu Ser Asp Val Arg Leu Val Leu Ser Ser Tyr
 165 170 175

Thr Arg Trp Leu Asp
180

<210> 296

<211> 124

<212> PRT

<213> Chlamydia

<400> 296

Ile Tyr Glu Val Met Asn Met Asp Leu Glu Thr Arg Arg Ser Phe Ala
5 10 15

Val Gln Gln Gly His Tyr Gln Asp Pro Arg Ala Ser Asp Tyr Asp Leu
20 25 30

Pro Arg Ala Ser Asp Tyr Asp Leu Pro Arg Ser Pro Tyr Pro Thr Pro
35 40 45

Pro Leu Pro Ser Arg Tyr Gln Leu Gln Asn Met Asp Val Glu Ala Gly
50 55 60

Phe Arg Glu Ala Val Tyr Ala Ser Phe Val Ala Gly Met Tyr Asn Tyr
65 70 75 80

Val Val Thr Gln Pro Gln Glu Arg Ile Pro Asn Ser Gln Gln Val Glu
85 90 95

Gly Ile Leu Arg Asp Met Leu Thr Asn Gly Ser Gln Thr Phe Ser Asn
100 105 110

Leu Met Gln Arg Trp Asp Arg Glu Val Asp Arg Glu
115 120

<210> 297

<211> 488

<212> PRT

<213> Chlamydia

<400> 297

Lys Gly Ser Leu Pro Ile Leu Gly Pro Phe Leu Asn Gly Lys Met Gly
5 10 15

Phe Trp Arg Thr Ser Ile Met Lys Met Asn Arg Ile Trp Leu Leu Leu
20 25 30

Leu Thr Phe Ser Ser Ala Ile His Ser Pro Val Arg Gly Glu Ser Leu
35 40 45

Val Cys Lys Asn Ala Leu Gln Asp Leu Ser Phe Leu Glu His Leu Leu
50 55 60

Gln Val Lys Tyr Ala Pro Lys Thr Trp Lys Glu Gln Tyr Leu Gly Trp
65 70 75 80

Asp Leu Val Gln Ser Ser Val Ser Ala Gln Gln Lys Leu Arg Thr Gln
85 90 95

Glu Asn Pro Ser Thr Ser Phe Cys Gln Gln Val Leu Ala Asp Phe Ile
100 105 110

Gly Gly Leu Asn Asp Phe His Ala Gly Val Thr Phe Phe Ala Ile Glu
 115 120 125
 Ser Ala Tyr Leu Pro Tyr Thr Val Gln Lys Ser Ser Asp Gly Arg Phe
 130 135 140
 Tyr Phe Val Asp Ile Met Thr Phe Ser Ser Glu Ile Arg Val Gly Asp
 145 150 155 160
 Glu Leu Leu Glu Val Asp Gly Ala Pro Val Gln Asp Val Leu Ala Thr
 165 170 175
 Leu Tyr Gly Ser Asn His Lys Gly Thr Ala Ala Glu Glu Ser Ala Ala
 180 185 190
 Leu Arg Thr Leu Phe Ser Arg Met Ala Ser Leu Gly His Lys Val Pro
 195 200 205
 Ser Gly Arg Thr Thr Leu Lys Ile Arg Arg Pro Phe Gly Thr Thr Arg
 210 215 220
 Glu Val Arg Val Lys Trp Arg Tyr Val Pro Glu Gly Val Gly Asp Leu
 225 230 235 240
 Ala Thr Ile Ala Pro Ser Ile Arg Ala Pro Gln Leu Gln Lys Ser Met
 245 250 255
 Arg Ser Phe Phe Pro Lys Lys Asp Asp Ala Phe His Arg Ser Ser Ser
 260 265 270
 Leu Phe Tyr Ser Pro Met Val Pro His Phe Trp Ala Glu Leu Arg Asn
 275 280 285
 His Tyr Ala Thr Ser Gly Leu Lys Ser Gly Tyr Asn Ile Gly Ser Thr
 290 295 300
 Asp Gly Phe Leu Pro Val Ile Gly Pro Val Ile Trp Glu Ser Glu Gly
 305 310 315 320
 Leu Phe Arg Ala Tyr Ile Ser Ser Val Thr Asp Gly Asp Gly Lys Ser
 325 330 335
 His Lys Val Gly Phe Leu Arg Ile Pro Thr Tyr Ser Trp Gln Asp Met
 340 345 350
 Glu Asp Phe Asp Pro Ser Gly Pro Pro Pro Trp Glu Glu Phe Ala Lys
 355 360 365
 Ile Ile Gln Val Phe Ser Ser Asn Thr Glu Ala Leu Ile Ile Asp Gln
 370 375 380
 Thr Asn Asn Pro Gly Gly Ser Val Leu Tyr Leu Tyr Ala Leu Leu Ser
 385 390 395 400
 Met Leu Thr Asp Arg Pro Leu Glu Leu Pro Lys His Arg Met Ile Leu
 405 410 415
 Thr Gln Asp Glu Val Val Asp Ala Leu Asp Trp Leu Thr Leu Leu Glu
 420 425 430

Asn Val Asp Thr Asn Val Glu Ser Arg Leu Ala Leu Gly Asp Asn Met
435 440 445

Glu Gly Tyr Thr Val Asp Leu Gln Val Ala Glu Tyr Leu Lys Ser Phe
450 455 460

Gly Arg Gln Val Leu Asn Cys Trp Ser Lys Gly Asp Ile Glu Leu Ser
465 470 475 480

Thr Pro Ile Pro Leu Phe Gly Phe
485

<210> 298
<211> 140
<212> PRT
<213> Chlamydia

<400> 298
Arg Ile Asp Ile Ser Ser Val Thr Phe Phe Ile Gly Ile Leu Leu Ala
5 10 15

Val Asn Ala Leu Thr Tyr Ser His Val Leu Arg Asp Leu Ser Val Ser
20 25 30

Met Asp Ala Leu Phe Ser Arg Asn Thr Leu Ala Val Leu Leu Gly Leu
35 40 45

Val Ser Ser Val Leu Asp Asn Val Pro Leu Val Ala Ala Thr Ile Gly
50 55 60

Met Tyr Asp Leu Pro Met Asn Asp Pro Leu Trp Lys Leu Ile Ala Tyr
65 70 75 80

Thr Ala Gly Thr Gly Gly Ser Ile Leu Ile Ile Gly Ser Ala Ala Gly
85 90 95

Val Ala Tyr Met Gly Met Glu Lys Val Ser Phe Gly Trp Tyr Val Lys
100 105 110

His Ala Ser Trp Ile Ala Leu Ala Ser Tyr Phe Gly Gly Leu Ala Val
115 120 125

Tyr Phe Leu Met Glu Asn Cys Val Asn Leu Phe Val
130 135 140

<210> 299
<211> 361
<212> PRT
<213> Chlamydia

<400> 299
His Gln Glu Ile Ala Asp Ser Pro Leu Val Lys Lys Ala Glu Glu Gln
5 10 15

Ile Asn Gln Ala Gln Gln Asp Ile Gln Thr Ile Thr Pro Ser Gly Leu
20 25 30

Asp Ile Pro Ile Val Gly Pro Ser Gly Ser Ala Ala Ser Ala Gly Ser
35 40 45

Ala Ala Gly Ala Leu Lys Ser Ser Asn Asn Ser Gly Arg Ile Ser Leu
 50 55 60
 Leu Leu Asp Asp Val Asp Asn Glu Met Ala Ala Ile Ala Met Gln Gly
 65 70 75 80
 Phe Arg Ser Met Ile Glu Gln Phe Asn Val Asn Asn Pro Ala Thr Ala
 85 90 95
 Lys Glu Leu Gln Ala Met Glu Ala Gln Leu Thr Ala Met Ser Asp Gln
 100 105 110
 Leu Val Gly Ala Asp Gly Glu Leu Pro Ala Glu Ile Gln Ala Ile Lys
 115 120 125
 Asp Ala Leu Ala Gln Ala Leu Lys Gln Pro Ser Ala Asp Gly Leu Ala
 130 135 140
 Thr Ala Met Gly Gln Val Ala Phe Ala Ala Lys Val Gly Gly Gly
 145 150 155 160
 Ser Ala Gly Thr Ala Gly Thr Val Gln Met Asn Val Lys Gln Leu Tyr
 165 170 175
 Lys Thr Ala Phe Ser Ser Thr Ser Ser Ser Tyr Ala Ala Leu Leu
 180 185 190
 Ser Asp Gly Tyr Ser Ala Tyr Lys Thr Leu Asn Ser Leu Tyr Ser Glu
 195 200 205
 Ser Arg Ser Gly Val Gln Ser Ala Ile Ser Gln Thr Ala Asn Pro Ala
 210 215 220
 Leu Ser Arg Ser Val Ser Arg Ser Gly Ile Glu Ser Gln Gly Arg Ser
 225 230 235 240
 Ala Asp Ala Ser Gln Arg Ala Ala Glu Thr Ile Val Arg Asp Ser Gln
 245 250 255
 Thr Leu Gly Asp Val Tyr Ser Arg Leu Gln Val Leu Asp Ser Leu Met
 260 265 270
 Ser Thr Ile Val Ser Asn Pro Gln Ala Asn Gln Glu Glu Ile Met Gln
 275 280 285
 Lys Leu Thr Ala Ser Ile Ser Lys Ala Pro Gln Phe Gly Tyr Pro Ala
 290 295 300
 Val Gln Asn Ser Val Asp Ser Leu Gln Lys Phe Ala Ala Gln Leu Glu
 305 310 315 320
 Arg Glu Phe Val Asp Gly Glu Arg Ser Leu Ala Glu Ser Gln Glu Asn
 325 330 335
 Ala Phe Arg Lys Gln Pro Ala Phe Ile Gln Gln Val Leu Val Asn Ile
 340 345 350
 Ala Ser Leu Phe Ser Gly Tyr Leu Ser
 355 360

<210> 300
 <211> 207
 <212> PRT
 <213> Chlamydia

<400> 300
 Ser Ser Lys Ile Val Ser Leu Cys Glu Gly Ala Val Ala Asp Ala Arg
 5 10 15
 Met Cys Lys Ala Glu Leu Ile Lys Lys Glu Ala Asp Ala Tyr Leu Phe
 20 25 30
 Cys Glu Lys Ser Gly Ile Tyr Leu Thr Lys Lys Glu Gly Ile Leu Ile
 35 40 45
 Pro Ser Ala Gly Ile Asp Glu Ser Asn Thr Asp Gln Pro Phe Val Leu
 50 55 60
 Tyr Pro Lys Asp Ile Leu Gly Ser Cys Asn Arg Ile Gly Glu Trp Leu
 65 70 75 80
 Arg Asn Tyr Phe Arg Val Lys Glu Leu Gly Val Ile Ile Thr Asp Ser
 85 90 95
 His Thr Thr Pro Met Arg Arg Gly Val Leu Gly Ile Gly Leu Cys Trp
 100 105 110
 Tyr Gly Phe Ser Pro Leu His Asn Tyr Ile Gly Ser Leu Asp Cys Phe
 115 120 125
 Gly Arg Pro Leu Gln Met Thr Gln Ser Asn Leu Val Asp Ala Leu Ala
 130 135 140
 Val Ala Ala Val Val Cys Met Gly Glu Gly Asn Glu Gln Thr Pro Leu
 145 150 155 160
 Ala Val Ile Glu Gln Ala Pro Asn Met Val Tyr His Ser Tyr Pro Thr
 165 170 175
 Ser Arg Glu Glu Tyr Cys Ser Leu Arg Ile Asp Glu Thr Glu Asp Leu
 180 185 190
 Tyr Gly Pro Phe Leu Gln Ala Val Thr Trp Ser Gln Glu Lys Lys
 195 200 205

<210> 301
 <211> 183
 <212> PRT
 <213> Chlamydia

<400> 301
 Ile Pro Pro Ala Pro Arg Gly His Pro Gln Ile Glu Val Thr Phe Asp
 5 10 15
 Ile Asp Ala Asn Gly Ile Leu His Val Ser Ala Lys Asp Ala Ala Ser
 20 25 30
 Gly Arg Glu Gln Lys Ile Arg Ile Glu Ala Ser Ser Gly Leu Lys Glu
 35 40 45

Asp Glu Ile Gln Gln Met Ile Arg Asp Ala Glu Leu His Lys Glu Glu
 50 55 60
 Asp Lys Gln Arg Lys Glu Ala Ser Asp Val Lys Asn Glu Ala Asp Gly
 65 70 75 80
 Met Ile Phe Arg Ala Glu Lys Ala Val Lys Asp Tyr His Asp Lys Ile
 85 90 95
 Pro Ala Glu Leu Val Lys Glu Ile Glu Glu His Ile Glu Lys Val Arg
 100 105 110
 Gln Ala Ile Lys Glu Asp Ala Ser Thr Thr Ala Ile Lys Ala Ala Ser
 115 120 125
 Asp Glu Leu Ser Thr Arg Met Gln Lys Ile Gly Glu Ala Met Gln Ala
 130 135 140
 Gln Ser Ala Ser Ala Ala Ser Ser Ala Ala Asn Ala Gln Gly Gly
 145 150 155 160
 Pro Asn Ile Asn Ser Glu Asp Leu Lys Lys His Ser Phe Ser Thr Arg
 165 170 175
 Pro Pro Ala Gly Gly Ser Ala
 180

<210> 302

<211> 232

<212> FRT

<213> Chlamydia

<400> 302

Met Thr Lys His Gly Lys Arg Ile Arg Gly Ile Gln Glu Thr Tyr Asp
 5 10 15
 Leu Ala Lys Ser Tyr Ser Leu Gly Glu Ala Ile Asp Ile Leu Lys Gln
 20 25 30
 Cys Pro Thr Val Arg Phe Asp Gln Thr Val Asp Val Ser Val Lys Leu
 35 40 45
 Gly Ile Asp Pro Arg Lys Ser Asp Gln Gln Ile Arg Gly Ser Val Ser
 50 55 60
 Leu Pro His Gly Thr Gly Lys Val Leu Arg Ile Leu Val Phe Ala Ala
 65 70 75 80
 Gly Asp Lys Ala Ala Glu Ala Ile Glu Ala Gly Ala Asp Phe Val Gly
 85 90 95
 Ser Asp Asp Leu Val Glu Lys Ile Lys Gly Gly Trp Val Asp Phe Asp
 100 105 110
 Val Ala Val Ala Thr Pro Asp Met Met Arg Glu Val Gly Lys Leu Gly
 115 120 125
 Lys Val Leu Gly Pro Arg Asn Leu Met Pro Thr Pro Lys Ala Gly Thr
 130 135 140

Val Thr Thr Asp Val Val Lys Thr Ile Ala Glu Leu Arg Lys Gly Lys
 145 150 155 160
 Ile Glu Phe Lys Ala Asp Arg Ala Gly Val Cys Asn Val Gly Val Ala
 165 170 175
 Lys Leu Ser Phe Asp Ser Ala Gln Ile Lys Glu Asn Val Glu Ala Leu
 180 185 190
 Cys Ala Ala Leu Val Lys Ala Lys Pro Ala Thr Ala Lys Gly Gln Tyr
 195 200 205
 Leu Val Asn Phe Thr Ile Ser Ser Thr Met Gly Pro Gly Val Thr Val
 210 215 220
 Asp Thr Arg Glu Leu Ile Ala Leu
 225 230

<210> 303
 <211> 238
 <212> PRT
 <213> chlamydia

<400> 303
 Ile Asn Ser Lys Leu Glu Thr Lys Asn Leu Ile Tyr Leu Lys Leu Lys
 5 10 15
 Ile Lys Lys Ser Phe Lys Met Gly Asn Ser Gly Phe Tyr Leu Tyr Asn
 20 25 30
 Thr Gln Asn Cys Val Phe Ala Asp Asn Ile Lys Val Gly Gln Met Thr
 35 40 45
 Glu Pro Leu Lys Asp Gln Gln Ile Ile Leu Gly Thr Thr Ser Thr Pro
 50 55 60
 Val Ala Ala Lys Met Thr Ala Ser Asp Gly Ile Ser Leu Thr Val Ser
 65 70 75 80
 Asn Asn Pro Ser Thr Asn Ala Ser Ile Thr Ile Gly Leu Asp Ala Glu
 85 90 95
 Lys Ala Tyr Gln Leu Ile Leu Glu Lys Leu Gly Asp Gln Ile Leu Gly
 100 105 110
 Gly Ile Ala Asp Thr Ile Val Asp Ser Thr Val Gln Asp Ile Leu Asp
 115 120 125
 Lys Ile Thr Thr Asp Pro Ser Leu Gly Leu Leu Lys Ala Phe Asn Asn
 130 135 140
 Phe Pro Ile Thr Asn Lys Ile Gln Cys Asn Gly Leu Phe Thr Pro Arg
 145 150 155 160
 Asn Ile Glu Thr Leu Leu Gly Gly Thr Glu Ile Gly Lys Phe Thr Val
 165 170 175
 Thr Pro Lys Ser Ser Gly Ser Met Phe Leu Val Ser Ala Asp Ile Ile
 180 185 190

Ala Ser Arg Met Glu Gly Gly Val Val Leu Ala Leu Val Arg Glu Gly
195 200 205

Asp Ser Lys Pro Tyr Ala Ile Ser Tyr Gly Tyr Ser Ser Gly Val Pro
210 215 220

Asn Leu Cys Ser Leu Arg Thr Arg Ile Ile Asn Thr Gly Leu
225 230 235

<210> 304

<211> 133

<212> PRT

<213> Chlamydia

<400> 304

His Met His His His His His His Met Ala Ser Ile Cys Gly Arg Leu
5 10 15

Gly Ser Gly Thr Gly Asn Ala Leu Lys Ala Phe Phe Thr Gln Pro Ser
20 25 30

Asn Lys Met Ala Arg Val Val Asn Lys Thr Lys Gly Met Asp Lys Thr
35 40 45

Val Lys Val Ala Lys Ser Ala Ala Glu Leu Thr Ala Asn Ile Leu Glu
50 55 60

Gln Ala Gly Gly Ala Gly Ser Ser Ala His Ile Thr Ala Ser Gln Val
65 70 75 80

Ser Lys Gly Leu Gly Asp Thr Arg Thr Val Val Ala Leu Gly Asn Ala
85 90 95

Phe Asn Gly Ala Leu Pro Gly Thr Val Gln Ser Ala Gln Ser Phe Phe
100 105 110

Ser His Met Lys Ala Ala Ser Gln Lys Thr Gln Glu Gly Asp Glu Gly
115 120 125

Leu Thr Ala Asp Leu
130

<210> 305

<211> 125

<212> PRT

<213> Chlamydia

<400> 305

Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
5 10 15

Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val Val Asn
20 25 30

Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala
35 40 45

Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
50 55 60

Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Thr Arg
 65 70 75 80

Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
 85 90 95

Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
 100 105 110

Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu
 115 120 125

<210> 306

<211> 38

<212> DNA

<213> *Chlamydia trachomatis*

<400> 306

gagagcggcc gctcatgttt ataacaaagg aacttatg

38

<210> 307

<211> 39

<212> DNA

<213> *Chlamydia trachomatis*

<400> 307

gagagcggcc gcttacttag gtgagaagaa gggagtttc

39

<210> 308

<211> 1860

<212> DNA

<213> *Chlamydia trachomatis*

<400> 308

atgcatcacc	atcaccatca	cacggccgcg	tccgataact	tccagctgtc	ccaggggtgg	60
cagggtatcg	ccattccgat	cgggcaggcg	atggcgatcg	cgggccagat	caagcttccc	120
accgttcata	tcgggctcac	cgccttctct	ggcttgggtg	ttgtcgacaa	caacggcacc	180
ggcgacgag	tcgaacggat	ggtcgggagc	gctccggcgg	caagtctcgg	catctccacc	240
ggcgacgtga	tcacccgggt	cgaacggcgt	cgcatacaat	cggccaccgc	gatggcggac	300
gcgcttaacg	ggcatcatcc	cggtagcgtc	atctcggtga	cctggcaaac	caagtccggc	360
ggcacgcgtg	cagggaacgt	gacattggcc	gagggaaccc	cggccgaatt	ctgcagatat	420
ccatcacact	ggcgccgct	catgtttata	acaaaggaa	ttatgaatcg	agttatagaa	480
atccatgctc	actacgatca	aagacaact	tctcaatctc	caaatacaaa	cttcttagta	540
catcatcctt	atcttactct	tattccaag	tttctactag	gagctcta	agtctatgct	600
ctttattcgt	ttgcagaaat	ggaattagct	atttctggac	ataaacaagg	taaagatcga	660
gataccttta	ccatgatctc	ttcctgtcct	gaaggcacta	attacatcat	ctatctagat	720
ctcatactca	gtgattttct	gttactaaat	aaagtctcat	caggggggagc	ctttcggaat	780
ctagcaggga	aaatttctct	cttaggaaaa	aatctctctg	cgtccattca	ttttaaaccac	840
attaataata	atggttttgg	agccggagtc	ttttctgaat	cctctattga	tttactagat	900
ttacgaaaac	ttgttgcctt	tggtatcgaa	agcacaggag	gaatttttac	tgcgaaagag	960
gacatctctt	ttaaaaacaa	ccaccacatt	gccttcgcga	ataatatcac	caaagggaaat	1020
gggtggcgta	tcacagctcca	aggagatgat	aaagggaagg	tatcctttgt	agatcaacgt	1080
ggagctatca	tttttaccaa	taaccaagct	gtaactcttt	catcaatgaa	acatagtggg	1140
cgtggaggag	caattagcgg	tgacttcgca	ggatccagaa	ttctttttct	taataaccaa	1200
caaatattct	tcgaaggcga	tagcgtctgt	catggaggtg	ctatctacaa	tcgaataggc	1260
cttgtcgagt	tcttaggaaa	tgcaggacct	cttgccttta	aagagaacac	aaacatagct	1320
aacggggagg	ctatatacac	aagtaatttc	aaagcgaalc	aacaaacatc	ccccatttct	1380
ttctctcaaa	atcatgcgaa	taagaaaggc	ggagcgattt	acgcgcaata	tgtgaactta	1440

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gaacagaaac aagatactat tcgctttgaa aaaaataccg ctaaagaagg cgggtggagcc 1500
atcacctctt ctaaatgctc aattactgct cataatacca tcactttttc cgataatgct 1560
gcgggagatc ttggaggagg agcaattctt ctagaaggga aaaaaccttc tctaacccttg 1620
sttgctcata ttggtaatat tgcatttagc ggcaatacca tgcttcatat caccacaaaaa 1680
gcttccctag atcgacacaa ttctatctta atcaagaag ctcctataa aaaccacactt 1740
gcagcgaaac aaaaaccattc tattcatttc tttgatctg tcattggcatt gtcagcatca 1800
tcttccctca tacaatatca tgctcctgag tatgaaactc ccttctcttc acctaatgaa 1860

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<210> 309
<211> 619
<212> FRT
<213> Chlamydia trachomatis

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<400> 309
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1 5 10 15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
20 25 30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
35 40 45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
50 55 60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65 70 75 80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
85 90 95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
100 105 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
115 120 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
130 135 140
Arg Pro Leu Met Phe Ile Thr Lys Glu Leu Met Asn Arg Val Ile Glu
145 150 155 160
Ile His Ala His Tyr Asp Gln Arg Gln Leu Ser Gln Ser Pro Asn Thr
165 170 175
Asn Phe Leu Val His His Pro Tyr Leu Thr Leu Ile Pro Lys Phe Leu
180 185 190
Leu Gly Ala Leu Ile Val Tyr Ala Pro Tyr Ser Phe Ala Glu Met Glu
195 200 205
Leu Ala Ile Ser Gly His Lys Gln Gly Lys Asp Arg Asp Thr Phe Thr
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225 230 235 240
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245 250 255
Ala Phe Arg Asn Leu Ala Gly Lys Ile Ser Phe Leu Gly Lys Asn Ser
260 265 270
Ser Ala Ser Ile His Phe Lys His Ile Asn Ile Asn Gly Phe Gly Ala
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Gly Val Phe Ser Glu Ser Ser Ile Glu Phe Thr Asp Leu Arg Lys Leu
290 295 300
Val Ala Phe Gly Ser Glu Ser Thr Gly Gly Ile Phe Thr Ala Lys Glu
305 310 315 320
Asp Ile Ser Phe Lys Asn Asn His His Ile Ala Phe Arg Asn Asn Ile
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Thr Lys Gly Asn Gly Gly Val Ile Gln Leu Gln Gly Asp Met Lys Gly
340 345 350
Ser Val Ser Phe Val Asp Gln Arg Gly Ala Ile Ile Phe Thr Asn Asn
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Gln Ala Val Thr Ser Ser Ser Met Lys His Ser Gly Arg Gly Gly Ala

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370
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 Gln Ile Thr Phe Glu Gly Asn Ser Ala Val His Gly Gly Ala Ile Tyr
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 Asn Lys Asn Gly Leu Val Glu Phe Leu Gly Asn Ala Gly Pro Leu Ala
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 Phe Lys Glu Asn Thr Thr Ile Ala Asn Gly Gly Ala Ile Tyr Thr Ser
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 Asn Phe Lys Ala Asn Gln Gln Thr Ser Pro Ile Leu Phe Ser Gln Asn
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 His Ala Asn Lys Lys Gly Gly Ala Ile Tyr Ala Gln Tyr Val Asn Leu
 465 470 475 480
 Glu Gln Asn Gln Asp Thr Ile Arg Phe Glu Lys Asn Thr Ala Lys Glu
 485 490 495
 Gly Gly Gly Ala Ile Thr Ser Ser Gln Cys Ser Ile Thr Ala His Asn
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 515 520 525
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 Ala Ser Leu Asp Arg His Asn Ser Ile Leu Ile Lys Glu Ala Pro Tyr
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<211> 691

<212> PRT

<213> Chlamydia trachomatis

<400> 313

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Phe	Leu	Gly	Leu	Gly	Val	Val	Asp	Asn	Asn	Gly	Asn	Gly	Ala	Arg	Val
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Gln	Arg	Val	Val	Gly	Ser	Ala	Pro	Ala	Ala	Ser	Leu	Gly	Ile	Ser	Thr
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Gly	Asp	Val	Ile	Thr	Ala	Val	Asp	Gly	Ala	Pro	Ile	Asn	Ser	Ala	Thr
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Leu	Ala	Glu	Gly	Pro	Pro	Ala	Glu	Phe	Cys	Arg	Tyr	Pro	Ser	His	Trp
				130				135			140				
Arg	Pro	Leu	His	Ser	Ile	His	Phe	Phe	Asp	Pro	Val	Met	Ala	Leu	Ser
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Ala	Ser	Ser	Ser	Pro	Ile	Gln	Ile	Asn	Ala	Pro	Glu	Tyr	Glu	Thr	Pro
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Phe	Phe	Ser	Pro	Lys	Gly	Met	Ile	Val	Phe	Ser	Gly	Ala	Asn	Leu	Leu
				180				185					190		
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 Leu Phe Tyr Glu Asn Arg Asp Thr Ala Ala Ser Pro Tyr Gln Met Glu
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 405 410 415
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 420 425 430
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 435 440 445
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 450 455 460
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 465 470 475
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 485 490 495
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 515 520 525
 Gly Lys Trp Asp Thr Phe Gly Met Arg Gly Thr Leu Gly Ala Ser Tyr
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 565 570 575
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 Ile Gly Ile Gly Tyr Glu Phe Cys Leu Gly Asn Ser Ser Phe Ala Leu
 595 600 605
 Leu Gly Lys Gly Ser Ile Gly Tyr Ser Arg Asp Ile Lys Arg Glu Asn
 610 615 620
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 625 630 635
 Asn Gly Cys Ser Val Pro Thr Ser Ala His Thr Leu Ala Asn Gln Leu
 645 650 655
 Ile Leu Arg Tyr Lys Ala Cys Ser Leu Tyr Ile Thr Ala Tyr Thr Ile
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<211> 646		
<212> PRT		

<213> Chlamydia trachomatis

<400> 317

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Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
 35      40      45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
 50      55      60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
 65      70      75      80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
 85      90      95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
100      105      110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
115      120      125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
130      135      140
Arg Pro Leu Met Ile Lys Arg Thr Ser Leu Ser Phe Ala Cys Leu Ser
145      150      155      160
Phe Phe Tyr Leu Ser Thr Ile Ser Ile Leu Gln Ala Asn Glu Thr Asp
165      170      175
Thr Leu Gln Phe Arg Arg Phe Thr Phe Ser Asp Arg Glu Ile Gln Phe
180      185      190
Val Leu Asp Pro Ala Ser Leu Ile Thr Ala Gln Asn Ile Val Leu Ser
195      200      205
Asn Leu Gln Ser Asn Gly Thr Gly Ala Cys Thr Ile Ser Gly Asn Thr
210      215      220
Gln Thr Gln Ile Phe Ser Asn Ser Val Asn Thr Thr Ala Asp Ser Gly
225      230      235      240
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245      250      255
Asn Leu Leu Phe Cys Asn Asn Tyr Cys Thr His Asn Lys Gly Gly Gly
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325      330      335
Asp Cys Gly Gly Ala Ile Ser Ala Asp Thr Gln Ile Ser Ile Thr Asp
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355      360      365
Pro Tyr Thr Gln Ala Glu Asn Met Ala Arg Gly Gly Ala Ile Cys Ser
370      375      380
Arg Arg Asp Leu Cys Ser Ile Ser Asn Asn Ser Gly Pro Ile Val Phe
385      390      395      400
Asn Tyr Asn Gln Gly Gly Lys Gly Gly Ala Ile Ser Ala Thr Arg Cys
405      410      415
Val Ile Asp Asn Asn Lys Glu Arg Ile Ile Phe Ser Asn Asn Ser Ser
420      425      430
Leu Gly Trp Ser Gln Ser Ser Ser Ala Ser Asn Gly Gly Ala Ile Gln
435      440      445
Thr Thr Gln Gly Phe Thr Leu Arg Asn Asn Lys Gly Ser Ile Tyr Phe
450      455      460

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<211> 34

<212> DNA

<213> *Chlamydia trachomatis*

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<211> 33

<212> DNA

<213> *Chlamydia trachomatis*

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33

<210> 320

<211> 2148

<212> DNA

<213> *Chlamydia trachomatis*

<400> 320

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<213> Chlamydia trachomatis

<400> 321

Met	His	His	His	His	His	His	Thr	Ala	Ala	Ser	Asp	Asn	Phe	Gln	Leu
1				5					10					15	
Ser	Gln	Gly	Gly	Gln	Gly	Phe	Ala	Ile	Pro	Ile	Gly	Gln	Ala	Met	Ala
				20				25						30	
Ile	Ala	Gly	Gln	Ile	Lys	Leu	Pro	Thr	Val	His	Ile	Gly	Pro	Thr	Ala
				35				40				45			
Phe	Leu	Gly	Leu	Gly	Val	Val	Asp	Asn	Asn	Gly	Asn	Gly	Ala	Arg	Val
				50				55				60			
Gln	Arg	Val	Val	Gly	Ser	Ala	Pro	Ala	Ala	Ser	Leu	Gly	Ile	Ser	Thr
				65				70				75		80	
Gly	Asp	Val	Ile	Thr	Ala	Val	Asp	Gly	Ala	Pro	Ile	Asn	Ser	Ala	Thr
				85				90				95			
Ala	Met	Ala	Asp	Ala	Leu	Asn	Gly	His	His	Pro	Gly	Asp	Val	Ile	Ser
				100				105				110			
Val	Thr	Trp	Gln	Thr	Lys	Ser	Gly	Gly	Thr	Arg	Thr	Gly	Asn	Val	Thr
				115				120				125			
Leu	Ala	Glu	Gly	Pro	Pro	Ala	Glu	Phe	Cys	Arg	Tyr	Pro	Ser	His	Trp
				130				135				140			
Arg	Pro	Leu	Asp	Ile	Arg	Thr	Leu	Met	Gly	Lys	Glu	His	Asn	Tyr	Ile
				145				150				155			160
Lys	Glu	Ala	Pro	Thr	Thr	Leu	Lys	Phe	Gly	Thr	Leu	Ala	Ile	Glu	Asp
				165				170				175			
Asp	Ala	Glu	Leu	Glu	Ile	Phe	Asn	Ile	Pro	Phe	Thr	Gln	Asn	Pro	Thr
				180				185				190			
Ser	Leu	Leu	Ala	Leu	Gly	Ser	Gly	Ala	Thr	Leu	Thr	Val	Gly	Lys	His
				195				200				205			
Gly	Lys	Leu	Asn	Ile	Thr	Asn	Leu	Gly	Val	Ile	Leu	Pro	Ile	Ile	Leu
				210				215				220			
Lys	Glu	Gly	Lys	Ser	Pro	Pro	Cys	Ile	Arg	Val	Asn	Pro	Gln	Asp	Met
				225				230				235			240
Thr	Gln	Asn	Thr	Gly	Thr	Gly	Gln	Thr	Pro	Ser	Ser	Thr	Ser	Ser	Ile
				245				250							255

Ser Thr Pro Met Ile Ile Phe Asn Gly Arg Leu Ser Ile Val Asp Glu
 260 265 270
 Asn Tyr Glu Ser Val Tyr Asp Ser Met Asp Leu Ser Arg Gly Lys Ala
 275 280 285
 Glu Gln Leu Ile Leu Ser Ile Glu Thr Thr Asn Asp Gly Gln Leu Asp
 290 295 300
 Ser Asn Trp Gln Ser Ser Leu Asn Thr Ser Leu Leu Ser Pro Pro His
 305 310 315 320
 Tyr Gly Tyr Gln Gly Leu Trp Thr Pro Asn Trp Ile Thr Thr Thr Tyr
 325 330 335
 Thr Ile Thr Leu Asn Asn Asn Ser Ser Ala Pro Thr Ser Ala Thr Ser
 340 345 350
 Ile Ala Glu Gln Lys Lys Thr Ser Glu Thr Phe Thr Pro Ser Asn Thr
 355 360 365
 Thr Thr Ala Ser Ile Pro Asn Ile Lys Ala Ser Ala Gly Ser Gly Ser
 370 375 380
 Gly Ser Ala Ser Asn Ser Gly Glu Val Thr Ile Thr Lys His Thr Leu
 385 390 395 400
 Val Val Asn Trp Ala Pro Val Gly Tyr Ile Val Asp Pro Ile Arg Arg
 405 410 415
 Gly Asp Leu Ile Ala Asn Ser Leu Val His Ser Gly Arg Asn Met Thr
 420 425 430
 Met Gly Leu Arg Ser Leu Leu Pro Asp Asn Ser Trp Phe Ala Leu Gln
 435 440 445
 Gly Ala Ala Thr Thr Leu Phe Thr Lys Gln Gln Lys Arg Leu Ser Tyr
 450 455 460
 His Gly Tyr Ser Ser Ala Ser Lys Gly Tyr Thr Val Ser Ser Gln Ala
 465 470 475 480
 Ser Gly Ala His Gly His Lys Phe Leu Leu Ser Phe Ser Gln Ser Ser
 485 490 495
 Asp Lys Met Lys Glu Lys Glu Thr Asn Asn Arg Leu Ser Ser Arg Tyr
 500 505 510
 Tyr Leu Ser Ala Leu Cys Phe Glu His Pro Met Phe Asp Arg Ile Ala
 515 520 525
 Leu Ile Gly Ala Ala Ala Cys Asn Tyr Gly Thr His Asn Met Arg Ser
 530 535 540
 Phe Tyr Gly Thr Lys Lys Ser Ser Lys Gly Lys Phe His Ser Thr Thr
 545 550 555
 Leu Gly Ala Ser Leu Arg Cys Glu Leu Arg Asp Ser Met Pro Leu Arg
 560 565 570 575
 Ser Ile Met Leu Thr Pro Phe Ala Gln Ala Leu Phe Ser Arg Thr Glu
 580 585 590
 Pro Ala Ser Ile Arg Glu Ser Gly Asp Leu Ala Arg Leu Phe Thr Leu
 595 600 605
 Glu Gln Ala His Thr Ala Val Val Ser Pro Ile Gly Ile Lys Gly Ala
 610 615 620
 Tyr Ser Ser Asp Thr Trp Pro Thr Leu Ser Trp Glu Met Glu Leu Ala
 625 630 635 640
 Tyr Gln Pro Thr Leu Tyr Trp Lys Arg Pro Leu Leu Asn Thr Leu Leu
 645 650 655
 Ile Gln Asn Asn Gly Ser Trp Val Thr Thr Asn Thr Pro Leu Ala Lys
 660 665 670
 His Ser Phe Tyr Gly Arg Gly Ser His Ser Leu Lys Phe Ser His Leu
 675 680 685
 Lys Leu Phe Ala Asn Tyr Gln Ala Glu Val Ala Thr Ser Thr Val Ser
 690 695 700
 His Tyr Ile Asn Ala Gly Gly Ala Leu Val Phe
 705 710 715

<210> 322

<211> 37

<212> DNA
<213> *Chlamydia trachomatis*

<400> 322
gagagcggcc gctcatgcct ttttctttga gatctac 37

<210> 323
<211> 36
<212> DNA
<213> *Chlamydia trachomatis*

<400> 323
gagagcggcc gcttacacag atccattacc ggactg 36

<210> 324
<211> 1896
<212> DNA
<213> *Chlamydia trachomatis*

<400> 324
atgcatcaac atcaccatca caagcgccgc tcgataaact tccagctgtc ccagggtggg 60
cagggtattcg ccattccgat cggcgaggcg atggcgatcg cgggccagat caagcttccc 120
accgttcata tcgggcctac cgccttcttc gcttgggtg ttgtcgacaa caacggcaac 180
ggcgacagag tccaaacggt ggtcggagcg gctccggcgg caagtctcgg catctccacc 240
ggcgacgtga tcacgcgggt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300
cgctttaacg ggcattccac cgtgacgtc atctcgttga cctggcaaac caagtggggc 360
ggcaccgcta cagggaacgt gacattggcc gagggaaccc cggccgaatt ctgcagatat 420
ccatcacact ggcggccgct catgcctttt tctttgagat ctacatcatt ttgtttttta 480
gctgttttgg gtttctattc gtatggatto cggagctctc ctcaagtgtt aacacctaat 540
gtaaccactc cttttaaagg ggaacgatgt tacttgaatg gagactcgcc ttttgtcaat 600
gtctatcgag ggccagagaa cggctcaatt atctcagcta atggcgacaa ttttaacgatt 660
accggacaaa accatacatt atcatttaca gattctcaag ggccagttct tcaaaattat 720
gccttcattt cagcaggaga gacacttact ctgaaagatt ttctcgattt gatgttctcg 780
aaaaatgttt ctgcgggaga aaagggaatg atctcaggga aaacgttgag tatttccgga 840
gcaggcggaag tgattttttg ggataactct gtggggattt ctctttgtc tatttgcca 900
gcactcgactc caactctctc agcaccagca ccagctctcg ctgcttcaag ctctttatct 960
ccaacagtta gtgatgctcg gaaagggtct atttttctg tagagactag ttggagatc 1020
tcaggcgctca aaaaaggggt catgttcgat aataatgccg ggaatttttg aacagttttt 1080
cgaggttaata gtaataataa tgctgttagt gggggttagt ggtctgctac aacaccaagt 1140
tttaccagta aaactgttaa agggaaagt tctttcacag ataacgtagc ctctctggga 1200
ggcgagtagt cctacaaagg aactgtgctt tccaaagaca atgaaggagg catattcttc 1260
cgagggaaaca cagcatcagca tgatttaggg attcttgctg ctactagtcg ggaacagaat 1320
acggagacag gaggcggtgg aggagttatt tgcttccag atgattctgt aagatttgaa 1380
ggcaataaag gttctattgt ttttgattac aactttgcaa aaggcagagg oggaagcatc 1440
ctaacgaaag aattctctct ttagacagat gattcgggtg tcttttagtaa caatacagca 1500
gaaaaaggcg gtggagctat ttatgctctc actatcgata taagcagaga tggaggatcg 1560
attctgtctg aaagaaacgg agctgcagaa ggaggcgcca tctcgttgag tgaagcaagc 1620
tctggttcaa ctggaaatct tacttttaag gcttctgat gggatatgtt ttttctggg 1680
aatatgacga gtgatcgctc tggagagcgc agcgacgcaa gaattttaag tgatggaaag 1740
actgtttctt taaatgcttc cggactatcg aagctgatct tttatgatac tttagtaca 1800
aataattcag cagcgggtgc atcgacacca tccactctct ctctctctat gctcgtgtct 1860
gtcacgatta atcagtcggt taatggatct gtgtaa 1896

<210> 325
<211> 631
<212> PRT
<213> *Chlamydia trachomatis*

<400> 325
Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1 5 10 15

Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
 20 25 30
 Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
 35 40 45
 Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
 50 55 60
 Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
 65 70 75 80
 Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
 85 90 95
 Ala Met Ala Asp Ala Leu Asn Gly His Pro Gly Asp Val Ile Ser
 100 105 110
 Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
 115 120 125
 Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
 130 135 140
 Arg Pro Leu Met Pro Phe Ser Leu Arg Ser Thr Ser Phe Cys Phe Leu
 145 150 155 160
 Ala Cys Leu Cys Ser Tyr Ser Tyr Gly Phe Ala Ser Ser Pro Gln Val
 165 170 175
 Leu Thr Pro Asn Val Thr Thr Pro Phe Lys Gly Asp Asp Val Tyr Leu
 180 185 190
 Asn Gly Asp Cys Ala Phe Val Asn Val Tyr Ala Gly Ala Glu Asn Gly
 195 200 205
 Ser Ile Ile Ser Ala Asn Gly Asp Asn Leu Thr Ile Thr Gln Asn
 210 215 220
 His Thr Leu Ser Phe Thr Asp Ser Gln Gly Pro Val Leu Gln Asn Tyr
 225 230 235 240
 Ala Phe Ile Ser Ala Gly Glu Thr Leu Thr Leu Lys Asp Phe Ser Ser
 245 250 255
 Leu Met Phe Ser Ser Lys Asn Val Ser Cys Gly Glu Lys Gly Met Ile Ser
 260 265 270
 Gly Lys Thr Val Ser Ile Ser Gly Ala Gly Glu Val Ile Phe Trp Asp
 275 280 285
 Asn Ser Val Gly Tyr Ser Pro Leu Ser Ile Val Pro Ala Ser Thr Pro
 290 295 300
 Thr Pro Pro Ala Pro Ala Pro Ala Ala Ser Ser Ser Leu Ser
 305 310 315 320
 Pro Thr Val Ser Asp Ala Arg Lys Gly Ser Ile Phe Ser Val Glu Thr
 325 330 335
 Ser Leu Glu Ile Ser Gly Val Lys Lys Gly Val Met Phe Asp Asn Asn
 340 345 350
 Ala Gly Asn Phe Gly Thr Val Phe Arg Gly Asn Ser Asn Asn Ala
 355 360 365
 Gly Ser Gly Gly Ser Gly Ser Ala Thr Thr Pro Ser Phe Thr Val Lys
 370 375 380
 Asn Cys Lys Gly Lys Val Ser Phe Thr Asp Asn Val Ala Ser Cys Gly
 385 390 395 400
 Gly Gly Val Val Tyr Lys Gly Thr Val Leu Phe Lys Asp Asn Glu Gly
 405 410 415
 Gly Ile Phe Phe Arg Gly Asn Thr Ala Tyr Asp Asp Leu Gly Ile Leu
 420 425 430
 Ala Ala Thr Ser Arg Asp Gln Asn Thr Glu Thr Gly Gly Gly Gly
 435 440 445
 Val Ile Cys Ser Pro Asp Asp Ser Val Lys Phe Glu Gly Asn Lys Gly
 450 455 460
 Ser Ile Val Phe Asp Tyr Asn Phe Ala Lys Gly Arg Gly Gly Ser Ile
 465 470 475 480
 Leu Thr Lys Glu Phe Ser Leu Val Ala Asp Asp Ser Val Val Phe Ser
 485 490 495
 Asn Asn Thr Ala Glu Lys Gly Gly Gly Ala Ile Tyr Ala Pro Thr Ile

500										505										510													
Asp	Ile	Ser	Thr	Asn	Gly	Gly	Ser	Ile	Leu	Phe	Glu	Arg	Asn	Arg	Ala	Asp	Ile	Leu	Phe	Glu	Arg	Asn	Arg	Ala	Asp	Ile	Leu	Phe	Glu	Arg	Asn	Arg	Ala
		515					520					525											530										
Ala	Glu	Gly	Gly	Ala	Ile	Cys	Val	Ser	Glu	Ala	Ser	Ser	Gly	Ser	Thr																		
		530				535						540																					
Gly	Asn	Leu	Thr	Leu	Ser	Ala	Ser	Asp	Gly	Asp	Ile	Val	Phe	Ser	Gly																		
		545				550					555				560																		
Asn	Met	Thr	Ser	Asp	Arg	Pro	Gly	Glu	Arg	Ser	Ala	Ala	Arg	Ile	Leu																		
				565						570				575																			
Ser	Asp	Gly	Thr	Thr	Val	Ser	Leu	Asn	Ala	Ser	Gly	Leu	Ser	Iys	Leu																		
				580					585				590																				
Ile	Phe	Tyr	Asp	Pro	Val	Val	Gln	Asn	Asn	Ser	Ala	Ala	Gly	Ala	Ser																		
		595					600					605																					
Thr	Pro	Ser	Pro	Ser	Ser	Ser	Ser	Met	Pro	Gly	Ala	Val	Thr	Ile	Asn																		
		610					615					620																					
Gln	Ser	Gly	Asn	Gly	Ser	Val																											
		625				630																											

<210> 326

<211> 40

<212> DNA

<213> Chlamydia trachomatis

<400> 326

gagagcgcc gctcgatcct gtagtacaaa ataattcagc

40

<210> 327

<211> 33

<212> DNA

<213> Chlamydia trachomatis

<400> 327

gagagcgcc gcttaaaaga ttctattcaa gcc

33

<210> 328

<211> 2148

<212> DNA

<213> Chlamydia trachomatis

<400> 328

atgcatacc	atcaccatca	cacggcgccg	tccgataaact	tccagctgtc	ccaggggtggg	60
cagggaattcg	ccattccgat	cgggcaggcg	atggcgatcg	cgggccagat	caagcttccc	120
accgttccata	tccgggctac	cgccttccct	ggcttgggtg	tgttcgacaa	caacggcaac	180
ggcgcaacgag	tccaaocggt	ggtcgggagc	gctccggggg	caagttctgg	catctccacc	240
ggcgacgtga	tcaccccggt	cgaaggcgct	ccgatcaact	cggccaccgc	gatggcgagc	300
gcgcttaacg	ggcatcatcc	cggtagcgtc	atctcggtga	cctggcaaac	caagtccggc	360
ggcacgcgt	cagggaacgt	gacattggcc	gaggggacccc	cggcgcaatt	ctgcagatat	420
ccatcacact	ggcgcccgct	cgatcctgta	gtacaaaata	attcagcagc	gggtgcacgc	480
acacatcac	catctttctc	ttctatgctc	ggtgtgtgca	cgattaatca	gtccggtaat	540
ggatctgtga	tttttacccg	cgagtcattg	actcctcag	aaaaacttca	agttcttaac	600
tctacttcta	acttccagg	agctctgact	gtgtcaggag	gggagttgtg	tgtgacggaa	660
ggagctacct	taactactgg	gaccattaca	gcacactctg	gacgagtgac	tttaggatcc	720
ggagcttcgt	tgtctgcgct	tgcagggtct	gcaataata	attatacttg	tacagtatct	780
aagtctggga	ttgattttag	atccttttta	actcctaact	ataagacggc	catactgggt	840
cgcgatggaa	cagttactgt	taacacgggc	tctactttag	acctagtgtat	ggagaatgag	900
gcgaggtctc	atgataatcc	gcttttttgt	ggatcgctga	caattccctt	tgttactcta	960
tctctagtta	gtgctagttaa	cggagtgtaca	aaaaattctg	tcaactattaa	tgatgcagac	1020
gctcgccact	atgggtatgt	aggtctcttg	tctgcagatt	ggacgaaacc	gcctctggct	1080
cctgtagcta	aggggatggt	acctcctaata	accaataaca	ctctgtatct	gacatggaga	1140
cctgcttcga	attacggtga	atatcgactg	gatcctcaga	gaaagggaga	actgtatccc	1200
aactctcttt	gggtagcggg	atctgcatta	agaaccttta	ctaattggtt	gaaagaacac	1260

305
 Ser Ser Ser Ser Ala 310 Ser Asn Gly Val Thr 315 Lys Asn Ser Val Thr Ile 320
 325 330 335
 Asn Asp Ala Asp Ala Ala His Tyr Gly Tyr Gln Gly Ser Trp Ser Ala 340 350
 345 355
 Asp Trp Thr Lys Pro Pro Leu Ala Pro Asp Ala Lys Gly Met Val Pro 360 365
 370 375 380
 Pro Asn Thr Asn Asn Thr Leu Tyr Leu Thr Trp Arg Pro Ala Ser Asn 385 390 395
 Tyr Gly Glu Tyr Arg Leu Asp Pro Gln Arg Lys Gly Glu Leu Val Pro 400 405
 410 415
 Asn Ser Leu Trp Val Ala Gly Ser Ala Leu Arg Thr Phe Thr Asn Gly 420 425
 430 435
 Leu Lys Glu His Tyr Val Ser Arg Asp Val Gly Phe Val Ala Ser Leu 440 445
 450 455 460 465
 His Ala Leu Gly Asp Tyr Ile Leu Asn Tyr Thr Gln Asp Asp Arg Asp 470 475
 Gly Phe Leu Ala Arg Tyr Gly Gly Phe Gln Ala Thr Ala Ala Ser His 480 485
 Tyr Glu Asn Gly Ser Ile Phe Gly Val Ala Phe Gly Gln Leu Tyr Gly 490 495
 500 505 510 515
 Gln Thr Lys Ser Arg Met Tyr Tyr Ser Lys Asp Ala Gly Asn Met Thr 520 525
 Met Leu Ser Cys Phe Gly Arg Ser Tyr Val Asp Ile Lys Gly Thr Glu 530 535
 Thr Val Met Tyr Trp Glu Thr Ala Tyr Gly Tyr Ser Val His Arg Met 540 545
 His Thr Gln Tyr Phe Asn Asp Lys Thr Gln Lys Phe Asp His Ser Lys 550 555
 Cys His Trp His Asn Asn Tyr Tyr Ala Phe Val Gly Ala Glu His 560 565
 570 575
 Asn Phe Leu Glu Tyr Cys Ile Pro Thr Arg Gln Leu Ala Arg Asp Tyr 580 585
 Glu Leu Thr Gly Phe Met Arg Phe Glu Met Ala Gly Gly Trp Ser Ser 590 595
 Ser Thr Arg Glu Thr Gly Ser Leu Thr Arg Tyr Phe Ala Arg Gly Ser 600 605
 Gly His Asn Met Ser Leu Pro Ile Gly Ile Val Ala His Ala Val Ser 610 615
 620 625
 His Val Arg Arg Ser Pro Ser Lys Leu Thr Leu Asn Met Gly Tyr 630 635
 Arg Pro Asp Ile Trp Arg Val Thr Pro His Cys Asn Met Glu Ile Ile 640 645
 650 655
 Ala Asn Gly Val Lys Thr Pro Ile Gln Gly Ser Pro Leu Ala Arg His 660 665
 670 675
 Ala Phe Phe Leu Glu Val His Asp Thr Leu Tyr Ile His His Phe Gly 680 685
 Arg Ala Tyr Met Asn Tyr Ser Leu Asp Ala Arg Arg Gln Thr Ala 690 700
 His Phe Val Ser Met Gly Leu Asn Arg Ile Phe 705 710 715

<210> 330

<211> 38

<212> DNA

<213> Chlamydia trachomatis

<400> 330

gagagcggcc gctcatgaaa tggctgtcag ctactgca

38

<210> 331

<211> 34
 <212> DNA
 <213> Chlymmedia trachomatis

<400> 331
 gagcgccgc ttacttaagt cgaattttct caag

34

<210> 332
 <211> 1557
 <212> DNA
 <213> Chlymmedia trachomatis

<400> 332
 atgcatcacc atcacatca cagggccgcg tcgataaact tccagctgtc ccaggggtggg 60
 cagggattcg cnatccgat cgggcaggcg atggcgatcg cgggccagat caagottccc 120
 accgttcata tggggccatc cgccttctct ggcttgggtg ttgtcgacaa caacggcaac 180
 ggcgacagag tccaacgcgt ggtcgggagc gctcggcgcg caagtctcgg catctccacc 240
 ggcgacgtga tcacccgggt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300
 gcgcttaacg ggcatcatcc cggtagcgtc atctcgggtga cctggcaaac caagtccgggc 360
 ggcaacgcgt cagggaacgt gacattggcc gagggacccc cggccgaatt ctgcagatat 420
 ccatacaact ggcgccgct catgaaatgt ctgtcagcta ctgcggtgtt tgctgctgtt 480
 ctccctccag ttccagggtt ttgottccca gaacctaaag aattaaattt ctctcgcgtg 540
 gaaactctt cctctaccac ttttactgaa acaattggag aagctggggc agaataatc 600
 ttctctgtga acgcatcttt caaaaaattt accaacattc ctactacgga tacaacaact 660
 cccacgaact caaactctct tagctctagc ggagaaactg ctccggtttc tgaggatagt 720
 gactctacaa caacgactcc tgatcctaaa ggtggcgcg cctttataa cgcgcactcc 780
 ggagttttgt cctttatgac acgatcagga acagaaggtt ccttaactct gtctgagata 840
 aaaatgactg gtgaaggcgg tgcctatctt tctcaaggag agctgctatt tacagatctg 900
 acaagctcaa accatcaaaa taacttatcc cagctatccg gaggaagcat ttttgaggga 960
 tctacaactc cctatcagg gattactaaa gcgaattttt cctgcaactc tgcagaagtt 1020
 cctgctcctg ttaagaaacc tacagaacct aaagctcaaa cagcaagcgt ttttgcgggt 1080
 tctagtgttt atcagcgaaa tgattcgggt tcttcccccga gttccagtag agctgaaccc 1140
 gcagcagcta atcttcaag tcaotttatt tgtgtacag ctactcctgc gtctcaaac 1200
 gatacagaaa catcaactcc ctctcataag ccaggatctg ggggagctgc ctatgctaaa 1260
 ggcaacctta ctatcgaga ctctcaagag gtactattct caataataa agctactaaa 1320
 gatggaggag cgatctttgc tgagaagat gtttctttcg agaataattc atcattaaaa 1380
 gtacaactca accgtctcga agaaaaggga ggagctatct atgctaaagg tgcctctcca 1440
 attcaattct ctaaacagag tctttttaat tctaactaca gtaaacagg tgggggggct 1500
 ctatatgttg aaggaggat aaactccaa gatcttgaag aaattcgcat taagtaa 1557

<210> 333
 <211> 518
 <212> FRT
 <213> Chlymmedia trachomatis

<400> 333
 Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
 1 5 10 15
 Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
 20 25 30
 Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
 35 40 45
 Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
 50 55 60
 Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
 65 70 75 80
 Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
 85 90 95
 Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
 100 105 110
 Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Thr

115 120 125
 Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
 130 135 140
 Arg Pro Leu Met Lys Trp Leu Ser Ala Thr Ala Val Phe Ala Ala Val
 145 150 155 160
 Leu Pro Ser Val Ser Gly Phe Cys Phe Pro Glu Pro Lys Glu Leu Asn
 165 170 175
 Phe Ser Arg Val Glu Thr Ser Ser Ser Thr Thr Phe Thr Glu Thr Ile
 180 185 190
 Gly Glu Ala Gly Ala Glu Tyr Ile Val Ser Gly Asn Ala Ser Phe Thr
 195 200 205
 Lys Phe Thr Asn Ile Pro Thr Thr Asp Thr Thr Thr Pro Thr Asn Ser
 210 215 220
 Asn Ser Ser Ser Ser Ser Gly Glu Thr Ala Ser Val Ser Glu Asp Ser
 225 230 235 240
 Asp Ser Thr Thr Thr Thr Pro Asp Pro Lys Gly Gly Gly Ala Phe Tyr
 245 250 255
 Asn Ala His Ser Gly Val Leu Ser Phe Met Thr Arg Ser Gly Thr Glu
 260 265 270
 Gly Ser Leu Thr Leu Ser Glu Ile Lys Met Thr Gly Glu Gly Gly Ala
 275 280 285
 Ile Phe Ser Gln Gly Glu Leu Leu Phe Thr Asp Leu Thr Ser Leu Thr
 290 295 300
 Ile Gln Asn Asn Leu Ser Gln Leu Ser Gly Gly Ala Ile Phe Gly Gly
 305 310 315 320
 Ser Thr Ile Ser Leu Ser Gly Ile Thr Lys Ala Thr Phe Ser Cys Asn
 325 330 335
 Ser Ala Glu Val Pro Ala Pro Val Lys Lys Pro Thr Glu Pro Lys Ala
 340 345 350
 Gln Thr Ala Ser Glu Thr Ser Gly Ser Ser Ser Ser Ser Gly Asn Asp
 355 360 365
 Ser Val Ser Ser Pro Ser Ser Ser Arg Ala Glu Pro Ala Ala Ala Asn
 370 375 380
 Leu Gln Ser His Phe Ile Cys Ala Thr Ala Thr Pro Ala Ala Gln Thr
 385 390 395 400
 Asp Thr Glu Thr Ser Thr Pro Ser His Lys Pro Gly Ser Gly Gly Ala
 405 410 415
 Ile Tyr Ala Lys Gly Asp Leu Thr Ile Ala Asp Ser Gln Glu Val Leu
 420 425 430
 Phe Ser Ile Asn Lys Ala Thr Lys Asp Gly Gly Ala Ile Phe Ala Glu
 435 440 445
 Lys Asp Val Ser Phe Glu Asn Ile Thr Ser Leu Lys Val Gln Thr Asn
 450 455 460
 Gly Ala Glu Glu Lys Gly Gly Ala Ile Tyr Ala Lys Gly Asp Leu Ser
 465 470 475 480
 Ile Gln Ser Ser Lys Gln Ser Leu Phe Asn Ser Asn Tyr Ser Lys Gln
 485 490 495
 Gly Gly Gly Ala Leu Tyr Val Glu Gly Gly Ile Asn Phe Gln Asp Leu
 500 505 510
 Glu Glu Ile Arg Ile Lys
 515

<210> 334

<211> 37

<212> DNA

<213> Chlamydia trachomatis

<400> 334

gagagcggcc gctcggtgac ctctcaattc aatcttc

37

<210> 335

<211> 39
 <212> DNA
 <213> Chlamydia trachomatis

<400> 335
 gagagcgccc gcttagttct ctgttacaga taaggagac 39

<210> 336
 <211> 1758
 <212> DNA
 <213> Chlamydia trachomatis

<400> 336
 atgcatcacc atcaccatca cagggcgcgc tccgataact tccagctgtc ccaggggtggg 60
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 accgttcata tggggcctac cgccttctct ggcttgggtg ttgtcgacaa caacggcacc 180
 ggcgacagag tccaacgcgt ggctcgggagc gctccggcgg caagtctcgg catctccacc 240
 ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300
 cgctctaacg ggcatcatcc cggtagcgtc atctcgggtg cctggcaaac caagtcgggc 360
 ggccacgcgt cagggaacgt gacattggcg gagggaaccc cggccgaatt ctgcagatat 420
 ccacacacat gcgcgcgcgt cggtagcctc tcaattcaat ottctaaaca gagtcttttt 480
 aattctaaat acagtaaaaca aggtgggggg gctctatatg ttgaaggagg tataaaattc 540
 caagattctg aagaaattcg cattaagtag aataaagctg gaacgttoga aacaaaaaaa 600
 atcactttac cttcttttaa agctcaagca tctgcaggaa atgcagatgc ttgggcctct 660
 tctctctctc aattctgggtc tggagcaact acagtctcgc actcaggaga ctctagctct 720
 ggctcagact cggatcacctc agaaacagtt ccagtccagc cttaaaggcgg tgggtcttat 780
 actgataaga atctttcgat tactaacatc acaggaatta tcgaaattgc aaataacaaa 840
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 cgtctacaat ttttgaaaaa ctcttcgat aaacaagtg gaggaaatct cggagaagac 960
 aacatcaccc tatctaattt gacagggag acctctattc aagagaatac tgcacaaaga 1020
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 agtttctgtg taattaataa cacatcagaa aacatcgtg gtggagcctt tgttaccaaa 1140
 gaaatctctc agacttacac ctctgatgtg gaaacaattc caggaatcac gccgtgtacat 1200
 ggtagaacag tcattactgg caataaatct acaggaggta atgttgaggg cgtgtgtaca 1260
 aaacgtcttg ccttatctaa ccttcaaacg atttctatat ccgggaattc tgcagacaga 1320
 aatggtggtg gagccacacac atgcccagat agcttcccaa cggcgagata tgcagaacag 1380
 cccgcagcag cttctgcgcg gacgtctact cccaaatctg ccccggtctc aactgctcta 1440
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 tctctgcmaa cctctaaata ggaaactcaa gatcctaagt ctgatacaga cttattgatc 1560
 gattatgtag ttgatacagc tatcagcaaa aacactgcta agaaaggcgg tggaaatctat 1620
 gctaaaaaag ccaagatgc cgcataagac caactgaata tctctgagaa ctccgctaca 1680
 gagatagggt gaggtagctg ctgtaaagaa tctttagaac tagatgctct agtctcctta 1740
 tctgtaacag agaactaa 1758

<210> 337
 <211> 585
 <212> PRT
 <213> Chlamydia trachomatis

<400> 337
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 20 25 30
 Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
 35 40 45
 Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
 50 55 60
 Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
 65 70 75 80
 Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr

			85				90			95					
Ala	Met	Ala	Asp	Ala	Leu	Asn	Gly	His	Pro	Gly	Asp	Val	Ile	Ser	
			100				105				110				
Val	Thr	Trp	Gln	Thr	Lys	Ser	Gly	Gly	Thr	Arg	Thr	Gly	Asn	Val	Thr
			115				120				125				
Leu	Ala	Glu	Gly	Pro	Pro	Ala	Glu	Phe	Cys	Arg	Tyr	Pro	Ser	His	Trp
			130				135				140				
Arg	Pro	Leu	Gly	Asp	Leu	Ser	Ile	Gln	Ser	Ser	Lys	Gln	Ser	Leu	Phe
			145				150				155				160
Asn	Ser	Asn	Tyr	Ser	Lys	Gln	Gly	Gly	Gly	Ala	Leu	Tyr	Val	Glu	Gly
			165				170				175				
Gly	Ile	Asn	Phe	Gln	Asp	Leu	Glu	Glu	Ile	Arg	Ile	Lys	Tyr	Asn	Lys
			180				185				190				
Ala	Gly	Thr	Phe	Glu	Thr	Lys	Lys	Ile	Thr	Leu	Pro	Ser	Leu	Lys	Ala
			195				200				205				
Gln	Ala	Ser	Ala	Gly	Asn	Ala	Asp	Ala	Trp	Ala	Ser	Ser	Ser	Pro	Gln
			210				215				220				
Ser	Gly	Ser	Gly	Ala	Thr	Thr	Val	Ser	Asp	Ser	Gly	Asp	Ser	Ser	Ser
			225				230				235				240
Gly	Ser	Asp	Ser	Asp	Thr	Ser	Glu	Thr	Val	Pro	Val	Thr	Ala	Lys	Gly
			245				250				255				
Gly	Gly	Leu	Tyr	Thr	Asp	Lys	Asn	Leu	Ser	Ile	Thr	Asn	Ile	Thr	Gly
			260				265				270				
Ile	Ile	Glu	Ile	Ala	Asn	Asn	Lys	Ala	Thr	Asp	Val	Gly	Gly	Gly	Ala
			275				280				285				
Tyr	Val	Lys	Gly	Thr	Leu	Thr	Cys	Glu	Asn	Ser	His	Arg	Leu	Gln	Phe
			290				295				300				
Leu	Lys	Asn	Ser	Ser	Asp	Lys	Gln	Gly	Gly	Gly	Ile	Tyr	Gly	Glu	Asp
			305				310				315				320
Asn	Ile	Thr	Leu	Ser	Asn	Leu	Thr	Gly	Lys	Thr	Leu	Phe	Gln	Glu	Asn
			325				330				335				
Thr	Ala	Lys	Glu	Glu	Gly	Gly	Gly	Leu	Phe	Ile	Lys	Gly	Thr	Asp	Lys
			340				345				350				
Ala	Leu	Thr	Met	Thr	Gly	Leu	Asp	Ser	Phe	Cys	Leu	Ile	Asn	Asn	Thr
			355				360				365				
Ser	Glu	Lys	His	Gly	Gly	Gly	Ala	Phe	Val	Thr	Lys	Glu	Ile	Ser	Gln
			370				375				380				
Thr	Tyr	Thr	Ser	Asp	Val	Glu	Thr	Ile	Pro	Gly	Ile	Thr	Pro	Val	His
			385				390				395				400
Gly	Glu	Thr	Val	Ile	Thr	Gly	Asn	Lys	Ser	Thr	Gly	Gly	Asn	Gly	Gly
			405				410				415				
Gly	Val	Cys	Thr	Lys	Arg	Leu	Ala	Leu	Ser	Asn	Leu	Gln	Ser	Ile	Ser
			420				425				430				
Ile	Ser	Gly	Asn	Ser	Ala	Ala	Glu	Asn	Gly	Gly	Gly	Ala	His	Thr	Cys
			435				440				445				
Pro	Asp	Ser	Phe	Pro	Thr	Ala	Asp	Thr	Ala	Glu	Gln	Pro	Ala	Ala	Ala
			450				455				460				
Ser	Ala	Ala	Thr	Ser	Thr	Pro	Lys	Ser	Ala	Pro	Val	Ser	Thr	Ala	Leu
			465				470				475				480
Ser	Thr	Pro	Ser	Ser	Ser	Thr	Val	Ser	Ser	Leu	Thr	Leu	Leu	Ala	Ala
			485				490				495				
Ser	Ser	Gln	Ala	Ser	Pro	Ala	Thr	Ser	Asn	Lys	Glu	Thr	Gln	Asp	Pro
			500				505				510				
Asn	Ala	Asp	Thr	Asp	Leu	Leu	Ile	Asp	Tyr	Val	Val	Asp	Thr	Thr	Ile
			515				520				525				
Ser	Lys	Asn	Thr	Ala	Lys	Lys	Gly	Gly	Gly	Ile	Tyr	Ala	Lys	Lys	Ala
			530				535				540				
Lys	Met	Ser	Arg	Ile	Asp	Gln	Leu	Asn	Ile	Ser	Glu	Asn	Ser	Ala	Thr
			545				550				555				560
Glu	Ile	Gly	Gly	Gly	Ile	Cys	Cys	Lys	Glu	Ser	Leu	Glu	Leu	Asp	Ala
			565				570				575				

Leu Val Ser Leu Ser Val Thr Glu Asn
580 585

<210> 338
<211> 38
<212> DNA
<213> Chlamydia trachomatis

<400> 338
gagagcggcc gctcgaccaa ctgaatatct ctgagaac

38

<210> 339
<211> 35
<212> DNA
<213> Chlamydia trachomatis

<400> 339
gagagcggcc gcttaagaga ctacgtggag ttctg

35

<210> 340
<211> 1965
<212> DNA
<213> Chlamydia trachomatis

<400> 340
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cagggatctcg ccattccgat. ogggcaggcg atggcgatcg ogggccagat caagcttccc 120
accgttccata tcgggcccac cgccttctct ggttgggtg ttgtcgacaa caacggcaca 180
ggcgacagag tccaaagggt ggctgggagc gctccgggg caagtctcgg catctccacc 240
ggcgacgtga tcacccgggt cgacggcgct ccgatcaact ogggccacgg gatggcgagc 300
ggccttaagg ggcatcatcc cggtgacgtc atctcgggtga cctggcaaac caagtccggc 360
ggcacgcgtc cagggaacgt gacattggcc gagggacccc ogggccgaatt ctgcagatat 420
ccatcacact ggccggccgt cgaccaaact aatatctctg agaactccgc tacagagata 480
gggtggaggta ttgtgtggaa agaactctta gaactagatg ctctagtctc ctattctgta 540
acagagaacc ttgttgggaa agaaggtgga ggcttacatg ctaaaactgt aaattttct 600
aatctgaat cagggtctct tttctcgaa caaaaagcaa actcctcatc cacaggagtc 660
gcaacaacag cttccagcacc tgcgtcagct gctgctccc tacaagcagc cgacgcagcc 720
gcaccatcat ctcacgcaac accaacttat tcagggttag taggaggagc tctctatgta 780
gaaaagggtta cattctctca atgtagcggg acttgtcagt tctctgggaa caagctalc 840
gataacaatc cctcccaatc atcgttgaa gtacaaggag gagccatcta tgcacaaacc 900
ttttgtctca ttgtgtcttc cgatgtgga accctctata tttctcggg gaacagctac 960
tccactggga aatctcaaac aacagggcaa atagcgggag gagcgaacta ctcccctact 1020
gttacattga gttgtcctgc gacattctct aacaaacag cctctatagc tacacggag 1080
acttctctcg aagatgggtc ctacggaat tctattaaag ataccattgg aggagccatt 1140
gcagggaacg ccattaccct atctggagtc tctcgatttt cagggaatac ggtgattata 1200
ggagctgcaa taggaaact agctaagta aatacaccca gtgcaactca cggatctcaa 1260
aatagcata cagaaaaaat tactttagaa aacggltctt ttattttga aagaacccaa 1320
gctaataaac gtggagcgat ttactctctc agcgtttcca tttaagggaa taattattcc 1380
tccaatacaa atacatccac tcatgtgga agcgtctatc actttacaaa agatgctaag 1440
attgagctct taggatctgt tctttttaca ggaataaag tlacagctac acaagctagt 1500
tctgcaacat ctggacaaaa tacaactatg gccactatg gggcagccat ctttggagat 1560
ccaggaacca cccaatcgct tcaaacagat gcatttttaa ccttcttgc ttctctgga 1620
aacattact ttgacacaaa cagtttacag aataaccaag gtgatactcc cgtagcaag 1680
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gaacttttag atattaatga agaagagaac agtaatccat atacaggaa tactgtgttc 1860
tctctgaat tacatgaaa caaatctac atcccaaga atgcaactct tcacacgga 1920
actttagttc ttaaagagaa aacagaactc cactgattct cttaa 1965

<210> 341
<211> 654

<212> PRT

<213> Chlamydia trachomatis

<400> 341

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 20 25 30
 Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
 35 40 45
 Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
 50 55 60
 Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
 65 70 75 80
 Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
 85 90 95
 Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
 100 105 110
 Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
 115 120 125
 Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
 130 135 140
 Arg Pro Leu Asp Gln Leu Asn Ile Ser Glu Asn Ser Ala Thr Glu Ile
 145 150 155 160
 Gly Gly Gly Ile Cys Cys Lys Glu Ser Leu Glu Leu Asp Ala Leu Val
 165 170 175
 Ser Leu Ser Val Thr Glu Asn Leu Val Gly Lys Glu Gly Gly Leu
 180 185 190
 His Ala Lys Thr Val Asn Ile Ser Asn Leu Lys Ser Gly Phe Ser Phe
 195 200 205
 Ser Asn Asn Lys Ala Asn Ser Ser Ser Thr Gly Val Ala Thr Ala
 210 215 220
 Ser Ala Pro Ala Ala Ala Ala Ser Leu Gln Ala Ala Ala Ala
 225 230 235 240
 Ala Pro Ser Ser Pro Ala Thr Pro Thr Tyr Ser Gly Val Val Gly Gly
 245 250 255
 Ala Ile Tyr Gly Glu Lys Val Thr Phe Ser Gln Cys Ser Thr Cys
 260 265 270
 Gln Phe Ser Gly Asn Gln Ala Ile Asp Asn Asn Pro Ser Gln Ser Ser
 275 280 285
 Leu Asn Val Gln Gly Gly Ala Ile Tyr Ala Lys Thr Ser Leu Ser Ile
 290 295 300
 Gly Ser Ser Asp Ala Gly Thr Ser Tyr Ile Phe Ser Gly Asn Ser Val
 305 310 315 320
 Ser Thr Gly Lys Ser Gln Thr Thr Gly Gln Ile Ala Gly Gly Ala Ile
 325 330 335
 Tyr Ser Pro Thr Val Thr Leu Asn Cys Pro Ala Thr Phe Ser Asn Asn
 340 345 350
 Thr Ala Ser Ile Ala Thr Pro Lys Thr Ser Ser Glu Asp Gly Ser Ser
 355 360 365
 Gly Asn Ser Ile Lys Asp Thr Ile Gly Gly Ala Ile Ala Gly Thr Ala
 370 375 380
 Ile Thr Leu Ser Gly Val Ser Arg Phe Ser Gly Asn Thr Ala Asp Leu
 385 390 395 400
 Gly Ala Ala Ile Gly Thr Leu Ala Asn Ala Asn Thr Pro Ser Ala Thr
 405 410 415
 Ser Gly Ser Gln Asn Ser Ile Thr Glu Lys Ile Thr Leu Glu Asn Gly
 420 425 430
 Ser Phe Ile Phe Glu Arg Asn Gln Ala Asn Lys Arg Gly Ala Ile Tyr
 435 440 445
 Ser Pro Ser Val Ser Ile Lys Gly Asn Asn Ile Thr Phe Asn Gln Asn

450 455 460
 Thr Ser Thr His Asp Gly Ser Ala Ile Tyr Phe Thr Lys Asp Ala Thr
 465 470 475 480
 Ile Glu Ser Leu Gly Ser Val Leu Phe Thr Gly Asn Asn Val Thr Ala
 485 490 495
 Thr Gln Ala Ser Ser Ala Thr Ser Gly Gln Asn Thr Asn Thr Ala Asn
 500 505 510
 Tyr Gly Ala Ala Ile Phe Gly Asp Pro Gly Thr Thr Gln Ser Ser Gln
 515 520 525
 Thr Asp Ala Ile Leu Thr Leu Leu Ala Ser Ser Gly Asn Ile Thr Phe
 530 535 540
 Ser Asn Asn Ser Leu Gln Asn Asn Gln Gly Asp Thr Pro Ala Ser Lys
 545 550 555 560
 Phe Cys Ser Ile Ala Gly Tyr Val Lys Leu Ser Leu Gln Ala Ala Lys
 565 570 575
 Gly Lys Thr Ile Ser Phe Phe Asp Cys Val His Thr Ser Thr Lys Lys
 580 585 590
 Thr Gly Ser Thr Gln Asn Val Tyr Glu Thr Leu Asp Ile Asn Lys Glu
 595 600 605
 Glu Asn Ser Asn Pro Tyr Thr Gly Thr Ile Val Phe Ser Ser Glu Leu
 610 615 620
 His Glu Asn Lys Ser Tyr Ile Pro Gln Asn Ala Ile Leu His Asn Gly
 625 630 635 640
 Thr Leu Val Leu Lys Glu Lys Thr Glu Leu His Val Val Ser
 645 650

<210> 342
 <211> 36
 <212> DNA
 <213> Chlamydia trachomatis

<400> 342
 gagagcgccc gctcggaact attgtgttct cttctg 36

<210> 343
 <211> 35
 <212> DNA
 <213> Chlamydia trachomatis

<400> 343
 gagagcgccc gcttagaaga tcatgagagc accgc 35

<210> 344
 <211> 2103
 <212> DNA
 <213> Chlamydia trachomatis

<400> 344
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 cagggtatcg ccattccgat cgggcaggcg atggcgatcg cgggocagat caagcttccc 120
 accgttccata tcgggctccac cgccttctct ggcttgggtg ttgtcgacaa caacggcaac 180
 ggccgacagag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240
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 ggccacgcgt cagggaacgt gacattggcc gagggacccc cggccgaatt ctgcagatat 420
 ccatcacact gcggccgcgt cggaaactatt gtgttctctt ctgaattaca tgaaaacaaa 480
 tcttatccac cacagaaatgc aatccttcac aacggaactt tagttcttaa agagaaaaca 540
 gaactccacg tagtctcttt tgagcagaaa gaagggtcta aattaattat ggaaccggga 600
 gctgtgttat ctaaccacaa catagctaac ggagctctag ctatcaatgg gttacgatt 660
 gatctttcca gatgtgggac tctcacaaga ggggaaatct tctctctccc agaattacgt 720
 atcgttgcca cgacctctag tgcatacggg ggaagcggg tcagcagtag tataccaaca 780

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agcgagaaaa aagttttctc aacaggagagc cttacttttaa tagatcctaa tggaaacttt      900
taccaaaaacc ctatgtttagg aagcgatcta gatgtaccac taattaagct tccgaactaac      960
acaagtgagc tccaagtccta tgattttaat ttatctgggg atctttttccc tcagaaaggg      1020
tacatgggaaa cctggacatt agattctaat ccaccaaacag ggaacttca agccagatgg      1080
acattcgata cctatcgctg ctgggtatac atacctaggg ataactattt ttatgcgaac      1140
tctatctttag gctcccaaaa ctcaatgatt gtgtgaagc aagggcttat caacaacatg      1200
ttgaataatg cccgcttcga tgatatcgct tacaataact tctgggttct aggagttaga      1260
actttcttag ctcaacaagg aactcctctt tcggaagaat tccagttact tcagttacta cagccgcgga      1320
acttcagtgg ccatcgatgc caaacctaga caagatttta tctcaggagc tgcatttagt      1380
aagatagtgg ggaaaaccaa agccatcaaa aaaatgcata attacttcca taagggtctct      1440
gagtagctctt accaagcttc tgtctatgga ggtaaaattcc tgtattttct gctcaataag      1500
caacatggtt gggcacttcc tttcctaata caaggagtcg tgtcctatgg acatatataa      1560
catgatataa caacacttta cctctctatc catgaaagaa ataaagagga ttgggaagat      1620
ttaggatggt tagcggtatc tctgtatctc atggatctta aagaaccttc taaagattct      1680
tctaaccgga tcactgtcta tggggaaactc gagtatccca gcattcgcca gaaacagttc      1740
acagaaatcg attacgatcc aagacacttc gatgattgtg cttacagaaa tctgtcgctt      1800
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cttgcattag cctacatgcc ttctatctac agaaataaact ctgtctgtaa atatcggyta      1920
tgtcttcgga atgaagctgg tcaagttatc tgcggagtcg caactagaac atctgctaga      1980
gcagaaataca gtactcaact atactttggt cctctctgga ctctctacg aaactatact      2040
atcgatgtag gcatgtatac gctatcgcaa atgactagct gcggtgctcg catgatcttc      2100
taa

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<210> 345
 <211> 700
 <212> PRT
 <213> Chlamydia trachomatis

<400> 345
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 20 25 30
 Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
 35 40 45
 Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
 50 55 60
 Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
 65 70 75 80
 Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
 85 90 95
 Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
 100 105 110
 Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
 115 120 125
 Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
 130 135 140
 Arg Pro Leu Gly Thr Ile Val Phe Ser Ser Glu Leu His Glu Asn Lys
 145 150 155 160
 Ser Tyr Ile Pro Gln Asn Ala Ile Leu His Asn Gly Thr Leu Val Leu
 165 170 175
 Lys Glu Lys Thr Glu Leu His Val Val Ser Phe Glu Gln Lys Glu Gly
 180 185 190
 Ser Lys Leu Ile Met Glu Pro Gly Ala Val Leu Ser Asn Gln Asn Ile
 195 200 205
 Ala Asn Gly Ala Leu Ala Ile Asn Gly Leu Thr Ile Asp Leu Ser Ser
 210 215 220
 Met Gly Thr Pro Gln Ala Gly Glu Ile Phe Ser Pro Pro Glu Leu Arg
 225 230 235 240
 Ile Val Ala Thr Thr Ser Ser Ala Ser Gly Gly Ser Gly Val Ser Ser

Ser	Ile	Pro	Thr	245	Asn	Pro	Lys	Arg	Ile	250	Ser	Ala	Ala	Val	Pro	255	Ser	Gly
				260						265						270		
Ser	Ala	Ala	Thr	Thr	Pro	Thr	Met	Ser	Glu	Asn	Lys	Val	Phe	Leu	Thr			
				275						280						285		
Gly	Asp	Leu	Thr	Leu	Ile	Asp	Pro	Asn	Gly	Asn	Phe	Tyr	Gln	Asn	Pro			
				290						295						300		
Met	Leu	Gly	Ser	Asp	Leu	Asp	Val	Pro	Leu	Ile	Lys	Leu	Pro	Thr	Asn			
				305						310						315		
Thr	Ser	Asp	Val	Gln	Val	Tyr	Asp	Leu	Thr	Leu	Ser	Gly	Asp	Leu	Phe			
				325						330						335		
Pro	Gln	Lys	Gly	Tyr	Met	Gly	Thr	Trp	Thr	Leu	Asp	Ser	Asn	Pro	Gln			
				340						345						350		
Thr	Gly	Lys	Leu	Gln	Ala	Arg	Trp	Thr	Phe	Asp	Thr	Tyr	Arg	Arg	Trp			
				355						360						365		
Val	Tyr	Ile	Pro	Arg	Asp	Asn	His	Phe	Tyr	Ala	Asn	Ser	Ile	Leu	Gly			
				370						375						380		
Ser	Gln	Asn	Ser	Met	Ile	Val	Val	Lys	Gln	Gly	Leu	Ile	Asn	Asn	Met			
				385						390						395		
Leu	Asn	Asn	Ala	Arg	Phe	Asp	Asp	Ile	Ala	Tyr	Asn	Asn	Phe	Trp	Val			
				405						410						415		
Ser	Gly	Val	Gly	Thr	Phe	Leu	Ala	Gln	Gln	Gly	Thr	Pro	Leu	Ser	Glu			
				420						425						430		
Glu	Phe	Ser	Tyr	Tyr	Ser	Arg	Gly	Thr	Ser	Val	Ala	Ile	Asp	Ala	Lys			
				435						440						445		
Pro	Arg	Gln	Asp	Phe	Ile	Leu	Gly	Ala	Ala	Phe	Ser	Lys	Ile	Val	Gly			
				450						455						460		
Lys	Thr	Lys	Ala	Ile	Lys	Lys	Met	His	Asn	Tyr	Phe	His	Lys	Gly	Ser			
				465						475						480		
Glu	Tyr	Ser	Tyr	Gln	Ala	Ser	Val	Tyr	Gly	Gly	Lys	Phe	Leu	Tyr	Phe			
				485						490						495		
Leu	Leu	Asn	Lys	Gln	His	Gly	Trp	Ala	Leu	Pro	Phe	Leu	Ile	Gln	Gly			
				500						505						510		
Val	Val	Ser	Tyr	Gly	His	Ile	Lys	His	Asp	Thr	Thr	Thr	Leu	Tyr	Pro			
				515						520						525		
Ser	Ile	His	Glu	Arg	Asn	Lys	Gly	Asp	Trp	Glu	Asp	Leu	Gly	Trp	Leu			
				530						535						540		
Ala	Asp	Leu	Arg	Ile	Ser	Met	Asp	Leu	Lys	Glu	Pro	Ser	Lys	Asp	Ser			
				545						550						555		
Ser	Lys	Arg	Ile	Thr	Val	Tyr	Gly	Glu	Leu	Glu	Tyr	Ser	Ser	Ile	Arg			
				565						570						575		
Gln	Lys	Gln	Phe	Thr	Glu	Ile	Asp	Tyr	Asp	Pro	Arg	His	Phe	Asp	Asp			
				580						585						590		
Cys	Ala	Tyr	Arg	Asn	Leu	Ser	Leu	Pro	Val	Gly	Cys	Ala	Val	Glu	Gly			
				595						600						605		
Ala	Ile	Met	Asn	Cys	Asn	Ile	Leu	Met	Tyr	Asn	Lys	Leu	Ala	Leu	Ala			
				610						615						620		
Tyr	Met	Pro	Ser	Ile	Tyr	Arg	Asn	Asn	Pro	Val	Cys	Lys	Tyr	Arg	Val			
				625						630						635		
Leu	Ser	Ser	Asn	Glu	Ala	Gly	Gln	Val	Ile	Cys	Gly	Val	Pro	Thr	Arg			
				645						650						655		
Thr	Ser	Ala	Arg	Ala	Glu	Tyr	Ser	Thr	Gln	Leu	Tyr	Leu	Gly	Pro	Phe			
				660						665						670		
Trp	Thr	Leu	Tyr	Gly	Asn	Tyr	Thr	Ile	Asp	Val	Gly	Met	Tyr	Thr	Leu			
				675						680						685		
Ser	Gln	Met	Thr	Ser	Cys	Gly	Ala	Arg	Met	Ile	Phe					700		
				690						695								

<210> 346

<211> 37

<212> DNA

<213> Chlamydia trachomatis

<400> 346

gagagcggcc gctcatgaaa ttatgtcag ctactgc

37

<210> 347

<211> 37

<212> DNA

<213> Chlamydia trachomatis

<400> 347

gagagcggcc gcttaccctg taattccagt gatggtc

37

<210> 348

<211> 1464

<212> DNA

<213> Chlamydia trachomatis

<400> 348

atgcatcacc	atcaccatca	cacgccgcgc	tccgataact	tccagctgtc	ccagggtggg	60
cagggattcg	ccattccgat	cgggcacggc	atggcgatcg	cgggcacgat	caagcttccc	120
accgttccata	tccggccctac	cgcccttctc	ggcttggtg	ttgtccgaca	caacggcacc	180
ggcgccacgag	tccaacgcag	ggcggggagc	gctccggggc	caagtctcgg	catctccacc	240
ggcgacgtga	tcaccgcggt	cgacggcgct	ccgatcaact	cggccacccg	gatggcgagc	300
cgctttaacg	ggcatcatcc	cggtgacgtc	atctcgggtg	cctggcacaac	caagtccggc	360
ggcacgcgtg	cagggaacgt	gacattggcc	gagggaaccc	cggccgaatt	ctgcagatat	420
ccatcacact	ggcggccgct	catgaatttt	atgtcagcta	ctgctgtatt	tgtcgagta	480
ctctctcccg	ttactgagcg	gagctogato	caagatcaaa	taaagaatac	cgactgcaat	540
gttagcaaaag	taggatattc	aacttctcaa	gcatttactg	atatgatgct	agcagacaac	600
acagagtatc	gagctgctga	tagtgtttca	ttctatgact	tttcgacatc	ttccggatta	660
cctagaaaaac	atcttagtag	tagtagtgaa	gcttctccaa	cgacagaagg	agtgtcttoa	720
tcttcactctg	gagaaaaaac	tgagaattca	caagattcag	ctccctcttc	tggagaaact	780
gataagaaaa	cagaagaaga	actagacaat	ggcggaatca	tttatgctag	agagaaacta	840
actatctcag	aatctcagga	ctctctctct	aatccaagca	tagaactcca	tgacaatagt	900
tttttctctg	gagaaggtga	agttatcttt	gatcacagag	ttgccctcaa	aaacggagga	960
gctattttcg	gagagaaga	ggtagtcttt	gaaaaacata	aatctctact	agtagaagta	1020
aatatctcgg	tcgagaaagg	ggtagcgctc	tatgcataag	aacgagtatc	tttagaaaat	1080
gttaccgaga	caacettctc	ctccaatggt	ggggaacaag	gtgtgtgtgt	aattctattca	1140
gaacaagaata	tgttaatcat	tgattgcaac	aatgtacatt	tccaaggagg	gtgtgcagga	1200
ccaacagcag	taaaacaagt	ctctggatga	gaaatgatcg	tattgtccac	agaatcgctt	1260
gatagcttat	ccgaagatgc	actggatagc	actccagaaa	cggaacagag	taagtcaaat	1320
ggaaatcaag	atggttctgc	tgaacaaaa	gatcacacaag	tatcagaatc	accagaatca	1380
actctagcc	ccgacgatgt	tttaggtaaa	ggtggtggtg	tctatacaga	aaaatctttg	1440
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<210> 349

<211> 487

<212> PRT

<213> Chlamydia trachomatis

<400> 349

Met	His	His	His	His	His	His	Thr	Ala	Ala	Ser	Asp	Asn	Phe	Gln	Leu
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Ser	Gln	Gly	Gly	Gln	Gly	Phe	Ala	Ile	Pro	Ile	Gly	Gln	Ala	Met	Ala
				20					25					30	
Ile	Ala	Gly	Gln	Ile	Lys	Leu	Pro	Thr	Val	His	Ile	Gly	Pro	Thr	Ala
				35					40					45	
Phe	Leu	Gly	Leu	Gly	Val	Val	Asp	Asn	Asn	Gly	Asn	Gly	Ala	Arg	Val
				50					55					60	
Gln	Arg	Val	Val	Gly	Ser	Ala	Pro	Ala	Ala	Ser	Leu	Gly	Ile	Ser	Thr
65				70					75					80	

Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
 85 90 95
 Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
 100 105 110
 Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
 115 120 125
 Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
 130 135 140
 Arg Pro Leu Met Lys Phe Met Ser Ala Thr Ala Val Phe Ala Ala Val
 145 150 155
 Leu Ser Ser Val Thr Glu Ala Ser Ser Ile Gln Asp Gln Ile Lys Asn
 165 170 175
 Thr Asp Cys Asn Val Ser Lys Val Gly Tyr Ser Thr Ser Gln Ala Phe
 180 185 190
 Thr Asp Met Met Leu Ala Asp Asn Thr Glu Tyr Arg Ala Ala Asp Ser
 195 200 205
 Val Ser Phe Tyr Asp Phe Ser Thr Ser Ser Gly Leu Pro Arg Lys His
 210 215 220
 Leu Ser Ser Ser Ser Glu Ala Ser Pro Thr Thr Glu Gly Val Ser Ser
 225 230 235
 Ser Ser Ser Gly Glu Asn Thr Glu Asn Ser Gln Asp Ser Ala Pro Ser
 245 250 255
 Ser Gly Glu Thr Asp Lys Lys Thr Glu Glu Leu Asp Asn Gly Gly
 260 265 270
 Ile Ile Tyr Ala Arg Glu Lys Leu Thr Ile Ser Glu Ser Gln Asp Ser
 275 280 285
 Leu Ser Asn Pro Ser Ile Glu Leu His Asp Asn Ser Phe Phe Gly
 290 295 300
 Glu Gly Glu Val Ile Phe Asp His Arg Val Ala Leu Lys Asn Gly Gly
 305 310 315
 Ala Ile Tyr Gly Glu Lys Glu Val Val Phe Glu Asn Ile Lys Ser Leu
 325 330 335
 Leu Val Glu Val Asn Ile Ser Val Glu Lys Gly Gly Ser Val Tyr Ala
 340 345 350
 Lys Glu Arg Val Ser Leu Glu Asn Val Thr Glu Ala Thr Phe Ser Ser
 355 360 365
 Asn Gly Gly Glu Gln Gly Gly Gly Ile Tyr Ser Glu Gln Asp Met
 370 375 380
 Leu Ile Ser Asp Cys Asn Asn Val His Phe Gln Gly Asn Ala Ala Gly
 385 390 395
 Ala Thr Ala Val Lys Gln Cys Leu Asp Glu Met Ile Val Leu Leu
 405 410 415
 Thr Glu Cys Val Asp Ser Leu Ser Glu Asp Thr Leu Asp Ser Thr Pro
 420 425 430
 Glu Thr Glu Gln Thr Lys Ser Asn Gly Asn Gln Asp Gly Ser Ser Glu
 435 440 445
 Thr Lys Asp Thr Gln Val Ser Glu Ser Pro Glu Ser Thr Pro Ser Pro
 450 455 460
 Asp Asp Val Leu Gly Lys Gly Gly Gly Ile Tyr Thr Glu Lys Ser Leu
 465 470 475
 Thr Ile Thr Gly Ile Thr Gly
 485

<210> 350

<211> 37

<212> DNA

<213> Chlamydia trachomatis

<400> 350

gagagcgagcc gctcgataca caagtatcag aatcacc

<210> 351
 <211> 37
 <212> DNA
 <213> Chlamydia trachomatis

<400> 351
 gagagcggcc gcttaagagg acgatgagac actctcg

37

<210> 352
 <211> 1752
 <212> DNA
 <213> Chlamydia trachomatis

<400> 352
 atgcataccc atcaccatca cagcgccggc tccgataact tccagctgtc ccaggggtgg 60
 cagggaattcg ccattccgat cgggcaggcg atggcgatcg cgggcccagat caagcttccc 120
 accgtttcata tcgggcctac cgccttctct ggttgggtg ttgtcgacaa caacggcaac 180
 ggcgcaacgag tccaaacggt ggtcgggagc gctcggcgcg caagtctcgg catctccacc 240
 ggacagctga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300
 cgcgttaacg gccatcatcc cgggtgacgt atctcgggtg cctggcaaac caagtccggc 360
 ggacgcgcta cagggaacgt gacattggcc gagggacccc cggccgaatt ctgcagatat 420
 ccatcacact ggccggcgct cgatacacaa gatatcagaat caccagaatt aactcctagc 480
 ccgcagcgtg ttttaggtta aggtgggtgt atctatacag aaaaatcttt gaccatcact 540
 ggaattacag ggaactataga tttgtcagt aacatagcta ccgattctctg agcaggtgta 600
 ttccactaaag aaaaacttgtc ttgcaccaac acgaatagcc tacagttttt gaaaaactcg 660
 gcaggccaac atggaggagg agcctacgtt actcaaaaca tgtctgttac taatacaact 720
 agtgaagata taactactcc cctctcgtg ggagaagtga tttctctga aaatacagct 780
 aaagggccagc gtggtgggat ctgcactaac aaactttctt tatctaattt aaaaacgggt 840
 actctcacta aaaaactctgc aaaggagtct ggaggagcta tttttacaga cttagcgtct 900
 ataccaacaa cagatacccc agagtcttct cccctctct cctcctcgcc tgaagcact 960
 ccggaagtga ttgctctcgc taaaataaat cgattctttg cctctaagcg agaacggca 1020
 gccctctctc taacagagcg tgagtctgat caaacggatc aaacagaaac tctgtatact 1080
 aatagcgata tagacgtgtc gattgagaac attttgaatg tcgctatcaa tcaaaact 1140
 tctgcgaaaa aaggaggggc tatttaacgg aaaaagcta aactttcccg tatatacaat 1200
 cttgaacttt cagggaattc atcccaggat gtaggaggag gtctctgttt aactgaaagg 1260
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 ggggtttatc attctaaaac ggttactcta tctaacctca agtctacctt caacttttgc 1380
 gataaacctg ttaaagcaat agtagaagcg actctcgaag ctccagaaga gattccctca 1440
 gtagaaggag aagagtctac agcaacagaa aatccgaatt ctaatacaga agtgaaggtg 1500
 gctaacacta accttgaagg atctcaaggg gatactgctg atacagggac tgggtgtttt 1560
 acaactgagt ctcaagacac atcagatact ggaacgcctg aatctggaga acaactacaa 1620
 gattctacac aatctaatta agaaaatacc cttcccaata gtgattatga tcaatctaac 1680
 gaaaacacag acgaatcac tgaatgccac actgagggaa taactgacga gagtgtctca 1740
 tgcctctctt aa 1752

<210> 353
 <211> 583
 <212> PRT
 <213> Chlamydia trachomatis

<400> 353
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 20 25 30
 Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
 35 40 45
 Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
 50 55 60
 Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
 65 70 75 80

Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
 85 90 95
 Ala Met Ala Asp Ala Leu Asn Gly His Pro Gly Asp Val Ile Ser
 100 105 110
 Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
 115 120 125
 Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
 130 135 140
 Arg Pro Leu Asp Thr Gln Val Ser Glu Ser Pro Glu Ser Thr Pro Ser
 145 150 155
 Pro Asp Asp Val Leu Gly Lys Gly Gly Ile Tyr Thr Glu Lys Ser
 165 170 175
 Leu Thr Ile Thr Gly Ile Thr Gly Thr Ile Asp Phe Val Ser Asn Ile
 180 185 190
 Ala Thr Asp Ser Gly Ala Gly Val Phe Thr Lys Glu Asn Leu Ser Cys
 195 200 205
 Thr Asn Thr Asn Ser Leu Gln Phe Leu Lys Asn Ser Ala Gly Gln His
 210 215 220
 Gly Gly Gly Ala Tyr Val Thr Gln Thr Met Ser Val Thr Asn Thr Thr
 225 230 235
 Ser Glu Ser Ile Thr Thr Pro Pro Leu Val Gly Glu Val Ile Phe Ser
 245 250 255
 Glu Asn Thr Ala Lys Gly His Gly Gly Ile Cys Thr Asn Lys Leu
 260 265 270
 Ser Leu Ser Asn Leu Lys Thr Val Thr Leu Thr Lys Asn Ser Ala Lys
 275 280 285
 Glu Ser Gly Gly Ala Ile Phe Thr Asp Leu Ala Ser Ile Pro Thr Thr
 290 295 300
 Asp Thr Pro Glu Ser Ser Thr Thr Pro Ser Ser Ser Pro Ala Ser Thr
 305 310 315
 Pro Glu Val Val Ala Ser Ala Lys Ile Asn Arg Phe Phe Ala Ser Thr
 325 330 335
 Ala Glu Pro Ala Ala Pro Ser Leu Thr Glu Ala Glu Ser Asp Gln Thr
 340 345 350
 Asp Gln Thr Glu Thr Ser Asp Thr Asn Ser Asp Ile Asp Val Ser Ile
 355 360 365
 Glu Asn Ile Leu Asn Val Ala Ile Asn Gln Asn Thr Ser Ala Lys Lys
 370 375 380
 Gly Gly Ala Ile Tyr Gly Lys Lys Ala Lys Leu Ser Arg Ile Asn Asn
 385 390 395
 Leu Glu Leu Ser Gly Asn Ser Ser Gln Asp Val Gly Gly Gly Leu Cys
 405 410 415
 Leu Thr Glu Ser Val Glu Phe Asp Ala Ile Gly Ser Leu Leu Ser His
 420 425 430
 Tyr Asn Ser Ser Ala Ala Lys Glu Gly Gly Val Ile His Ser Lys Thr Val
 435 440 445
 Thr Leu Ser Asn Leu Lys Ser Thr Phe Thr Phe Ala Asp Asn Thr Val
 450 455 460
 Lys Ala Ile Val Glu Ser Thr Pro Glu Ala Pro Glu Glu Ile Pro Pro
 465 470 475
 Val Glu Gly Glu Glu Ser Thr Ala Thr Glu Asn Pro Asn Ser Asn Thr
 485 490 495
 Glu Gly Ser Ser Ala Asn Thr Asn Leu Glu Gly Ser Gln Gly Asp Thr
 500 505 510
 Ala Asp Thr Gly Thr Gly Val Val Asn Asn Glu Ser Gln Asp Thr Ser
 515 520 525
 Asp Thr Gly Asn Ala Glu Ser Gly Glu Gln Leu Gln Asp Ser Thr Gln
 530 535 540
 Ser Asn Glu Glu Asn Thr Leu Pro Asn Ser Ser Ile Asp Gln Ser Asn
 545 550 555
 Glu Asn Thr Asp Glu Ser Ser Asp Ser His Thr Glu Glu Ile Thr Asp
 560

565
Glu Ser Val Ser Ser Ser Ser
580

570

575

<210> 354
<211> 39
<212> DNA
<213> Chlamydia trachomatis

<400> 354
gagagcggcc gctcgatcaa tctaacgaaa acacagacg

39

<210> 355
<211> 36
<212> DNA
<213> Chlamydia trachomatis

<400> 355
gagagcggcc gcttagacca aagctccatc agcaac

36

<210> 356
<211> 2052
<212> DNA
<213> Chlamydia trachomatis

<400> 356
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cagggtattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc 120
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gcgcttaacg ggcatactcc cgttagcgtc atctcgttga cctggcaaac caagtggggc 360
ggcaccgcta cagggaacgt gacattggcc gagggaccoc cggccgaatt ctgcagatat 420
ccatcacact ggcggccgct cgatcaatct aacgaaaaca cagacgaatt atctgatagc 480
cacactgagg aaataactga cgagagtgtc tcactgctct ctaaaagtgg atcatctact 540
cctcaagatt gagggacgag ttcttcaggg gctccctcag gagatcaatc tatctctgca 600
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gtctggagact ctgaagacct gactgagcga gaagctggtt ctacacaga aactcctact 780
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tacgcacctg tcgtttccat taaagcctat actgogacat ttaacaaaaa cagatctcta 1380
gaagaaggaa gcgcgattca ctttacaaaa gaagcatctc ttgagtcctt aggcctgttt 1440
ctcttcacag gaaacttagt aaccccaacg ctaagcacia ctacagaagg cacaccagcc 1500
acaacctcag gagatgtaac aaaaataggt gctgctatct ttggacaaat agcaagctca 1560
aacggatctc agacgggata ccttccctct aaactcattg cttcaggagg aaatatgttt 1620
ttcgaaaaaa atgaatacgc tctactttct tctgatcagc gaacctctac cgtactctc 1680
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gatgcaatc ggacctctac taagaaaaa ggtacacagg caactgccta cgtactctc 1800
gatatttaata aatctggagg ttacagaaat gtaaacctcg cgtttacagg aacgatctct 1860
ttctctctcg aatttacaag aaataaatcc tatattccac aaaaactagt tctacacagt 1920
ggatctcttg tattgaagcc aaataccgag ctctcatgca tttcttttga gcagaaagaa 1980
ggctctcttc tegttagtac aactggatct gttcttccga accagactgt tgctgatgga 2040
gctttggtct aa 2052

<210> 357
 <211> 683
 <212> PRT
 <213> Chlamydia trachomatis

<400> 357
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 1 5 10 15
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 20 25 30
 Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
 35 40 45
 Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
 50 55 60
 Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
 65 70 75 80
 Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
 85 90 95
 Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
 100 105 110
 Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
 115 120 125
 Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
 130 135 140
 Arg Pro Leu Asp Gln Ser Asn Glu Asn Thr Asp Glu Ser Ser Asp Ser
 145 150 155 160
 His Thr Glu Glu Ile Thr Asp Glu Ser Val Ser Ser Ser Ser Lys Ser
 165 170 175
 Gly Ser Ser Thr Pro Gln Asp Gly Gly Ala Ala Ser Ser Gly Ala Pro
 180 185 190
 Ser Gly Asp Gln Ser Ile Ser Ala Asn Ala Cys Leu Ala Lys Ser Tyr
 195 200 205
 Ala Ala Ser Thr Asp Ser Ser Pro Val Ser Asn Ser Ser Gly Ser Asp
 210 215 220
 Val Thr Ala Ser Ser Asp Asn Pro Asp Ser Ser Ser Ser Gly Asp Ser
 225 230 235 240
 Ala Gly Asp Ser Glu Gly Pro Thr Glu Pro Glu Ala Gly Ser Thr Thr
 245 250 255
 Glu Thr Pro Thr Leu Ile Gly Gly Gly Ala Ile Tyr Gly Glu Thr Val
 260 265 270
 Lys Ile Glu Asn Phe Ser Gly Gln Gly Ile Phe Ser Gly Asn Lys Ala
 275 280 285
 Ile Asp Asn Thr Thr Glu Gly Ser Ser Ser Lys Ser Asn Val Leu Gly
 290 295 300
 Gly Ala Val Tyr Ala Lys Thr Leu Phe Asn Leu Asp Ser Gly Ser Ser
 305 310 315 320
 Arg Arg Thr Val Thr Phe Ser Gly Asn Thr Val Ser Ser Gln Ser Thr
 325 330 335
 Thr Gly Gln Val Ala Gly Gly Ala Ile Tyr Ser Pro Thr Val Thr Ile
 340 345 350
 Ala Thr Pro Val Val Phe Ser Lys Asn Ser Ala Thr Asn Asn Ala Asn
 355 360 365
 Asn Ala Thr Asp Thr Gln Arg Lys Asp Thr Phe Gly Gly Ala Ile Gly
 370 375 380
 Ala Thr Ser Ala Val Ser Leu Ser Gly Gly Ala His Phe Leu Glu Asn
 385 390 395 400
 Val Ala Asp Leu Gly Ser Ala Ile Gly Leu Val Pro Asp Thr Gln Asn
 405 410 415
 Thr Glu Thr Val Lys Leu Glu Ser Gly Ser Tyr Tyr Phe Glu Lys Asn
 420 425 430

Lys Ala Leu Lys Arg Ala Thr Ile Tyr Ala Pro Val Val Ser Ile Lys
 435 440 445
 Ala Tyr Thr Ala Thr Phe Asn Gln Asn Arg Ser Leu Glu Glu Gly Ser
 450 455 460
 Ala Ile Tyr Phe Thr Lys Glu Ala Ser Ile Glu Ser Leu Gly Ser Val
 465 470 475 480
 Leu Phe Thr Gly Asn Leu Val Thr Pro Thr Leu Ser Thr Thr Thr Glu
 485 490 495
 Gly Thr Pro Ala Thr Thr Ser Gly Asp Val Thr Lys Tyr Gly Ala Ala
 500 505 510
 Ile Phe Gly Gln Ile Ala Ser Ser Asn Gly Ser Gln Thr Asp Asn Leu
 515 520 525
 Pro Leu Lys Leu Ile Ala Ser Gly Gly Asn Ile Cys Phe Arg Asn Asn
 530 535 540
 Glu Tyr Arg Pro Thr Ser Ser Asp Thr Gly Thr Ser Thr Phe Cys Ser
 545 550 555 560
 Ile Ala Gly Asp Val Lys Leu Thr Met Gln Ala Ala Lys Gly Lys Thr
 565 570 575
 Ile Ser Phe Phe Asp Ala Ile Arg Thr Ser Thr Lys Lys Thr Gly Thr
 580 585 590
 Gln Ala Thr Ala Tyr Asp Thr Leu Asp Ile Asn Lys Ser Glu Asp Ser
 595 600 605
 Glu Thr Val Asn Ser Ala Phe Thr Gly Thr Ile Leu Phe Ser Ser Glu
 610 615 620
 Leu His Glu Asn Lys Ser Tyr Ile Pro Gln Asn Val Val Leu His Ser
 625 630 635 640
 Gly Ser Leu Val Leu Lys Pro Asn Thr Glu Leu His Val Ile Ser Phe
 645 650 655 660
 Glu Gln Lys Glu Gly Ser Ser Leu Val Met Thr Pro Gly Ser Val Leu
 660 665 670
 Ser Asn Gln Thr Val Ala Asp Gly Ala Leu Val
 675 680

<210> 358

<211> 1248

<212> DNA

<213> Chlamydia

<400> 358

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 gctttatttt ctactctctt cagagaagag ctctctggat taaccctctc tctggtctcc 180
 tctatcaag tttcggaaga cggcggttt tatcgttttt gtattcgtaa agatgctaaag 240
 tggagtgaag gctctctttt actttgcagaa gatgtaatag ctgcttgga acacactaaa 300
 caagctgggc gatattccct actttttgaa aagctatctt ttgcgcctc ttcttcttcg 360
 gaaatcctta ttgaactcaa agaaccogag cctcaactat tggcgatatt agoctctccg 420
 tttttgtct tgtatgtctc agaaaatcct tttctttct ctggaccttt ttgccaanaa 480
 aactatgctc aaggccaaac gctcgttcta caaaaaacc ctattacta tgcacatgcg 540
 catgtggaat tacattccat agactttcgc atcattccca acattttacac agctctacac 600
 ctcttaagaa gaggtgacgt ggattgggtg gggcagcctt ggcaccaagg gattcctttt 660
 gagcttcgga ctacctctgc tctctacacc cattaccctg tatctggcac attctggctt 720
 attcttaact ccaaagatcc tgaactttcc tctctatcta atcgctcagc attgattgct 780
 gccatccaaa agaaaaaact ggtgaagcaa gctttaggaa cacaatatcg attagctgaa 840
 agctctccat ctccagaggg aatcatagct catcaagaag ctcttactcc ttttctcggg 900
 aaaaattact tgatalatcc caataatatt acgcgctgtc agcgtttggc cggaggtattg 960
 caagaacaat gcgcagacgc aggtatccag ctgactcttg aaggactcga ataccagtta 1020
 tttgttcaaa ccaagagccac tcaagatttc tctgtctcca cagcaacttc atagctttc 1080
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 <213> Chlamydia

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<210> 362

<211> 412

<212> PRT

<213> Chlamydia

<400> 362

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                    20                               25           30
Phe His Phe Ser Leu Ser Lys Ala Leu Phe Ala Thr Leu Phe Arg Glu
                    35                               40           45
Glu Leu Ser Gly Leu Thr Pro Ala Leu Val Ser Ser Tyr Gln Val Ser
                    50                               55           60
Glu Asp Gly Arg Phe Tyr Arg Phe Cys Ile Arg Lys Asp Ala Lys Trp
                    65                               70           75           80
Ser Asp Gly Ser Leu Leu Leu Ala Glu Asp Val Ile Ala Ala Trp Glu
                    85                               90           95
His Thr Lys Gln Ala Gly Arg Tyr Ser Leu Leu Phe Glu Lys Leu Ser
                    100                              105          110
Phe Arg Ala Ser Ser Ser Ser Glu Ile Leu Ile Glu Leu Lys Glu Pro
                    115                              120          125
Glu Pro Gln Leu Leu Ala Ile Leu Ala Ser Pro Phe Phe Ala Val Tyr
                    130                              135          140
Arg Pro Glu Asn Pro Phe Leu Ser Ser Gly Pro Phe Met Pro Lys Thr
                    145                              150          155          160
Tyr Val Gln Gly Gln Thr Leu Val Leu Gln Lys Asn Pro Tyr Tyr Tyr
                    165                              170          175
Asp His Ala His Val Glu Leu His Ser Ile Asp Phe Arg Ile Ile Pro
                    180                              185          190
Asn Ile Tyr Thr Ala Leu His Leu Leu Arg Arg Gly Asp Val Asp Trp
                    195                              200          205
Val Gly Gln Pro Trp His Gln Gly Ile Pro Phe Glu Leu Arg Thr Thr
                    210                              215          220
Ser Ala Leu Tyr Thr His Tyr Pro Val Asp Gly Thr Phe Trp Leu Ile
                    225                              230          235          240
Leu Asn Pro Lys Asp Pro Val Leu Ser Ser Leu Ser Asn Arg Gln Arg
                    245                              250          255
Leu Ile Ala Ala Ile Gln Lys Glu Lys Leu Val Lys Gln Ala Leu Gly
                    260                              265          270
Thr Gln Tyr Arg Val Ala Glu Ser Ser Pro Ser Pro Glu Gly Ile Ile
                    275                              280          285
Ala His Gln Glu Ala Ser Thr Pro Phe Pro Gly Lys Ile Thr Leu Ile
                    290                              295          300
Tyr Pro Asn Asn Ile Thr Arg Cys Gln Arg Leu Ala Glu Val Leu Gln
                    305                              310          315          320
Glu Gln Cys Arg Asp Ala Gly Ile Gln Leu Thr Leu Glu Gly Leu Glu
                    325                              330          335
Tyr His Val Phe Val Gln Lys Arg Ala Thr Gln Asp Phe Ser Val Ser
                    340                              345          350
Thr Ala Thr Ser Ile Ala Phe His Pro Leu Ala Lys Ser Lys Phe Asp

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	355		360		365
Gln Thr	Ala Leu Asp Asn Phe	Thr Cys Leu Pro Leu	Tyr His Ile Glu		
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Tyr Asp Tyr Ile Leu Ser Arg Pro Leu Asp Gln Ile	Val His Tyr Pro				
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Ser Gly Ser Val Asp Leu Thr Tyr Ala His Phe His					
	405	410			

<210> 363

<211> 433

<212> PRT

<213> Chlamydia

<400> 363

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	20								
Gly Leu Ile Ile Ala Ile His Asp Asp Pro Arg Ser Leu Ser Pro Glu						40			45
	35								
Lys Gly Glu Asn Ala Phe His Phe Ser Leu Ser Lys Ala Leu Phe Ala						55			60
	50								
Thr Leu Phe Arg Glu Glu Leu Ser Gly Leu Thr Pro Ala Leu Val Ser						70			80
	65								
Ser Tyr Gln Val Ser Glu Asp Gly Arg Phe Tyr Arg Phe Cys Ile Arg						90			95
	85								
Lys Asp Ala Lys Trp Ser Asp Gly Ser Leu Leu Leu Ala Glu Asp Val						105			110
	100								
Ile Ala Ala Trp Glu His Thr Lys Gln Ala Gly Arg Tyr Ser Leu Leu						120			125
	115								
Phe Glu Lys Leu Ser Phe Arg Ala Ser Ser Ser Ser Glu Ile Leu Ile						135			140
	130								
Glu Leu Lys Glu Pro Glu Pro Gln Leu Leu Ala Ile Leu Ala Ser Pro						150			155
	145								
Phe Phe Ala Val Tyr Arg Pro Glu Asn Pro Phe Leu Ser Ser Gly Pro						170			175
	165								
Phe Met Pro Lys Thr Tyr Val Gln Gly Gln Thr Leu Val Leu Gln Lys						185			190
	180								
Asn Pro Tyr Tyr Tyr Asp His Ala His Val Glu Leu His Ser Ile Asp						200			205
	195								
Phe Arg Ile Ile Pro Asn Ile Tyr Thr Ala Leu His Leu Leu Arg Arg						215			220
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Gly Asp Val Asp Trp Val Gly Gln Pro Trp His Gln Gly Ile Pro Phe						235			240
	225								
Glu Leu Arg Thr Thr Ser Ala Leu Tyr Thr His Tyr Pro Val Asp Gly						250			255
	245								
Thr Phe Trp Leu Ile Leu Asn Pro Lys Asp Pro Val Leu Ser Ser Leu						265			270
	260								
Ser Asn Arg Gln Arg Leu Ile Ala Ala Ile Gln Lys Glu Lys Leu Val						280			285
	275								
Lys Gln Ala Leu Gly Thr Gln Tyr Arg Val Ala Glu Ser Ser Pro Ser						295			300
	290								
Pro Glu Gly Ile Ile Ala His Gln Glu Ala Ser Thr Pro Phe Pro Gly						310			315
	305								
Lys Ile Thr Leu Ile Tyr Pro Asn Asn Ile Thr Arg Cys Gln Arg Leu						330			335
	325								
Ala Glu Val Leu Gln Glu Gln Cys Arg Asp Ala Gly Ile Gln Leu Thr						345			350
	340								
Leu Glu Gly Leu Glu Tyr His Val Phe Val Gln Lys Arg Ala Thr Gln						360			365
	355								

Asp Phe Ser Val Ser Thr Ala Thr Ser Ile Ala Phe His Pro Leu Ala
 370 375 380
 Lys Ser Lys Phe Asp Gln Thr Ala Leu Asp Asn Phe Thr Cys Leu Pro
 385 390 395
 Leu Tyr His Ile Glu Tyr Asp Tyr Ile Leu Ser Arg Pro Leu Asp Gln
 405 410 415
 Ile Val His Tyr Tyr Pro Ser Gly Ser Val Asp Leu Thr Tyr Ala His Phe
 420 425 430
 His

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<211> 264

<212> PRT

<213> Chlamydia

<400> 364

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 Gln Ile Ile Leu Gly Thr Thr Ser Thr Pro Val Ala Ala Lys Met Thr
 35 40 45
 Ala Ser Asp Gly Ile Ser Leu Thr Val Ser Asn Asn Pro Ser Thr Asn
 50 55 60
 Ala Ser Ile Thr Ile Gly Leu Asp Ala Glu Lys Ala Tyr Gln Leu Ile
 65 70 75 80
 Leu Glu Lys Leu Gly Asp Gln Ile Leu Gly Gly Ile Ala Asp Thr Ile
 85 90 95
 Val Asp Ser Thr Val Gln Asp Ile Leu Asp Lys Ile Thr Thr Asp Pro
 100 105 110
 Ser Leu Gly Leu Leu Lys Ala Phe Asn Asn Phe Pro Ile Thr Asn Lys
 115 120 125
 Ile Gln Cys Asn Gly Leu Phe Thr Pro Arg Asn Ile Glu Thr Leu Leu
 130 135 140
 Gly Gly Thr Glu Ile Gly Lys Phe Thr Val Thr Pro Lys Ser Ser Gly
 145 150 155 160
 Ser Met Phe Leu Val Ser Ala Asp Ile Ile Ala Ser Arg Met Glu Gly
 165 170 175
 Gly Val Val Leu Ala Leu Val Arg Glu Gly Asp Ser Lys Pro Tyr Ala
 180 185 190
 Ile Ser Tyr Gly Tyr Ser Ser Gly Val Pro Asn Leu Cys Ser Leu Arg
 195 200 205
 Thr Arg Ile Ile Asn Thr Gly Leu Thr Pro Thr Thr Tyr Ser Leu Arg
 210 215 220
 Val Gly Gly Leu Glu Ser Gly Val Val Trp Val Asn Ala Leu Ser Asn
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<210> 365

<211> 249

<212> PRT

<213> Chlamydia

<400> 365

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 Pro Leu Gln Glu Arg Ser Val Val Val Ser Ser Lys Ile Val Ser
 35 40 45
 Leu Cys Glu Gly Ala Val Ala Asp Ala Arg Met Cys Lys Ala Glu Leu
 50 55 60
 Ile Lys Lys Glu Ala Asp Ala Tyr Leu Phe Cys Glu Lys Ser Gly Ile
 65 70 75 80
 Tyr Leu Thr Lys Lys Glu Gly Ile Leu Ile Pro Ser Ala Gly Ile Asp
 85 90 95
 Glu Ser Asn Thr Asp Gln Pro Phe Val Leu Tyr Pro Lys Asp Ile Leu
 100 105 110
 Gly Ser Cys Asn Arg Ile Gly Glu Trp Leu Arg Asn Tyr Phe Arg Val
 115 120 125
 Lys Glu Leu Gly Val Ile Ile Thr Asp Ser His Thr Thr Pro Met Arg
 130 135 140
 Arg Gly Val Leu Gly Ile Gly Leu Cys Trp Tyr Gly Phe Ser Pro Leu
 145 150 155 160
 His Asn Tyr Ile Gly Ser Leu Asp Cys Phe Gly Arg Pro Leu Gln Met
 165 170 175
 Thr Gln Ser Asn Leu Val Asp Ala Leu Ala Val Ala Val Val Cys
 180 185 190
 Met Gly Glu Gly Asn Glu Gln Thr Pro Leu Ala Val Ile Glu Gln Ala
 195 200 205
 Pro Asn Met Val Tyr His Ser Tyr Pro Thr Ser Arg Glu Glu Tyr Cys
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 <213> Chlamydia pneumoniae

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 <212> DNA
 <213> Chlamydia pneumoniae

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<210> 368
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 <212> DNA
 <213> Chlamydia pneumoniae

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 <212> DNA
 <213> Chlamydia pneumoniae

<400> 369

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<210> 370

<211> 774

<212> DNA

<213> Chlamydia pneumoniae

<400> 370

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<211> 3759

<212> DNA

<213> Chlamydia pneumoniae

<400> 376

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<210> 377

<211> 675

<212> DNA

<213> Chlamydia pneumoniae

<400> 377

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<210> 378

<211> 1671

<212> DNA

<213> Chlamydia pneumoniae

<400> 378

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<210> 379

<211> 1386

<212> DNA

<213> Chlamydia pneumoniae

<400> 379

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<210> 380
<211> 1635
<212> DNA
<213> Chlamydia pneumoniae

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<210> 381
<211> 1995
<212> DNA
<213> Chlamydia pneumoniae

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<210> 382

<211> 987

<212> DNA

<213> Chlamydia pneumoniae

<400> 382

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ttagtacact	ccgtgcagaa	ctcgtggaag	gctgtaattg	aagcaagagg	gaaatctctg	720
gcagcatccg	catctcagag	acttgcgcag	gcccgccgat	ctattttttg	tcctaaaaat	780
gacgagtggt	tttctctctg	agtggttctg	gatcataatc	cttatgggat	tctcgaagac	840
gttttttttg	gttttccatg	tctgatgttg	octcttgag	attatgaat	catctcctga	900
tgtcctttgg	agccttttat	cagaaataag	attcaaaatt	ccctggatga	aattgctcag	960
gaaaaagcta	cgctgtcttc	gttataa				987

<210> 383

<211> 654

<212> DNA

<213> Chlamydia pneumoniae

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<400> 383
atgaaaagag   tcatttataa   aaccatattt   tgcgggttaa   ctttacttac   aagtttgagt   60
agttgttccc   tggatcctaa   aggatataac   ctagagacaa   aaaactcgag   ggactttaat   120
caagagtctg   ttatactgaa   ggaataccgt   gaaacacctt   ctcttgtaa   gagaactctt   180
cgctgtctct   gaagactctt   cgctcgacgt   gatcaaacct   agaaggatac   gctgcaagtg   240
caagctaaact   ttaagacctt   cgcaaaaaag   atttcagagc   aggcagaaag   agacotttct   300
ttcgtttgct   cgtctgtcgc   agaaaagctc   tcaatttcgt   tagctttgtc   tcagggtgaa   360
attaaggatg   ctttgtacgc   tatccgagaa   gtccaccctc   tagctttaat   agaagctctt   420
gctgaaaacc   ctgccttgat   agaagggatg   aaaaagatgc   aaggccgtga   ttggatttgg   480
aatcttttct   taacacaatt   aagtgaaagta   ttttctcaag   ctgtgtctca   aggggttaac   540
tctgaagaag   atatcgccgc   atttgccctc   acctaggtt   tggactcgg   gaccgttgog   600
tcattgtctc   aaggggaaag   gtggcccgag   cttgtggata   tagtgataac   ttaa         654

<210> 384
<211> 813
<212> DNA
<213> Chlamydia pneumoniae

<400> 384
atgatcataa   taaaaaacia   tgagctcatg   ataagacgtt   ttttcaaaac   gcttttccct   60
cgggttccct   aataactctt   atgttatgct   togatcctga   tcgttttgag   ttcccttggt   120
tgtgttctct   cattttggtg   gttatttctc   cctgaactgt   ctttatcctc   attcaactct   180
tctccattta   ggaactctat   tttagtttcc   tcaactctat   ccaaagtcct   tctactcgcg   240
attgcagaac   atttaagctt   ttctgcggat   gcaactacat   atctccatga   attctctatt   300
aaagaagctg   agtcgagctt   gcatgctctt   gggatttttt   cctctttagt   tatagaaaaa   360
tctctcgata   ataaggcgat   tacaattttc   tatacctttac   aaacacctac   ggtttatggt   420
gggaaccgat   tgaatctccc   atgcaatctc   gaggggagct   gottttctgg   tcaaccgtac   480
ttccctctct   tgaatctccc   tcagattttt   ttctctcaag   aagatttaaa   aatgcaaaaa   540
ctccctaaga   aaaaaatgct   ttttaccgaag   attctcttta   aggagcttgc   tatggagctc   600
cgaataatca   ttgatttctc   ttatatcgat   gcataccctg   gagaatttat   agtcaagctc   660
tcttcaggca   gtcgtgtaag   acttccaatt   aagaacctag   atcgtgctct   agacctgtat   720
aagcacatga   aaaaaagctc   tgtaactcag   agcgaataac   aatatgtcta   tgatttgctg   780
tttccaatt   tcttattatt   aaaagctcta   tga         813

<210> 385
<211> 1956
<212> DNA
<213> Chlamydia pneumoniae

<400> 385
atggttaate   ctatttgctc   aggtcctata   gacgaacacg   aacgcacacc   tcccgcagat   60
ctttcttctc   aaggatgga   ggcgagtga   gcaataaaga   gtgcggaagc   tcaagaata   120
gcagggtgct   agctcaagcc   taagaatct   aagaccgatt   ctgtagagct   atggagcatc   180
ttgcgttctg   cagtgaatgc   tctcatgagt   ctggcgagata   agctgggtat   tgctttcagt   240
aacagctcgt   ctctctactg   cagatctgca   gacgtggact   caacgcacgc   gacgcgaact   300
acgcctctct   cccccagtt   tgatgattat   aagaactcaag   cgcaaacacg   ttacgatact   360
atctttactc   caacatcact   agctgaacata   caggctgctt   tggtagcctc   ccaggagctg   420
gtcaactaata   taaggagatc   agcggtact   gatgaggaaa   ccgcaatcgc   tgcggagtgg   480
gaactcaaga   atgcogagtc   agttaaagt   ggcgcgaaga   ttacagaatt   tcttaagaat   540
gcttcggata   accaagcgat   tcttgaactc   ttaggtaaac   tgacttctct   cgaactctta   600
caggctgctc   ttctccaatc   ttagcaaaac   aataacaaag   agctgcagct   tcttaagag   660
atgcaagata   acccagtagt   cccagggaag   acgcctgcac   ttgctcaact   tttagttgat   720
cacagcagtg   ctacagcgac   acagatagag   aaagatggaa   atcgcatatt   ggtgcatat   780
tttgacggac   agaacgctag   tggagctgta   gaaatgccta   aatctaataa   cagtataagc   840
aacatagatt   cagctaagc   agcaatcgct   actgctaaga   cacaaatagc   tgaagctcag   900
aaaaagtctc   ccgactctcc   aattctcaa   gaagcggaac   aaatggtaac   acagctgcag   960
aaagatcttc   aaaaatcaaa   acctgcagat   ggttctgatg   ttccaaatct   aggaactaca   1020
gttgaggctc   ccaagcaaca   aggaagtatg   attggtagta   tctgtgttca   catgctgtca   1080
gatgatgctg   aaatgagac   cgcttccatt   ttgatgtctg   ggttctcgta   gaggattcac   1140
atgttcaata   cggaaaatcc   tgattctcaa   gctgcccaac   aggagctcgc   agcacaagct   1200

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```

agagcagcga aagccgctgg agatgacagt gctgctgcag cgctggcaga tgctcagaaa 1260
gctttagaag cggctctagg taaagctggg caacaacagg gcataactcaa tgcttttagga 1320
cagatcgctt ctgctgctgt tgtgagcgca ggagttcctc cgctgagcag aagttctata 1380
gggtcatctg taaaacagct ttacaagacc tcaaaatcta caggttctga ttataaaaca 1440
cagatatcag caggttatga tgcttacaata tccatcaatg atgcttatgg tagggcagca 1500
aatgatcgca ctgctgatgt gataaacaat gtaagtaccc ccgctctcac acgatccgtt 1560
cctagagcac gaacagaagc tcgaaggcca gaaaaaacag atcaagccct cgctagggtg 1620
atctctggca atagcagaac tcttggagat gtctatagtc aagtttcggc actacaactc 1680
gtaatcgaga tcatccagtc gaatcctcaa gcgaataatg aggagatcag acaaaagctt 1740
acatcgcgag tgacaaagcc tccacagttt ggctatcctt atgtgcaact tcttaatgac 1800
tctacacaga agttcatagc taaattagaa agtttgtttg ctgaaggatc taggcacaga 1860
gctgaataaa aagcactttc ctttgaacag aactccttgt ttattcagca ggtgctggtc 1920
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```

<210> 386

<211> 805

<212> PRT

<213> *Chlamydia pneumoniae*

<400> 386

```

Met Asp Pro Lys Glu Lys Asn Tyr Asp Ala Ser Ala Ile Thr Val Leu
                    5              10              15

```

```

Glu Gly Leu Gln Ala Val Arg Glu Arg Pro Gly Met Tyr Ile Gly Asp
                    20              25              30

```

```

Thr Gly Ile Thr Gly Leu His His Leu Val Tyr Glu Val Val Asp Asn
                    35              40              45

```

```

Ser Ile Asp Glu Ala Met Ala Gly Tyr Cys Ser Arg Ile Asp Val Arg
                    50              55              60

```

```

Ile Leu Glu Asp Gly Gly Ile Val Ile Val Asp Asn Gly Arg Gly Ile
                    65              70              75              80

```

```

Pro Ile Glu Val His Glu Arg Glu Ser Ala Lys Gln Gly Arg Glu Val
                    85              90              95

```

```

Ser Ala Leu Glu Val Val Leu Thr Val Leu His Ala Gly Gly Lys Phe
                    100             105             110

```

```

Asp Lys Asp Ser Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val
                    115             120             125

```

```

Ser Cys Val Asn Ala Leu Ser Glu Lys Leu Val Ala Thr Val Phe Lys
                    130             135             140

```

```

Asp Lys Lys Cys Tyr Gln Met Glu Phe Ser Arg Gly Ile Pro Val Thr
                    145             150             155             160

```

```

Pro Leu Gln Tyr Val Ser Val Ser Asp Arg Gln Gly Thr Glu Ile Val
                    165             170             175

```

```

Phe Tyr Pro Asp Pro Lys Ile Phe Ser Thr Cys Thr Phe Asp Arg Ser
                    180             185             190

```

```

Ile Leu Met Lys Arg Leu Arg Glu Leu Ala Phe Leu Asn Arg Gly Ile
                    195             200             205

```

```

Thr Ile Val Phe Glu Asp Asp Arg Asp Val Ser Phe Asp Lys Val Thr

```

210		215		220	
Phe Phe Tyr Glu Gly Gly Ile Gln Ser	Phe Val Ser Tyr Leu Asn Gln				
225	230	235		240	
Asn Lys Glu Ser Leu Phe Ser Glu Pro	Ile Tyr Ile Cys Gly Thr Arg				
	245	250	255		
Val Gly Asp Asp Gly Glu Ile Glu Phe	Glu Ala Ala Leu Gln Trp Asn				
	260	265	270		
Ser Gly Tyr Ser Ser Glu Leu Val Tyr	Ser Tyr Ala Asn Asn Ile Pro Thr				
	275	280	285		
Arg Gln Gly Gly Thr His Leu Thr Gly	Phe Ser Thr Ala Leu Thr Arg				
	290	295	300		
Val Ile Asn Thr Tyr Ile Lys Ala His	Asn Leu Ala Lys Asn Asn Lys				
	305	310	315	320	
Leu Ala Leu Thr Gly Glu Asp Ile Arg	Glu Gly Leu Thr Ala Val Ile				
	325	330	335		
Ser Val Lys Val Pro Asn Pro Gln Phe	Glu Gly Gln Thr Lys Gln Lys				
	340	345	350		
Leu Gly Asn Ser Asp Val Ser Ser Val	Ala Gln Gln Val Val Gly Glu				
	355	360	365		
Ala Leu Thr Ile Phe Phe Glu Glu Asn	Pro Gln Ile Ala Arg Met Ile				
	370	375	380		
Val Asp Lys Val Phe Val Ala Ala Gln	Ala Arg Glu Ala Ala Lys Lys				
	385	390	395	400	
Ala Arg Glu Leu Thr Leu Arg Lys Ser	Ala Leu Asp Ser Ala Arg Leu				
	405	410	415		
Pro Gly Lys Leu Ile Asp Cys Leu Glu	Lys Asp Pro Glu Lys Cys Glu				
	420	425	430		
Met Tyr Ile Val Glu Gly Asp Ser Ala	Gly Gly Ser Ala Lys Gln Gly				
	435	440	445		
Arg Asp Arg Arg Phe Gln Ala Ile Leu	Pro Ile Arg Gly Lys Ile Leu				
	450	455	460		
Asn Val Glu Lys Ala Arg Leu Gln Lys	Ile Phe Gln Asn Gln Glu Ile				
	465	470	475	480	
Gly Thr Ile Ile Ala Ala Leu Gly Cys	Gly Ile Gly Ala Asp Asn Phe				
	485	490	495		
Asn Leu Ser Lys Leu Arg Tyr Arg Arg	Ile Ile Ile Met Thr Asp Ala				
	500	505	510		
Asp Val Asp Gly Ser His Ile Arg Thr	Leu Leu Leu Thr Phe Phe Tyr				
	515	520	525		
Arg His Met Thr Ala Leu Ile Glu Asn	Glu Cys Val Tyr Ile Ala Gln				
	530	535	540		

Pro Pro Leu Tyr Lys Val Ser Lys Lys Lys Asp Phe Arg Tyr Ile Leu
 545 550 555
 Ser Glu Lys Glu Met Asp Ser Tyr Leu Leu Met Leu Gly Thr Asn Glu
 565 570 575
 Ser Ser Ile Leu Phe Lys Ser Thr Glu Arg Glu Leu Arg Gly Glu Ala
 580 585 590
 Leu Glu Ser Phe Ile Asn Val Ile Leu Asp Val Glu Ser Phe Ile Asn
 595 600 605
 Thr Leu Glu Lys Lys Ala Ile Pro Phe Ser Glu Phe Leu Glu Met Tyr
 610 615 620
 Lys Glu Gly Ile Gly Tyr Pro Leu Tyr Tyr Leu Ala Pro Ala Thr Gly
 625 630 635 640
 Met Gln Gly Gly Arg Tyr Leu Tyr Ser Asp Glu Glu Lys Glu Glu Ala
 645 650 655
 Leu Ala Gln Glu Glu Thr His Lys Phe Lys Ile Ile Glu Leu Tyr Lys
 660 665 670
 Val Ala Val Phe Val Asp Ile Gln Asn Gln Leu Lys Glu Tyr Gly Leu
 675 680 685
 Asp Ile Ser Ser Tyr Leu Ile Pro Gln Lys Asn Glu Ile Val Ile Gly
 690 695 700
 Asn Glu Asp Ser Pro Ser Cys Asn Tyr Ser Cys Tyr Thr Leu Glu Glu
 705 710 715 720
 Val Ile Asn Tyr Leu Lys Asn Leu Gly Arg Lys Gly Ile Glu Ile Gln
 725 730 735
 Arg Tyr Lys Gly Leu Gly Glu Met Asn Ala Asp Gln Leu Trp Asp Thr
 740 745 750
 Thr Met Asn Pro Glu Gln Arg Thr Leu Ile His Val Ser Leu Lys Asp
 755 760 765
 Ala Val Glu Ala Asp His Ile Phe Thr Met Leu Met Gly Glu Glu Val
 770 775 780
 Pro Pro Arg Arg Glu Phe Ile Glu Ser His Ala Leu Ser Ile Arg Ile
 785 790 795 800
 Asn Asn Leu Asp Ile
 805

<210> 387

<211> 295

<212> PRT

<213> Chlamydia pneumoniae

<400> 387

Met Glu Lys Leu Leu Val Thr Asp Ile Asp Gly Thr Ile Thr His Gln
 5 10 15

Ser His His Leu Asp Lys Lys Val Tyr Glu Arg Leu Tyr Ala Leu His
 20 25 30
 Gln Ala Gly Trp Lys Leu Phe Phe Leu Thr Gly Arg Tyr Tyr Lys Tyr
 35 40 45
 Ala Ala Arg Leu Phe Ser Asp Phe Asp Ala Pro Tyr Leu Leu Gly Cys
 50 55 60
 Gln Asn Gly Ala Ser Val Trp Ser Ser Thr Ser Ser Asn Leu Leu Tyr
 65 70 75 80
 Ser Lys Ser Leu Pro Ser Asp Leu Leu Cys Ile Leu Gln Asp Cys Met
 85 90 95
 Glu Gly Ala Thr Ala Leu Phe Ser Val Glu Ser Gly Ala Pro Tyr Gly
 100 105 110
 Asp His Tyr Tyr Arg Phe Ser Pro Thr Pro Ile Ala Gln Asp Leu His
 115 120 125
 Glu Tyr Val Asp Pro Arg Tyr Phe Pro Asn Ala Lys Glu Arg Glu Ile
 130 135 140
 Leu Phe Glu Thr Arg Ser Leu Lys Asp Asp Tyr Ala Phe Pro Ser Phe
 145 150 155 160
 Ala Ala Ala Lys Val Phe Gly Leu Arg Asp Glu Val Ile Arg Ile Gln
 165 170 175
 Lys Glu Leu Glu Arg Gln Glu Ala Leu Thr Ser Val Ala Thr Met Thr
 180 185 190
 Leu Met Arg Trp Pro Phe Asp Phe Arg Tyr Ala Ile Leu Phe Leu Thr
 195 200 205
 Asp Lys Ser Val Ser Lys Gly Lys Ala Leu Asp Arg Val Val Asn Ile
 210 215 220
 Leu Tyr Asp Gly Lys Lys Pro Phe Val Met Ala Ser Gly Asp Asp Ala
 225 230 235 240
 Asn Asp Leu Asp Leu Ile Glu Arg Gly Asp Phe Lys Ile Val Met Ser
 245 250 255
 Ser Ala Pro Glu Glu Met His Val His Ala Asp Phe Leu Ala Pro Pro
 260 265 270
 Ala Asp Lys Asn Gly Ile Leu Ser Ala Trp Glu Ala Gly Val Arg Tyr
 275 280 285
 Tyr Asp Asp Leu Met Ser Leu
 290 295

<210> 388

<211> 78

<212> PRT

<213> Chlamydia pneumoniae

<400> 388

Met	Lys	Glu	Phe	Leu	Ala	Tyr	Ile	Ile	Lys	Asn	Leu	Val	Asp	Arg	Pro
			5						10					15	
Glu	Glu	Val	Arg	Ile	Lys	Glu	Val	Gln	Gly	Thr	His	Thr	Ile	Ile	Tyr
			20					25					30		
Glu	Leu	Ser	Val	Ala	Lys	Pro	Asp	Ile	Gly	Lys	Ile	Ile	Gly	Lys	Glu
		35					40					45			
Gly	Arg	Thr	Ile	Lys	Ala	Ile	Arg	Thr	Leu	Leu	Val	Ser	Val	Ala	Ser
	50					55					60				
Arg	Asn	Asn	Val	Arg	Val	Ser	Leu	Glu	Ile	Met	Glu	Glu	Lys		
65					70					75					

<210> 389

<211> 478

<212> PRT

<213> Chlamydia pneumoniae

<400> 389

Met	Arg	Asp	Val	Ser 5	Glu	Leu	Phe	Arg	Thr 10	His	Phe	Met	His	Tyr 15	Ala
Ser	Tyr	Val	Ile 20	Leu	Glu	Arg	Ala	Ile 25	Pro	His	Ile	Leu	Asp 30	Gly	Leu
Lys	Pro	Val 35	Gln	Arg	Arg	Leu	Leu 40	Trp	Thr	Leu	Phe	Leu 45	Met	Asp	Asp
Gly	Lys 50	Met	His	Lys	Val	Ala 55	Asn	Ile	Ala	Gly	Arg 60	Thr	Met	Ala	Leu
His 65	Pro	His	Gly	Asp	Ala 70	Pro	Ile	Val	Glu	Ala 75	Leu	Val	Val	Leu	Ala 80
Asn	Lys	Gly	Tyr 85	Leu	Ile	Asp	Thr	Gln	Gly 90	Asn	Phe	Gly	Asn	Pro 95	Leu
Thr	Gly	Asp	Pro 100	His	Ala	Ala	Ala	Arg 105	Tyr	Ile	Glu	Ala	Arg 110	Leu	Ser
Pro	Leu	Ala 115	Arg	Glu	Thr	Leu	Phe 120	Asn	Thr	Asp	Leu	Ile 125	Ala	Phe	His
Asp	Ser 130	Tyr	Asp	Gly	Arg	Glu 135	Lys	Glu	Pro	Asp	Ile 140	Leu	Pro	Ala	Lys
Leu 145	Pro	Val	Leu	Leu	Leu 150	His	Gly	Val	Asp	Gly 155	Ile	Ala	Val	Gly	Met 160
Thr	Thr	Lys	Ile 165	Phe	Pro	His	Asn	Phe	Ala 170	Glu	Leu	Leu	Lys	Ala 175	Gln
Ile	Ala	Ile	Leu 180	Asn	Asp	Lys	Lys	Phe 185	Thr	Val	Phe	Pro	Asp 190	Phe	Pro
Ser	Gly	Gly 195	Leu	Met	Asp	Pro	Ser 200	Glu	Tyr	Gln	Asp	Gly 205	Leu	Gly	Ser

Ile Thr Leu Arg Ala Ser Ile Asp Ile Ile Asn Asp Lys Thr Leu Val
 210 215 220
 Val Lys Gln Ile Cys Pro Gln Ser Thr Thr Glu Thr Leu Ile Arg Ser
 225 230 235 240
 Ile Glu Asn Ala Ala Lys Arg Gly Thr Ile Lys Ile Asp Thr Ile Gln
 245 250 255
 Asp Phe Ser Thr Asp Val Pro His Ile Glu Ile Lys Leu Pro Lys Gly
 260 265 270
 Ser Arg Ala Lys Glu Met Leu Pro Leu Leu Phe Glu His Thr Glu Cys
 275 280 285
 Gln Val Ile Leu Tyr Ser Lys Pro Thr Val Ile Tyr Glu Asn Lys Pro
 290 295 300
 Val Glu Cys Ser Ile Ser Glu Ile Leu Lys Leu His Thr Thr Ala Leu
 305 310 315 320
 Gln Gly Tyr Leu Glu Lys Glu Leu Leu Leu Gln Glu Gln Leu Thr
 325 330 335
 Leu Asp His Tyr His Lys Thr Leu Glu Tyr Ile Phe Ile Lys His Lys
 340 345 350
 Leu Tyr Asp Ser Val Arg Glu Val Leu Ala Ile Asn Lys Lys Ile Ser
 355 360 365
 Ala Asp Asp Leu His Gln Ala Val Leu His Ala Leu Glu Pro Trp Leu
 370 375 380
 His Glu Leu Ala Thr Pro Val Thr Lys Gln Asp Thr Ser Gln Leu Ala
 385 390 395 400
 Ser Leu Thr Ile Lys Lys Ile Leu Cys Phe Asn Glu Glu Ala Cys Thr
 405 410 415
 Lys Glu Leu Leu Ala Ile Glu Lys Lys Gln Ala Ala Ile Gln Lys Asp
 420 425 430
 Leu Gly Arg Ile Lys Glu Val Thr Val Lys Tyr Leu Lys Gly Leu Leu
 435 440 445
 Glu Arg His Gly His Leu Gly Glu Arg Lys Thr Gln Ile Thr Asn Phe
 450 455 460
 Lys Thr Ala Lys Thr Ser Ile Leu Lys Gln Gln Thr Leu Ile
 465 470 475

<210> 390

<211> 257

<212> PRT

<213> Chlamydia pneumoniae

<400> 390

Met Ala Phe Tyr Ser Pro Ser Thr Ile Ser Lys Tyr Phe Ile Tyr Ser
 5 10 15

Gly	Ala	Gly	Asn	Arg	Phe	Leu	Leu	Gly	Glu	Thr	Leu	Pro	Glu	Val	Glu
			20					25					30		
Asp	Val	Arg	Phe	Leu	Cys	Gln	Glu	Thr	Arg	Val	Asp	Gly	Phe	Leu	Tyr
		35					40					45			
Leu	Lys	Pro	Ser	Ser	Cys	Ala	Asp	Ala	Gln	Leu	Ile	Ile	Phe	Asn	Ser
	50					55					60				
Asp	Gly	Ser	Arg	Pro	Thr	Met	Cys	Gly	Asn	Gly	Leu	Arg	Cys	Ala	Ile
65					70					75					80
Ala	His	Leu	Ala	Ser	Gln	Lys	Gly	Lys	Ser	Asp	Ile	Ser	Val	Ser	Thr
				85					90					95	
Asp	Ser	Gly	Leu	Tyr	Ser	Gly	Tyr	Phe	Tyr	Ser	Trp	Asp	Arg	Val	Leu
		100						105					110		
Val	Asp	Met	Thr	Leu	Ala	Asp	Trp	Arg	Ala	Ser	Val	His	Arg	Leu	Glu
		115					120					125			
Ser	Arg	Pro	Asp	Pro	Leu	Pro	Lys	Glu	Val	Val	Cys	Ile	His	Thr	Gly
		130				135					140				
Val	Pro	His	Ala	Val	Val	Ile	Leu	Pro	Glu	Ile	Ser	Thr	Leu	Asp	Leu
145				150						155					160
Ser	Ile	Leu	Gly	Pro	Phe	Leu	Arg	Tyr	His	Gln	Thr	Phe	Ser	Pro	Asp
				165					170					175	
Gly	Val	Asn	Val	Asn	Phe	Val	Gln	Ile	Leu	Gly	His	Cys	Gln	Leu	Arg
		180						185					190		
Val	Arg	Thr	Tyr	Glu	Arg	Gly	Val	Glu	Gly	Glu	Thr	Ala	Ala	Cys	Gly
		195					200					205			
Thr	Gly	Ala	Leu	Ala	Ser	Ala	Leu	Val	Val	Ser	Asn	Ser	Tyr	Gly	Trp
210					215						220				
Lys	Glu	Ser	Ile	Gln	Ile	His	Thr	Trp	Gly	Gly	Glu	Leu	Met	Thr	Val
225				230						235					240
Ser	Gln	Asn	Arg	Gly	Arg	Val	Tyr	Leu	Gln	Gly	Ser	Val	Thr	Arg	Asp
			245						250					255	

Leu

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<210> 391
<211> 191
<212> PRT
<213> Chlamydia pneumoniae
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<400> 391
Met Ala Asp Gly Glu Val His Lys Leu Arg Asp Ile Ile Glu Lys Glu
          5              10              15
Leu Leu Glu Ala Arg Arg Val Phe Phe Ser Glu Pro Val Thr Glu Lys
          20              25              30

```

Ser Ala Ser Asp Ala Ile Lys Lys Leu Trp Tyr Leu Glu Leu Lys Asp
 35 40 45
 Pro Gly Lys Pro Ile Val Phe Val Ile Asn Ser Pro Gly Gly Ser Val
 50 55 60
 Asp Ala Gly Phe Ala Val Trp Asp Gln Ile Lys Met Leu Thr Ser Pro
 65 70 75 80
 Val Thr Thr Val Val Thr Gly Leu Ala Ala Ser Met Gly Ser Val Leu
 85 90 95
 Ser Leu Cys Ala Ala Pro Gly Arg Arg Phe Ala Thr Pro His Ser Arg
 100 105 110
 Ile Met Ile His Gln Pro Ser Ile Gly Gly Pro Ile Thr Gly Gln Ala
 115 120 125
 Thr Asp Leu Asp Ile His Ala Arg Glu Ile Leu Lys Thr Lys Ala Arg
 130 135 140
 Ile Ile Asp Val Tyr Val Glu Ala Thr Asn Gln Pro Arg Asp Ile Ile
 145 150 155 160
 Glu Lys Ala Ile Asp Arg Asp Met Trp Met Thr Ala Asn Glu Ala Lys
 165 170 175
 Asp Phe Gly Leu Leu Asp Gly Ile Leu Ser Phe Asn Asp Leu
 180 185 190

<210> 392

<211> 232

<212> PRT

<213> Chlamydia pneumoniae

<400> 392

Met Thr Lys His Gly Lys Arg Ile Arg Gly Ile Leu Lys Asn Tyr Asp
 5 10 15
 Phe Ser Lys Ser Tyr Ser Leu Arg Glu Ala Ile Asp Ile Leu Lys Gln
 20 25 30
 Cys Pro Pro Val Arg Phe Asp Gln Thr Val Asp Val Ser Ile Lys Leu
 35 40 45
 Gly Ile Asp Pro Lys Lys Ser Asp Gln Gln Ile Arg Gly Ala Val Phe
 50 55 60
 Leu Pro Asn Gly Thr Gly Lys Thr Leu Arg Ile Leu Val Phe Ala Ser
 65 70 75 80
 Gly Asn Lys Val Lys Glu Ala Val Glu Ala Gly Ala Asp Phe Met Gly
 85 90 95
 Ser Asp Asp Leu Val Glu Lys Ile Lys Ser Gly Trp Leu Glu Phe Asp
 100 105 110
 Val Ala Val Ala Thr Pro Asp Met Met Arg Glu Val Gly Lys Leu Gly
 115 120 125

Lys Val Leu Gly Pro Arg Asn Leu Met Pro Thr Pro Lys Thr Gly Thr
 130 135 140
 Val Thr Thr Asp Val Ala Lys Ala Ile Ser Glu Leu Arg Lys Gly Lys
 145 150 155 160
 Ile Glu Phe Lys Ala Asp Arg Ala Gly Val Cys Asn Val Gly Val Gly
 165 170 175
 Lys Leu Ser Phe Glu Ser Ser Gln Ile Lys Glu Asn Ile Glu Ala Leu
 180 185 190
 Ser Ser Ala Leu Ile Lys Ala Lys Pro Pro Ala Ala Lys Gly Lys Tyr
 195 200 205
 Leu Val Ser Phe Thr Ile Ser Ser Thr Met Gly Pro Gly Ile Ser Ile
 210 215 220
 Asp Thr Arg Glu Leu Met Ala Ser
 225 230

<210> 393

<211> 122

<212> PRT

<213> Chlamydia pneumoniae

<400> 393

Met Pro Arg Ile Ile Gly Ile Asp Ile Pro Ala Lys Lys Lys Leu Lys
 5 10 15
 Ile Ser Leu Thr Tyr Ile Tyr Gly Ile Gly Ser Ala Arg Ser Asp Glu
 20 25 30
 Ile Ile Lys Lys Leu Lys Leu Asp Pro Glu Ala Arg Ala Ser Glu Leu
 35 40 45
 Thr Glu Glu Glu Val Gly Arg Leu Asn Ser Leu Leu Gln Ser Glu Tyr
 50 55 60
 Thr Val Glu Gly Asp Leu Arg Arg Arg Val Gln Ser Asp Ile Lys Arg
 65 70 75 80
 Leu Ile Ala Ile His Ser Tyr Arg Gly Gln Arg His Arg Leu Ser Leu
 85 90 95
 Pro Val Arg Gly Gln Arg Thr Lys Thr Asn Ser Arg Thr Arg Lys Gly
 100 105 110
 Lys Arg Lys Thr Val Ala Gly Lys Lys Lys
 115 120

<210> 394

<211> 1723

<212> PRT

<213> Chlamydia pneumoniae

<400> 394

Met Lys Trp Leu Pro Ala Thr Ala Val Phe Ala Ala Val Leu Pro Ala

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		20						25					30		
Thr	Gly	Ser	Gly	Asp	Pro	Thr	Ser	Asp	Ala	Ala	Leu	Thr	Gly	Phe	Thr
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Gln	Ser	Ser	Thr	Glu	Thr	Asp	Gly	Thr	Thr	Tyr	Thr	Ile	Val	Gly	Asp
		50					55					60			
Ile	Thr	Phe	Ser	Thr	Phe	Thr	Asn	Ile	Pro	Val	Pro	Val	Val	Thr	Pro
		65				70					75				80
Asp	Ala	Asn	Asp	Ser	Ser	Ser	Asn	Ser	Ser	Lys	Gly	Gly	Ser	Ser	Ser
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Ser	Gly	Ala	Thr	Ser	Leu	Ile	Arg	Ser	Ser	Asn	Leu	His	Ser	Asp	Phe
			100					105					110		
Asp	Phe	Thr	Lys	Asp	Ser	Val	Leu	Asp	Leu	Tyr	His	Leu	Phe	Phe	Pro
		115					120					125			
Ser	Ala	Ser	Asn	Thr	Leu	Asn	Pro	Ala	Leu	Leu	Ser	Ser	Ser	Ser	Ser
		130				135					140				
Gly	Gly	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Gly	Ser	Ala	Ser	
		145				150			155				160		
Ala	Val	Val	Ala	Ala	Asp	Pro	Lys	Gly	Gly	Ala	Ala	Phe	Tyr	Ser	Asn
			165					170					175		
Glu	Ala	Asn	Gly	Thr	Leu	Thr	Phe	Thr	Thr	Asp	Ser	Gly	Asn	Pro	Gly
		180					185						190		
Ser	Leu	Thr	Leu	Gln	Asn	Leu	Lys	Met	Thr	Gly	Asp	Gly	Ala	Ala	Ile
		195				200					205				
Tyr	Ser	Lys	Gly	Pro	Leu	Val	Phe	Thr	Gly	Leu	Lys	Asn	Leu	Thr	Phe
		210				215					220				
Thr	Gly	Asn	Glu	Ser	Gln	Lys	Ser	Gly	Gly	Ala	Ala	Tyr	Thr	Glu	Gly
		225				230			235					240	
Ala	Leu	Thr	Thr	Gln	Ala	Ile	Val	Glu	Ala	Val	Thr	Phe	Thr	Gly	Asn
			245					250						255	
Thr	Ser	Ala	Gly	Gln	Gly	Gly	Ala	Ile	Tyr	Val	Lys	Glu	Ala	Thr	Leu
		260					265						270		
Phe	Asn	Ala	Leu	Asp	Ser	Leu	Lys	Phe	Glu	Lys	Asn	Thr	Ser	Gly	Gln
		275					280					285			
Ala	Gly	Gly	Gly	Ile	Tyr	Thr	Glu	Ser	Thr	Leu	Thr	Ile	Ser	Asn	Ile
		290				295					300				
Thr	Lys	Ser	Ile	Glu	Phe	Ile	Ser	Asn	Lys	Ala	Ser	Val	Pro	Ala	Pro
		305				310			315					320	
Ala	Pro	Glu	Pro	Thr	Ser	Pro	Ala	Pro	Ser	Ser	Leu	Ile	Asn	Ser	Thr
			325					330						335	

Thr Ile Asp Thr Ser Thr Leu Gln Thr Arg Ala Ala Ser Ala Thr Pro
 340 345 350
 Ala Val Ala Pro Val Ala Ala Val Thr Pro Thr Pro Ile Ser Thr Gln
 355 360 365
 Glu Thr Ala Gly Asn Gly Gly Ala Ile Tyr Ala Lys Gln Gly Ile Ser
 370 375 380
 Ile Ser Thr Phe Lys Asp Leu Thr Phe Lys Ser Asn Ser Ala Ser Val
 385 390 395 400
 Asp Ala Thr Leu Thr Val Asp Ser Ser Thr Ile Gly Glu Ser Gly Gly
 405 410 415
 Ala Ile Phe Ala Ala Asp Ser Ile Gln Ile Gln Gln Cys Thr Gly Thr
 420 425 430
 Thr Leu Phe Ser Gly Asn Thr Ala Asn Lys Ser Gly Gly Ile Tyr
 435 440 445
 Ala Val Gly Gln Val Thr Leu Glu Asp Ile Ala Asn Leu Lys Met Thr
 450 455 460
 Asn Asn Thr Cys Lys Gly Glu Gly Gly Ala Ile Tyr Thr Lys Lys Ala
 465 470 475 480
 Leu Thr Ile Asn Asn Gly Ala Ile Leu Thr Thr Phe Ser Gly Asn Thr
 485 490 495
 Ser Thr Asp Asn Gly Gly Ala Ile Phe Ala Val Gly Gly Ile Thr Leu
 500 505 510
 Ser Asp Leu Val Glu Val Arg Phe Ser Lys Asn Lys Thr Gly Asn Tyr
 515 520 525
 Ser Ala Pro Ile Thr Lys Ala Ala Ser Asn Thr Ala Pro Val Val Ser
 530 535 540
 Ser Ser Thr Thr Ala Ala Ser Pro Ala Val Pro Ala Ala Ala Ala
 545 550 555 560
 Pro Val Thr Asn Ala Ala Lys Gly Gly Ala Leu Tyr Ser Thr Glu Gly
 565 570 575
 Leu Thr Val Ser Gly Ile Thr Ser Ile Leu Ser Phe Glu Asn Asn Glu
 580 585 590
 Cys Gln Asn Gln Gly Gly Gly Ala Tyr Val Thr Lys Thr Phe Gln Cys
 595 600 605
 Ser Asp Ser His Arg Leu Gln Phe Thr Ser Asn Lys Ala Ala Asp Glu
 610 615 620
 Gly Gly Gly Leu Tyr Cys Gly Asp Asp Val Thr Leu Thr Asn Leu Thr
 625 630 635 640
 Gly Lys Thr Leu Phe Gln Glu Asn Ser Ser Glu Lys His Gly Gly Gly
 645 650 655

Leu Ser Leu Ala Ser Gly Lys Ser Leu Thr Met Thr Ser Leu Glu Ser
 660 665 670
 Phe Cys Leu Asn Ala Asn Thr Ala Lys Glu Asn Gly Gly Glu Ala Asn
 675 680 685
 Val Pro Glu Asn Ile Val Leu Thr Phe Thr Tyr Thr Pro Thr Pro Asn
 690 695 700
 Glu Pro Ala Pro Val Gln Gln Pro Val Tyr Gly Glu Ala Leu Val Thr
 705 710 715 720
 Gly Asn Thr Ala Thr Lys Ser Gly Gly Gly Ile Tyr Thr Lys Asn Ala
 725 730 735
 Ala Phe Ser Asn Leu Ser Ser Val Thr Phe Asp Gln Asn Thr Ser Ser
 740 745 750
 Glu Asn Gly Gly Ala Leu Leu Thr Gln Lys Ala Ala Asp Lys Thr Asp
 755 760 765
 Cys Ser Phe Thr Tyr Ile Thr Asn Val Asn Ile Thr Asn Asn Thr Ala
 770 775 780
 Thr Gly Asn Gly Gly Gly Ile Ala Gly Gly Lys Ala His Phe Asp Arg
 785 790 795 800
 Ile Asp Asn Leu Thr Val Gln Ser Asn Gln Ala Lys Lys Gly Gly Gly
 805 810 815
 Val Tyr Leu Glu Asp Ala Leu Ile Leu Glu Lys Val Ile Thr Gly Ser
 820 825 830
 Val Ser Gln Asn Thr Ala Thr Glu Ser Gly Gly Gly Ile Tyr Ala Lys
 835 840 845
 Asp Ile Gln Leu Gln Ala Leu Pro Gly Ser Phe Thr Ile Thr Asp Asn
 850 855 860
 Lys Val Glu Thr Ser Leu Thr Thr Ser Thr Asn Leu Tyr Gly Gly Gly
 865 870 875 880
 Ile Tyr Ser Ser Gly Ala Val Thr Leu Thr Asn Ile Ser Gly Thr Phe
 885 890 895
 Gly Ile Thr Gly Asn Ser Val Ile Asn Thr Ala Thr Ser Gln Asp Ala
 900 905 910
 Asp Ile Gln Gly Gly Gly Ile Tyr Ala Thr Thr Ser Leu Ser Ile Asn
 915 920 925
 Gln Cys Asn Thr Pro Ile Leu Phe Ser Asn Asn Ser Ala Ala Thr Lys
 930 935 940
 Lys Thr Ser Thr Thr Lys Gln Ile Ala Gly Gly Ala Ile Phe Ser Ala
 945 950 955 960
 Ala Val Thr Ile Glu Asn Asn Ser Gln Pro Ile Ile Phe Leu Asn Asn
 965 970 975
 Ser Ala Lys Ser Glu Ala Thr Thr Ala Ala Thr Ala Gly Asn Lys Asp

980	985	990
Ser Cys Gly Gly Ala Ile Ala Ala Asn Ser Val Thr Leu Thr Asn Asn 995 1000 1005		
Pro Glu Ile Thr Phe Lys Gly Asn Tyr Ala Glu Thr Gly Gly Ala Ile 1010 1015 1020		
Gly Cys Ile Asp Leu Thr Asn Gly Ser Pro Pro Arg Lys Val Ser Ile 1025 1030 1035 1040		
Ala Asp Asn Gly Ser Val Leu Phe Gln Asp Asn Ser Ala Leu Asn Arg 1045 1050 1055		
Gly Gly Ala Ile Tyr Gly Glu Thr Ile Asp Ile Ser Arg Thr Gly Ala 1060 1065 1070		
Thr Phe Ile Gly Asn Ser Ser Lys His Asp Gly Ser Ala Ile Cys Cys 1075 1080 1085		
Ser Thr Ala Leu Thr Leu Ala Pro Asn Ser Gln Leu Ile Phe Glu Asn 1090 1095 1100		
Asn Lys Val Thr Glu Thr Thr Ala Thr Thr Lys Ala Ser Ile Asn Asn 1105 1110 1115 1120		
Leu Gly Ala Ala Ile Tyr Gly Asn Asn Glu Thr Ser Asp Val Thr Ile 1125 1130 1135		
Ser Leu Ser Ala Glu Asn Gly Ser Ile Phe Phe Lys Asn Asn Leu Cys 1140 1145 1150		
Thr Ala Thr Asn Lys Tyr Cys Ser Ile Ala Gly Asn Val Lys Phe Thr 1155 1160 1165		
Ala Ile Glu Ala Ser Ala Gly Lys Ala Ile Ser Phe Tyr Asp Ala Val 1170 1175 1180		
Asn Val Ser Thr Lys Glu Thr Asn Ala Gln Glu Leu Lys Leu Asn Glu 1185 1190 1195 1200		
Lys Ala Thr Ser Thr Gly Thr Ile Leu Phe Ser Gly Glu Leu His Glu 1205 1210 1215		
Asn Lys Ser Tyr Ile Pro Gln Lys Val Thr Phe Ala His Gly Asn Leu 1220 1225 1230		
Ile Leu Gly Lys Asn Ala Glu Leu Ser Val Val Ser Phe Thr Gln Ser 1235 1240 1245		
Pro Gly Thr Thr Ile Thr Met Gly Pro Gly Ser Val Leu Ser Asn His 1250 1255 1260		
Ser Lys Glu Ala Gly Gly Ile Ala Ile Asn Asn Val Ile Ile Asp Phe 1265 1270 1275 1280		
Ser Glu Ile Val Pro Thr Lys Asp Asn Ala Thr Val Ala Pro Pro Thr 1285 1290 1295		
Leu Lys Leu Val Ser Arg Thr Asn Ala Asp Ser Lys Asp Lys Ile Asp 1300 1305 1310		

Ile Thr Gly Thr Val Thr Leu Leu Asp Pro Asn Gly Asn Leu Tyr Gln
 1315 1320 1325
 Asn Ser Tyr Leu Gly Glu Asp Arg Asp Ile Thr Leu Phe Asn Ile Asp
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 Asn Ser Ala Ser Gly Ala Val Thr Ala Thr Asn Val Thr Leu Gln Gly
 1345 1350 1355 1360
 Asn Leu Gly Ala Lys Lys Gly Tyr Leu Gly Thr Trp Asn Leu Asp Pro
 1365 1370 1375
 Asn Ser Ser Gly Ser Lys Ile Ile Leu Lys Trp Thr Phe Asp Lys Tyr
 1380 1385 1390
 Leu Arg Trp Pro Tyr Ile Pro Arg Asp Asn His Phe Tyr Ile Asn Ser
 1395 1400 1405
 Ile Trp Gly Ala Gln Asn Ser Leu Val Thr Val Lys Gln Gly Ile Leu
 1410 1415 1420
 Gly Asn Met Leu Asn Asn Ala Arg Phe Glu Asp Pro Ala Phe Asn Asn
 1425 1430 1435 1440
 Phe Trp Ala Ser Ala Ile Gly Ser Phe Leu Arg Lys Glu Val Ser Arg
 1445 1450 1455
 Asn Ser Asp Ser Phe Thr Tyr His Gly Arg Gly Tyr Thr Ala Ala Val
 1460 1465 1470
 Asp Ala Lys Pro Arg Gln Glu Phe Ile Leu Gly Ala Ala Phe Ser Gln
 1475 1480 1485
 Val Phe Gly His Ala Glu Ser Glu Tyr His Leu Asp Asn Tyr Lys His
 1490 1495 1500
 Lys Gly Ser Gly His Ser Thr Gln Ala Ser Leu Tyr Ala Gly Asn Ile
 1505 1510 1515 1520
 Phe Tyr Phe Pro Ala Ile Arg Ser Arg Pro Ile Leu Phe Gln Gly Val
 1525 1530 1535
 Ala Thr Tyr Gly Tyr Met Gln His Asp Thr Thr Thr Tyr Tyr Pro Ser
 1540 1545 1550
 Ile Glu Glu Lys Asn Met Ala Asn Trp Asp Ser Ile Ala Trp Leu Phe
 1555 1560 1565
 Asp Leu Arg Phe Ser Val Asp Leu Lys Glu Pro Gln Pro His Ser Thr
 1570 1575 1580
 Ala Arg Leu Thr Phe Tyr Thr Glu Ala Glu Tyr Thr Arg Ile Arg Gln
 1585 1590 1595 1600
 Glu Lys Phe Thr Glu Leu Asp Tyr Asp Pro Arg Ser Phe Ser Ala Cys
 1605 1610 1615
 Ser Tyr Gly Asn Leu Ala Ile Pro Thr Gly Phe Ser Val Asp Gly Ala
 1620 1625 1630

Leu Ala Trp Arg Glu Ile Ile Leu Tyr Asn Lys Val Ser Ala Ala Tyr
 1635 1640 1645
 Leu Pro Val Ile Leu Arg Asn Asn Pro Lys Ala Thr Tyr Glu Val Leu
 1650 1655 1660
 Ser Thr Lys Glu Lys Gly Asn Val Val Asn Val Leu Pro Thr Arg Asn
 1665 1670 1675 1680
 Ala Ala Arg Ala Glu Val Ser Ser Gln Ile Tyr Leu Gly Ser Tyr Trp
 1685 1690 1695
 Thr Leu Tyr Gly Thr Tyr Thr Ile Asp Ala Ser Met Asn Thr Leu Val
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 Gln Met Ala Asn Gly Gly Ile Arg Phe Val Phe
 1715 1720

<210> 395

<211> 1723

<212> PRT

<213> Chlamydia pneumoniae

<400> 395

Met Lys Trp Leu Pro Ala Thr Ala Val Phe Ala Ala Val Leu Pro Ala
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 Thr Gly Ser Gly Asp Pro Thr Ser Asp Ala Ala Leu Thr Gly Phe Thr
 35 40 45
 Gln Ser Ser Thr Glu Thr Asp Gly Thr Thr Tyr Thr Ile Val Gly Asp
 50 55 60
 Ile Thr Phe Ser Thr Phe Thr Asn Ile Pro Val Pro Val Val Thr Pro
 65 70 75 80
 Asp Ala Asn Asp Ser Ser Ser Asn Ser Ser Lys Gly Gly Ser Ser Ser
 85 90 95
 Ser Gly Ala Thr Ser Leu Ile Arg Ser Ser Asn Leu His Ser Asp Phe
 100 105 110
 Asp Phe Thr Lys Asp Ser Val Leu Asp Leu Tyr His Leu Phe Phe Pro
 115 120 125
 Ser Ala Ser Asn Thr Leu Asn Pro Ala Leu Leu Ser Ser Ser Ser
 130 135 140
 Gly Gly Ser Ser Ser Ser Ser Ser Ser Ser Gly Ser Ala Ser
 145 150 155 160
 Ala Val Val Ala Ala Asp Pro Lys Gly Gly Ala Ala Phe Tyr Ser Asn
 165 170 175
 Glu Ala Asn Gly Thr Leu Thr Phe Thr Thr Asp Ser Gly Asn Pro Gly
 180 185 190
 Ser Leu Thr Leu Gln Asn Leu Lys Met Thr Gly Asp Gly Ala Ala Ile
 195 200 205
 Tyr Ser Lys Gly Pro Leu Val Phe Thr Gly Leu Lys Asn Leu Thr Phe
 210 215 220
 Thr Gly Asn Glu Ser Gln Lys Ser Gly Gly Ala Ala Tyr Thr Glu Gly
 225 230 235 240
 Ala Leu Thr Thr Gln Ala Ile Val Glu Ala Val Thr Phe Thr Gly Asn
 245 250 255
 Thr Ser Ala Gly Gln Gly Gly Ala Ile Tyr Val Lys Glu Ala Thr Leu
 260 265 270
 Phe Asn Ala Leu Asp Ser Leu Lys Phe Glu Lys Asn Thr Ser Gly Gln
 275 280 285

Ala Gly Gly Gly Ile Tyr Thr Glu Ser Thr Leu Thr Ile Ser Asn Ile
 290 295 300
 Thr Lys Ser Ile Glu Phe Ile Ser Asn Lys Ala Ser Val Pro Ala Pro
 305 310 315 320
 Ala Pro Glu Pro Thr Ser Pro Ala Pro Ser Ser Leu Ile Asn Ser Thr
 325 330 335
 Thr Ile Asp Thr Ser Thr Leu Gln Thr Arg Ala Ala Ser Ala Thr Pro
 340 345 350
 Ala Val Ala Pro Val Ala Ala Val Thr Pro Thr Pro Ile Ser Thr Gln
 355 360 365
 Glu Thr Ala Gly Asn Gly Gly Ala Ile Tyr Ala Lys Gln Gly Ile Ser
 370 375 380
 Ile Ser Thr Phe Lys Asp Leu Thr Phe Lys Ser Asn Ser Ala Ser Val
 385 390 395 400
 Asp Ala Thr Leu Thr Val Asp Ser Ser Thr Ile Gly Glu Ser Gly Gly
 405 410 415
 Ala Ile Phe Ala Ala Asp Ser Ile Gln Ile Gln Gln Cys Thr Gly Thr
 420 425 430
 Thr Leu Phe Ser Gly Asn Thr Ala Asn Lys Ser Gly Gly Gly Ile Tyr
 435 440 445
 Ala Val Gly Gln Val Thr Leu Glu Asp Ile Ala Asn Leu Lys Met Thr
 450 455 460
 Asn Asn Thr Cys Lys Gly Glu Gly Ala Ile Tyr Thr Lys Lys Ala
 465 470 475 480
 Leu Thr Ile Asn Asn Gly Ala Ile Leu Thr Thr Phe Ser Gly Asn Thr
 485 490 495
 Ser Thr Asp Asn Gly Gly Ala Ile Phe Ala Val Gly Gly Ile Thr Leu
 500 505 510
 Ser Asp Leu Val Glu Val Arg Phe Ser Lys Asn Lys Thr Gly Asn Tyr
 515 520 525
 Ser Ala Pro Ile Thr Lys Ala Ala Ser Asn Thr Ala Pro Val Val Ser
 530 535 540
 Ser Ser Thr Thr Ala Ala Ser Pro Ala Val Pro Ala Ala Ala Ala
 545 550 555 560
 Pro Val Thr Asn Ala Ala Lys Gly Gly Ala Leu Tyr Ser Thr Glu Gly
 565 570 575
 Leu Thr Val Ser Gly Ile Thr Ser Ile Leu Ser Phe Glu Asn Asn Glu
 580 585 590
 Cys Gln Asn Gln Gly Gly Gly Ala Tyr Val Thr Lys Thr Phe Gln Cys
 595 600 605
 Ser Asp Ser His Arg Leu Gln Phe Thr Ser Asn Lys Ala Ala Asp Glu
 610 615 620
 Gly Gly Gly Leu Tyr Cys Gly Asp Asp Val Thr Leu Thr Asn Leu Thr
 625 630 635 640
 Gly Lys Thr Leu Phe Gln Glu Asn Ser Ser Glu Lys His Gly Gly Gly
 645 650 655
 Leu Ser Leu Ala Ser Gly Lys Ser Leu Thr Met Thr Ser Leu Glu Ser
 660 665 670
 Phe Cys Leu Asn Ala Asn Thr Ala Lys Glu Asn Gly Gly Gly Ala Asn
 675 680 685
 Val Pro Glu Asn Ile Val Leu Thr Phe Thr Tyr Thr Pro Thr Pro Asn
 690 695 700
 Glu Pro Ala Pro Val Gln Gln Pro Val Tyr Gly Glu Ala Leu Val Thr
 705 710 715 720
 Gly Asn Thr Ala Thr Lys Ser Gly Gly Gly Ile Tyr Thr Lys Asn Ala
 725 730 735
 Ala Phe Ser Asn Leu Ser Ser Val Thr Phe Asp Gln Asn Thr Ser Ser
 740 745 750
 Glu Asn Gly Gly Ala Leu Leu Thr Gln Lys Ala Ala Asp Lys Thr Asp
 755 760 765
 Cys Ser Phe Thr Tyr Ile Thr Asn Val Asn Ile Thr Asn Asn Thr Ala

770	775	780
Thr Gly Asn Gly Gly Gly	Ile Ala Gly Gly Lys	Ala His Phe Asp Arg
785	790	795
Ile Asp Asn Leu Thr Val	Gln Ser Asn Gln Ala Lys	Lys Gly Gly Gly
805	810	815
Val Tyr Leu Glu Asp Ala	Leu Ile Leu Glu Lys	Val Ile Thr Gly Ser
820	825	830
Val Ser Gln Asn Thr Ala	Thr Glu Ser Gly Gly	Ile Tyr Ala Lys
835	840	845
Asp Ile Gln Leu Gln Ala	Leu Pro Gly Ser Phe	Thr Ile Thr Asp Asn
850	855	860
Lys Val Glu Thr Ser Leu	Thr Thr Ser Thr Asn	Leu Tyr Gly Gly
865	870	875
Ile Tyr Ser Ser Gly Ala	Val Thr Leu Thr Asn	Ile Ser Gly Thr Phe
885	890	895
Gly Ile Thr Gly Asn Ser	Val Ile Asn Thr Ala	Thr Ser Gln Asp Ala
900	905	910
Asp Ile Gln Gly Gly Gly	Ile Tyr Ala Thr Thr	Ser Leu Ser Ile Asn
915	920	925
Gln Cys Asn Thr Pro Ile	Leu Phe Ser Asn Asn	Ser Ala Ala Thr Lys
930	935	940
Lys Thr Ser Thr Thr Lys	Gln Ile Ala Gly Gly	Ala Ile Phe Ser Ala
945	950	955
Ala Val Thr Ile Glu Asn	Asn Ser Gln Pro Ile	Ile Phe Leu Asn Asn
965	970	975
Ser Ala Lys Ser Glu Ala	Thr Thr Ala Ala Thr	Ala Gly Asn Lys Asp
980	985	990
Ser Cys Gly Gly Ala Ile	Ala Ala Asn Ser Val	Thr Leu Thr Asn Asn
995	1000	1005
Pro Glu Ile Thr Phe Lys	Gly Asn Tyr Ala Glu	Thr Gly Gly Ala Ile
1010	1015	1020
Gly Cys Ile Asp Leu Thr	Asn Gly Ser Pro Pro	Arg Lys Val Ser Ile
1025	1030	1035
Ala Asp Asn Gly Ser Val	Leu Phe Gln Asp Asn	Ser Ala Leu Asn Arg
1045	1050	1055
Gly Gly Ala Ile Tyr Gly	Glu Thr Ile Asp Ile	Ser Arg Thr Gly Ala
1060	1065	1070
Thr Phe Ile Gly Asn Ser	Ser Lys His Asp Gly	Ser Ala Ile Cys Cys
1075	1080	1085
Ser Thr Ala Leu Thr Leu	Ala Pro Asn Ser Gln	Leu Ile Phe Glu Asn
1090	1095	1100
Asn Lys Val Thr Glu Thr	Thr Thr Lys Ala Ser	Ile Asn Asn
1105	1110	1115
Leu Gly Ala Ala Ile Tyr	Gly Asn Asn Glu Thr	Ser Asp Ile Thr Ile
1125	1130	1135
Ser Leu Ser Ala Glu Asn	Gly Ser Ile Phe Phe	Lys Asn Asn Leu Cys
1140	1145	1150
Thr Ala Thr Asn Lys Tyr	Cys Ser Ile Ala Gly	Asn Val Lys Phe Thr
1155	1160	1165
Ala Ile Glu Ala Ser Ala	Gly Lys Ala Ile Ser	Phe Tyr Asp Ala Val
1170	1175	1180
Asn Val Ser Thr Lys Glu	Thr Asn Ala Gln Glu	Leu Lys Leu Asn Glu
1185	1190	1195
Lys Ala Thr Ser Thr Gly	Thr Ile Leu Phe Ser	Gly Glu Leu His Glu
1205	1210	1215
Asn Lys Ser Tyr Ile Pro	Gln Lys Val Thr Phe	Ala His Gly Asn Leu
1220	1225	1230
Ile Leu Gly Lys Asn Ala	Glu Leu Ser Val Val	Ser Phe Thr Gln Ser
1235	1240	1245
Pro Gly Thr Thr Ile Thr	Met Gly Pro Gly Ser	Val Leu Ser Asn His
1250	1255	1260

Ser Lys Glu Ala Gly Gly Ile Ala Ile Asn Asn Val Ile Ile Asp Phe 1265 1270 1275 1280
 Ser Glu Ile Val Pro Thr Lys Asp Asn Ala Thr Val Ala Pro Pro Thr 1285 1290 1295
 Leu Lys Leu Val Ser Arg Thr Asn Ala Asp Ser Lys Asp Lys Ile Asp 1300 1305 1310
 Ile Thr Gly Thr Val Thr Leu Leu Asp Pro Asn Gly Asn Leu Tyr Gln 1315 1320 1325
 Asn Ser Tyr Leu Gly Glu Asp Arg Asp Ile Thr Leu Phe Asn Ile Asp 1330 1335 1340
 Asn Ser Ala Ser Gly Ala Val Thr Ala Thr Asn Val Thr Leu Gln Gly 1345 1350 1355 1360
 Asn Leu Gly Ala Lys Lys Gly Tyr Leu Gly Thr Trp Asn Leu Asp Pro 1365 1370 1375
 Asn Ser Ser Gly Ser Lys Ile Ile Leu Lys Trp Thr Phe Asp Lys Tyr 1380 1385 1390
 Leu Arg Trp Pro Tyr Ile Pro Arg Asp Asn His Phe Tyr Ile Asn Ser 1395 1400 1405
 Ile Trp Gly Ala Gln Asn Ser Leu Val Thr Val Lys Gln Gly Ile Leu 1410 1415 1420
 Gly Asn Met Leu Asn Asn Ala Arg Phe Glu Asp Pro Ala Phe Asn Asn 1425 1430 1435 1440
 Phe Trp Ala Ser Ala Ile Gly Ser Phe Leu Arg Lys Glu Val Ser Arg 1445 1450 1455
 Asn Ser Asp Ser Phe Thr Tyr His Gly Arg Gly Tyr Thr Ala Ala Val 1460 1465 1470
 Asp Ala Lys Pro Arg Gln Glu Phe Ile Leu Gly Ala Ala Phe Ser Gln 1475 1480 1485
 Val Phe Gly His Ala Glu Ser Glu Tyr His Leu Asp Asn Tyr Lys His 1490 1495 1500
 Lys Gly Ser Gly His Ser Thr Gln Ala Ser Leu Tyr Ala Gly Asn Ile 1505 1510 1515 1520
 Phe Tyr Phe Pro Ala Ile Arg Ser Arg Pro Ile Leu Phe Gln Gly Val 1525 1530 1535
 Ala Thr Tyr Gly Tyr Met Gln His Asp Thr Thr Tyr Tyr Pro Ser 1540 1545 1550
 Ile Glu Glu Lys Asn Met Ala Asn Trp Asp Ser Ile Ala Trp Leu Phe 1555 1560 1565
 Asp Leu Arg Phe Ser Val Asp Leu Lys Glu Pro Gln Pro His Ser Thr 1570 1575 1580
 Ala Arg Leu Thr Phe Tyr Thr Glu Ala Glu Tyr Thr Arg Ile Arg Gln 1585 1590 1595 1600
 Glu Lys Phe Thr Glu Leu Asp Tyr Asp Pro Arg Ser Phe Ser Ala Cys 1605 1610 1615
 Ser Tyr Gly Asn Leu Ala Ile Pro Thr Gly Phe Ser Val Asp Gly Ala 1620 1625 1630
 Leu Ala Trp Arg Glu Ile Ile Leu Tyr Asn Lys Val Ser Ala Ala Tyr 1635 1640 1645
 Leu Pro Val Ile Leu Arg Asn Asn Pro Lys Ala Thr Tyr Glu Val Leu 1650 1655 1660
 Ser Thr Lys Glu Lys Gly Asn Val Val Asn Val Leu Pro Thr Arg Asn 1665 1670 1675 1680
 Ala Ala Arg Ala Glu Val Ser Ser Gln Ile Tyr Leu Gly Ser Tyr Trp 1685 1690 1695
 Thr Leu Tyr Gly Thr Tyr Thr Ile Asp Ala Ser Met Asn Thr Leu Val 1700 1705 1710
 Gln Met Ala Asn Gly Gly Ile Arg Phe Val Phe 1715 1720

<211> 1252

<212> PRT

<213> Chlamydia pneumoniae

<400> 396

Met Leu Lys Cys Pro Glu Arg Val Ser Val Lys Lys Lys Glu Asp Ile
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Pro Asp Leu Pro Asn Leu Ile Glu Ile Gln Ile Lys Ser Tyr Lys Gln
20 25 30

Phe Leu Gln Ile Gly Lys Leu Ala Glu Glu Arg Glu Asn Ile Gly Leu
35 40 45

Glu Glu Val Phe Arg Glu Ile Phe Pro Ile Lys Ser Tyr Asn Glu Ala
50 55 60

Thr Val Leu Glu Tyr Leu Ser Tyr Asn Leu Gly Val Pro Lys Tyr Ser
65 70 75 80

Pro Glu Glu Cys Ile Arg Arg Gly Ile Thr Tyr Ser Val Thr Leu Lys
85 90 95

Val Arg Phe Arg Leu Thr Asp Glu Thr Gly Ile Lys Glu Glu Glu Val
100 105 110

Tyr Met Gly Thr Ile Pro Leu Met Thr Asp Lys Gly Thr Phe Ile Ile
115 120 125

Asn Gly Ala Glu Arg Val Val Val Ser Gln Val His Arg Ser Pro Gly
130 135 140

Ile Asn Phe Glu Gln Glu Lys His Ser Lys Gly Asn Ile Leu Phe Ser
145 150 155 160

Phe Arg Ile Ile Pro Tyr Arg Gly Ser Trp Leu Glu Ala Ile Phe Asp
165 170 175

Ile Asn Asp Leu Ile Tyr Ile His Ile Asp Arg Lys Lys Arg Arg Arg
180 185 190

Lys Ile Leu Ala Ile Thr Phe Ile Arg Ala Leu Gly Tyr Ser Ser Asp
195 200 205

Ala Asp Ile Ile Glu Glu Phe Phe Thr Ile Gly Glu Ser Ser Leu Arg
210 215 220

Ser Glu Lys Asp Phe Ala Leu Leu Val Gly Arg Ile Leu Ala Asp Asn
225 230 235 240

Ile Ile Asp Glu Ala Ser Ser Leu Val Tyr Gly Lys Ala Gly Glu Lys
245 250 255

Leu Ser Thr Ala Met Leu Lys Arg Met Leu Asp Ala Gly Ile Ala Ser
260 265 270

Val Lys Ile Ala Val Asp Ala Asp Glu Asn His Pro Ile Ile Lys Met
275 280 285

Leu Ala Lys Asp Pro Thr Asp Ser Tyr Glu Ala Ala Leu Lys Asp Phe
290 295 300

Tyr Arg Arg Leu Arg Pro Gly Glu Pro Ala Thr Leu Ala Asn Ala Arg
 305 310 315 320
 Ser Thr Ile Met Arg Leu Phe Phe Asp Pro Lys Arg Tyr Asn Leu Gly
 325 330 335
 Arg Val Gly Arg Tyr Lys Leu Asn Arg Lys Leu Gly Phe Ser Ile Asp
 340 345 350
 Asp Glu Ala Leu Ser Gln Val Thr Leu Arg Lys Glu Asp Val Ile Gly
 355 360 365
 Ala Leu Lys Tyr Leu Ile Arg Leu Lys Met Gly Asp Glu Lys Ala Cys
 370 375 380
 Val Asp Asp Ile Asp His Leu Ala Asn Arg Arg Val Arg Ser Val Gly
 385 390 395 400
 Glu Leu Ile Gln Asn Gln Cys Arg Ser Gly Leu Ala Arg Met Glu Lys
 405 410 415
 Ile Val Arg Glu Arg Met Asn Leu Phe Asp Phe Ser Ser Asp Thr Leu
 420 425 430
 Thr Pro Gly Lys Val Val Ser Ala Lys Gly Leu Ala Ser Val Leu Lys
 435 440 445
 Asp Phe Phe Gly Arg Ser Gln Leu Ser Gln Phe Met Asp Gln Thr Asn
 450 455 460
 Pro Val Ala Glu Leu Thr His Lys Arg Arg Leu Ser Ala Leu Gly Pro
 465 470 475 480
 Gly Gly Leu Asn Arg Glu Arg Ala Gly Phe Glu Val Arg Asp Val His
 485 490 495
 Ala Ser His Tyr Gly Arg Ile Cys Pro Ile Glu Thr Pro Glu Gly Pro
 500 505 510
 Asn Ile Gly Leu Ile Thr Ser Leu Ser Ser Phe Ala Lys Ile Asn Glu
 515 520 525
 Phe Gly Phe Ile Glu Thr Pro Tyr Arg Ile Val Arg Asp Gly Ile Val
 530 535 540
 Thr Asp Glu Ile Glu Tyr Met Thr Ala Asp Val Glu Glu Glu Cys Val
 545 550 555 560
 Ile Ala Gln Ala Ser Ala Ser Leu Asp Glu Tyr Asn Met Phe Thr Glu
 565 570 575
 Pro Val Cys Trp Val Arg Tyr Ala Gly Glu Ala Phe Glu Ala Asp Thr
 580 585 590
 Ser Thr Val Thr His Met Asp Val Ser Pro Lys Gln Leu Val Ser Ile
 595 600 605
 Val Thr Gly Leu Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala
 610 615 620

Leu Met Gly Ser Asn Met Gln Arg Gln Ala Val Pro Leu Leu Lys Thr
 625 630 635 640
 Glu Ala Pro Val Val Gly Thr Gly Leu Glu Cys Arg Ala Ala Lys Asp
 645 650 655
 Ser Gly Ala Ile Val Val Ala Glu Glu Asp Gly Val Val Asp Phe Val
 660 665 670
 Asp Gly Tyr Lys Val Val Val Ala Ala Lys His Asn Pro Thr Ile Lys
 675 680 685
 Arg Thr Tyr His Leu Lys Lys Phe Leu Arg Ser Asn Ser Gly Thr Cys
 690 695 700
 Ile Asn Gln Gln Pro Leu Cys Ala Val Gly Asp Val Ile Thr Lys Gly
 705 710 715 720
 Asp Val Ile Ala Asp Gly Pro Ala Thr Asp Arg Gly Glu Leu Ala Leu
 725 730 735
 Gly Lys Asn Val Leu Val Ala Phe Met Pro Trp Tyr Gly Tyr Asn Phe
 740 745 750
 Glu Asp Ala Ile Ile Ile Ser Glu Lys Leu Ile Arg Glu Asp Ala Tyr
 755 760 765
 Thr Ser Ile Tyr Ile Glu Glu Phe Glu Leu Thr Ala Arg Asp Thr Lys
 770 775 780
 Leu Gly Lys Glu Glu Ile Thr Arg Asp Ile Pro Asn Val Ser Asp Glu
 785 790 795 800
 Val Leu Ala Asn Leu Gly Glu Asp Gly Ile Ile Arg Ile Gly Ala Glu
 805 810 815
 Val Lys Pro Gly Asp Ile Leu Val Gly Lys Ile Thr Pro Lys Ser Glu
 820 825 830
 Thr Glu Leu Ala Pro Glu Glu Arg Leu Leu Arg Ala Ile Phe Gly Glu
 835 840 845
 Lys Ala Ala Asp Val Lys Asp Ala Ser Leu Thr Val Pro Pro Gly Thr
 850 855 860
 Glu Gly Val Val Met Asp Val Lys Val Phe Ser Arg Lys Asp Arg Leu
 865 870 875 880
 Ser Lys Ser Asp Asp Glu Leu Val Glu Glu Ala Val His Leu Lys Asp
 885 890 895
 Leu Gln Lys Gly Tyr Lys Asn Gln Val Ala Thr Leu Lys Thr Glu Tyr
 900 905 910
 Arg Glu Lys Leu Gly Ala Leu Leu Asn Glu Lys Ala Pro Ala Ala
 915 920 925
 Ile Ile His Arg Arg Thr Ala Glu Ile Val Val His Glu Gly Leu Leu
 930 935 940
 Phe Asp Gln Glu Thr Ile Glu Arg Ile Glu Gln Glu Asp Leu Val Asp

945 950 955 960
 Leu Leu Met Pro Asn Cys Glu Met Tyr Glu Val Leu Lys Gly Leu Leu
 965 970 975
 Ser Asp Tyr Glu Thr Ala Leu Gln Arg Leu Glu Ile Asn Tyr Lys Thr
 980 985 990
 Glu Val Glu His Ile Arg Glu Gly Asp Ala Asp Leu Asp His Gly Val
 995 1000 1005
 Ile Arg Gln Val Lys Val Tyr Val Ala Ser Lys Arg Lys Leu Gln Val
 1010 1015 1020
 Gly Asp Lys Met Ala Gly Arg His Gly Asn Lys Gly Val Val Ser Lys
 1025 1030 1035 1040
 Ile Val Pro Glu Ala Asp Met Pro Tyr Leu Ser Asn Gly Glu Thr Val
 1045 1050 1055
 Gln Met Ile Leu Asn Pro Leu Gly Val Pro Ser Arg Met Asn Leu Gly
 1060 1065 1070
 Gln Val Leu Glu Thr His Leu Gly Tyr Ala Ala Lys Thr Ala Gly Ile
 1075 1080 1085
 Tyr Val Lys Thr Pro Val Phe Glu Gly Phe Pro Glu Gln Arg Ile Trp
 1090 1095 1100
 Asp Met Met Ile Glu Gln Gly Leu Pro Glu Asp Gly Lys Ser Phe Leu
 1105 1110 1115 1120
 Tyr Asp Gly Lys Thr Gly Glu Arg Phe Asp Asn Lys Val Val Ile Gly
 1125 1130 1135
 Tyr Ile Tyr Met Leu Lys Leu Ser His Leu Ile Ala Asp Lys Ile His
 1140 1145 1150
 Ala Arg Ser Ile Gly Pro Tyr Ser Leu Val Thr Gln Gln Pro Leu Gly
 1155 1160 1165
 Gly Lys Ala Gln Met Gly Gly Gln Arg Phe Gly Glu Met Glu Val Trp
 1170 1175 1180
 Ala Leu Glu Ala Tyr Gly Val Ala His Met Leu Gln Glu Ile Leu Thr
 1185 1190 1195 1200
 Val Lys Ser Asp Asp Val Ser Gly Arg Thr Arg Ile Tyr Glu Ser Ile
 1205 1210 1215
 Val Lys Gly Glu Asn Leu Leu Arg Ser Gly Thr Pro Glu Ser Phe Asn
 1220 1225 1230
 Val Leu Ile Lys Glu Met Gln Gly Leu Gly Leu Asp Val Arg Pro Met
 1235 1240 1245
 Val Val Asp Ala
 1250

<211> 224

<212> FRT

<213> Chlamydia pneumoniae

<400> 397

Met Thr Ser Trp Ile Glu Leu Leu Asp Lys Gln Ile Glu Asp Gln His
5 10 15

Met Leu Lys His Glu Phe Tyr Gln Arg Trp Ser Glu Gly Lys Leu Glu
20 25 30

Lys Gln Gln Leu Gln Ala Tyr Ala Lys Asp Tyr Tyr Leu His Ile Lys
35 40 45

Ala Phe Pro Cys Tyr Leu Ser Ala Leu His Ala Arg Cys Asp Asp Leu
50 55 60

Gln Ile Arg Arg Gln Ile Leu Glu Asn Leu Met Asp Glu Glu Ala Gly
65 70 75 80

Asn Pro Asn His Ile Asp Leu Trp Arg Gln Phe Ala Leu Ser Leu Gly
85 90 95

Val Ser Glu Glu Glu Leu Ala Asn His Glu Phe Ser Gln Ala Ala Gln
100 105 110

Asp Met Val Ala Thr Phe Arg Arg Leu Cys Asp Met Pro Gln Leu Ala
115 120 125

Val Gly Leu Gly Ala Leu Tyr Thr Tyr Glu Ile Gln Ile Pro Gln Val
130 135 140

Cys Val Glu Lys Ile Arg Gly Leu Lys Glu Tyr Phe Gly Val Ser Ala
145 150 155 160

Arg Gly Tyr Ala Tyr Phe Thr Val His Gln Glu Ala Asp Ile Lys His
165 170 175

Ala Ser Glu Glu Lys Glu Met Leu Gln Thr Leu Val Gly Arg Glu Asn
180 185 190

Pro Asp Ala Val Leu Gln Gly Ser Gln Glu Val Leu Asp Thr Leu Trp
195 200 205

Asn Phe Leu Ser Ser Phe Ile Asn Ser Thr Glu Pro Cys Ser Cys Lys
210 215 220

<210> 398

<211> 556

<212> PRT

<213> Chlamydia pneumoniae

<400> 398

Met Ser Lys Leu Ile Arg Arg Val Val Thr Val Leu Ala Leu Thr Ser
5 10 15

Met Ala Ser Cys Phe Ala Ser Gly Gly Ile Glu Ala Ala Val Ala Glu
20 25 30

Ser Leu Ile Thr Lys Ile Val Ala Ser Ala Glu Thr Lys Pro Ala Pro

35					40					45					
Val	Pro	Met	Thr	Ala	Lys	Lys	Val	Arg	Leu	Val	Arg	Arg	Asn	Lys	Gln
50					55					60					
Pro	Val	Glu	Gln	Lys	Ser	Arg	Gly	Ala	Phe	Cys	Asp	Lys	Glu	Phe	Tyr
65					70					75					
Pro	Cys	Glu	Glu	Gly	Arg	Cys	Gln	Pro	Val	Glu	Ala	Gln	Gln	Glu	Ser
85					90					95					
Cys	Tyr	Gly	Arg	Leu	Tyr	Ser	Val	Lys	Val	Asn	Asp	Asp	Cys	Asn	Val
100					105					110					
Glu	Ile	Cys	Gln	Ser	Val	Pro	Glu	Tyr	Ala	Thr	Val	Gly	Ser	Pro	Tyr
115					120					125					
Pro	Ile	Glu	Ile	Leu	Ala	Ile	Gly	Lys	Lys	Asp	Cys	Val	Asp	Val	Val
130					135					140					
Ile	Thr	Gln	Gln	Leu	Pro	Cys	Glu	Ala	Glu	Phe	Val	Ser	Ser	Asp	Pro
145					150					155					
Glu	Thr	Thr	Pro	Thr	Ser	Asp	Gly	Lys	Leu	Val	Trp	Lys	Ile	Asp	Arg
165					170					175					
Leu	Gly	Ala	Gly	Asp	Lys	Cys	Lys	Ile	Thr	Val	Trp	Val	Lys	Pro	Leu
180					185					190					
Lys	Glu	Gly	Cys	Cys	Phe	Thr	Ala	Ala	Thr	Val	Cys	Ala	Cys	Pro	Glu
195					200					205					
Leu	Arg	Ser	Tyr	Thr	Lys	Cys	Gly	Gln	Pro	Ala	Ile	Cys	Ile	Lys	Gln
210					215					220					
Glu	Gly	Pro	Asp	Cys	Ala	Cys	Leu	Arg	Cys	Pro	Val	Cys	Tyr	Lys	Ile
225					230					235					
Glu	Val	Val	Asn	Thr	Gly	Ser	Ala	Ile	Ala	Arg	Asn	Val	Thr	Val	Asp
245					250					255					
Asn	Pro	Val	Pro	Asp	Gly	Tyr	Ser	His	Ala	Ser	Gly	Gln	Arg	Val	Leu
260					265					270					
Ser	Phe	Asn	Leu	Gly	Asp	Met	Arg	Pro	Gly	Asp	Lys	Lys	Val	Phe	Thr
275					280					285					
Val	Glu	Phe	Cys	Pro	Gln	Arg	Arg	Gly	Gln	Ile	Thr	Asn	Val	Ala	Thr
290					295					300					
Val	Thr	Tyr	Cys	Gly	Gly	His	Lys	Cys	Ser	Ala	Asn	Val	Thr	Thr	Val
305					310					315					
Val	Asn	Glu	Pro	Cys	Val	Gln	Val	Asn	Ile	Ser	Gly	Ala	Asp	Trp	Ser
325					330					335					
Tyr	Val	Cys	Lys	Pro	Val	Glu	Tyr	Ser	Ile	Ser	Val	Ser	Asn	Pro	Gly
340					345					350					
Asp	Leu	Val	Leu	His	Asp	Val	Val	Ile	Gln	Asp	Thr	Leu	Pro	Ser	Gly
355					360					365					

Val Thr Val Leu Glu Ala Pro Gly Gly Glu Ile Cys Cys Asn Lys Val
 370 375 380
 Val Trp Arg Ile Lys Glu Met Cys Pro Gly Glu Thr Leu Gln Phe Lys
 385 390 395 400
 Leu Val Val Lys Ala Gln Val Pro Gly Arg Phe Thr Asn Gln Val Ala
 405 410 415
 Val Thr Ser Glu Ser Asn Cys Gly Thr Cys Thr Ser Cys Ala Glu Thr
 420 425 430
 Thr Thr His Trp Lys Gly Leu Ala Ala Thr His Met Cys Val Leu Asp
 435 440 445
 Thr Asn Asp Pro Ile Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys
 450 455 460
 Val Thr Asn Arg Gly Ser Ala Glu Asp Thr Asn Val Ser Leu Ile Leu
 465 470 475 480
 Lys Phe Ser Lys Glu Leu Gln Pro Ile Ala Ser Ser Gly Pro Thr Lys
 485 490 495
 Gly Thr Ile Ser Gly Asn Thr Val Val Phe Asp Ala Leu Pro Lys Leu
 500 505 510
 Gly Ser Lys Glu Ser Val Glu Phe Ser Val Thr Leu Lys Gly Ile Ala
 515 520 525
 Pro Gly Asp Ala Arg Gly Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr
 530 535 540
 Ser Pro Val Ser Asp Thr Glu Asn Thr His Val Tyr
 545 550 555

 <210> 399
 <211> 461
 <212> PRT
 <213> Chlamydia pneumoniae

 <400> 399
 Met Thr Gln Glu Phe Asp Cys Val Val Ile Gly Ala Gly Pro Ser Gly
 5 10 15
 Tyr Val Ala Ala Ile Thr Ala Ala Gln Ser Lys Leu Arg Thr Ala Leu
 20 25 30
 Ile Glu Glu Asp Gln Ala Gly Gly Thr Cys Leu Asn Arg Gly Cys Ile
 35 40 45
 Pro Ser Lys Ala Leu Ile Ala Gly Ala Asn Val Val Ser His Ile Lys
 50 55 60
 His Ala Glu Gln Phe Gly Ile His Val Asp Gly Tyr Thr Ile Asp Tyr
 65 70 75 80
 Pro Ala Met Ala Lys Arg Lys Asn Thr Val Val Gln Gly Ile Arg Gln
 85 90 95

Gly Leu Glu Gly Leu Ile Arg Ser Asn Lys Ile Thr Val Leu Lys Gly
 100 105 110
 Thr Gly Ser Leu Val Ser Ser Thr Glu Val Lys Val Ile Gly Gln Asp
 115 120 125
 Thr Thr Ile Ile Lys Ala Asn His Ile Ile Leu Ala Thr Gly Ser Glu
 130 135 140
 Pro Arg Pro Phe Pro Gly Val Pro Phe Ser Ser Arg Ile Leu Ser Ser
 145 150 155 160
 Thr Gly Ile Leu Glu Leu Glu Val Leu Pro Lys Lys Leu Ala Ile Ile
 165 170 175
 Gly Gly Gly Val Ile Gly Cys Glu Phe Ala Ser Leu Phe His Thr Leu
 180 185 190
 Gly Val Glu Ile Thr Val Ile Glu Ala Leu Asp His Ile Leu Ala Val
 195 200 205
 Asn Asn Lys Glu Val Ser Gln Thr Val Thr Asn Lys Phe Thr Lys Gln
 210 215 220
 Gly Ile Arg Ile Leu Thr Lys Ala Ser Ile Ser Ala Ile Glu Glu Ser
 225 230 235 240
 Gln Asn Gln Val Arg Ile Thr Val Asn Asp Gln Val Glu Glu Phe Asp
 245 250 255
 Tyr Val Leu Val Ala Ile Gly Arg Gln Phe Asn Thr Ala Ser Ile Gly
 260 265 270
 Leu Asp Asn Ala Gly Val Ile Arg Asp Asp Arg Gly Val Ile Pro Val
 275 280 285
 Asp Glu Thr Met Arg Thr Asn Val Pro Asn Ile Tyr Ala Ile Gly Asp
 290 295 300
 Ile Thr Gly Lys Trp Leu Leu Ala His Val Ala Ser His Gln Gly Val
 305 310 315 320
 Ile Ala Ala Lys Asn Ile Ser Gly His His Glu Val Met Asp Tyr Ser
 325 330 335
 Ala Ile Pro Ser Val Ile Phe Thr His Pro Glu Ile Ala Met Val Gly
 340 345 350
 Leu Ser Leu Gln Glu Ala Glu Gln Gln Asn Leu Pro Ala Lys Leu Thr
 355 360 365
 Lys Phe Pro Phe Lys Ala Ile Gly Lys Ala Val Ala Leu Gly Ala Ser
 370 375 380
 Asp Gly Phe Ala Ala Ile Val Ser His Glu Ile Thr Gln Gln Ile Leu
 385 390 395 400
 Gly Ala Tyr Val Ile Gly Pro His Ala Ser Ser Leu Ile Gly Glu Met
 405 410 415

Thr Leu Ala Ile Arg Asn Glu Leu Thr Leu Pro Cys Ile Tyr Glu Thr
 420 425 430
 Val His Ala His Pro Thr Leu Ser Glu Val Trp Ala Glu Gly Ala Leu
 435 440 445
 Leu Ala Thr Asn His Pro Leu His Phe Pro Pro Lys Ser
 450 455 460
 <210> 400
 <211> 544
 <212> PRT
 <213> Chlamydia pneumoniae
 <400> 400
 Met Ala Ala Lys Asn Ile Lys Tyr Asn Glu Glu Ala Arg Lys Lys Ile
 5 10 15
 His Lys Gly Val Lys Thr Leu Ala Glu Val Lys Val Thr Leu Gly
 20 25 30
 Pro Lys Gly Arg His Val Val Ile Asp Lys Ser Phe Gly Ser Pro Gln
 35 40 45
 Val Thr Lys Asp Gly Val Thr Val Ala Lys Glu Ile Glu Leu Glu Asp
 50 55 60
 Lys His Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys
 65 70 75 80
 Thr Ala Asp Lys Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala
 85 90 95
 Glu Ala Ile Tyr Ser Glu Gly Leu Arg Asn Val Thr Ala Gly Ala Asn
 100 105 110
 Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Lys Val Val Val
 115 120 125
 Asp Glu Leu Lys Lys Ile Ser Lys Pro Val Gln His His Lys Glu Ile
 130 135 140
 Ala Gln Val Ala Thr Ile Ser Ala Asn Asn Asp Ser Glu Ile Gly Asn
 145 150 155 160
 Leu Ile Ala Glu Ala Met Glu Lys Val Gly Lys Asn Gly Ser Ile Thr
 165 170 175
 Val Glu Glu Ala Lys Gly Phe Glu Thr Val Leu Asp Val Val Glu Gly
 180 185 190
 Met Asn Phe Asn Arg Gly Tyr Leu Ser Ser Tyr Phe Ser Thr Asn Pro
 195 200 205
 Glu Thr Gln Glu Cys Val Leu Glu Asp Ala Leu Ile Leu Ile Tyr Asp
 210 215 220
 Lys Lys Ile Ser Gly Ile Lys Asp Phe Leu Pro Val Leu Gln Gln Val
 225 230 235 240

<213> Chlamydia pneumoniae

<400> 401

Met Glu Lys Val Ser Ser Tyr Pro Ser Val Pro Leu Pro Leu Gly Ala
5 10 15

Ser Lys Ile Ser Pro Asn Arg Tyr Arg Phe Ala Leu Tyr Ala Ser Gln
20 25 30

Ala Thr Glu Val Ile Leu Ala Leu Thr Asp Glu Asn Ser Glu Val Ile
35 40 45

Glu Val Pro Leu Tyr Pro Asp Thr His Arg Thr Gly Ala Ile Trp His
50 55 60

Ile Glu Ile Glu Gly Ile Ser Asp Gln Ser Ser Tyr Ala Phe Arg Val
65 70 75 80

His Gly Pro Lys Lys His Gly Met Gln Tyr Ser Phe Lys Glu Tyr Leu
85 90 95

Ala Asp Pro Tyr Ala Lys Asn Ile His Ser Pro Gln Ser Phe Gly Ser
100 105 110

Arg Lys Lys Gln Gly Asp Tyr Ala Phe Cys Tyr Leu Lys Glu Glu Pro
115 120 125

Phe Pro Trp Asp Gly Asp Gln Pro Leu His Leu Pro Lys Glu Glu Met
130 135 140

Ile Ile Tyr Glu Met His Val Arg Ser Phe Thr Gln Ser Ser Ser Ser
145 150 155 160

Arg Val His Ala Pro Gly Thr Phe Leu Gly Ile Ile Glu Lys Ile Asp
165 170 175

His Leu His Lys Leu Gly Ile Asn Ala Val Glu Leu Leu Pro Ile Phe
180 185 190

Glu Phe Asp Glu Thr Ala His Pro Phe Arg Asn Ser Lys Phe Pro Tyr
195 200 205

Leu Cys Asn Tyr Trp Gly Tyr Ala Pro Leu Asn Phe Phe Ser Pro Cys
210 215 220

Arg Arg Tyr Ala Tyr Ala Ser Asp Pro Cys Ala Pro Ser Arg Glu Phe
225 230 235 240

Lys Thr Leu Val Lys Thr Leu His Gln Glu Gly Ile Glu Val Ile Leu
245 250 255

Asp Val Val Phe Asn His Thr Gly Leu Gln Gly Thr Thr Cys Ser Leu
260 265 270

Pro Trp Ile Asp Thr Pro Ser Tyr Tyr Ile Leu Asp Ala Gln Gly His
275 280 285

Phe Thr Asn Tyr Ser Gly Cys Gly Asn Thr Leu Asn Thr Asn Arg Ala
290 295 300

Pro Thr Thr Gln Trp Ile Leu Asp Ile Leu Arg Tyr Trp Val Glu Glu

303					310				315				320			
Met	His	Val	Asp	Gly	Phe	Arg	Phe	Asp	Leu	Ala	Ser	Val	Phe	Ser	Arg	
				325					330				335			
Gly	Pro	Ser	Gly	Ser	Pro	Leu	Gln	Phe	Ala	Pro	Val	Leu	Glu	Ala	Ile	
				340					345				350			
Ser	Phe	Asp	Pro	Leu	Leu	Ala	Ser	Thr	Lys	Ile	Ile	Ala	Glu	Pro	Trp	
				355					360				365			
Asp	Ala	Gly	Gly	Leu	Tyr	Gln	Val	Gly	Tyr	Phe	Pro	Thr	Leu	Ser	Pro	
				370					375				380			
Arg	Trp	Ser	Glu	Trp	Asn	Gly	Pro	Tyr	Arg	Asp	Asn	Val	Lys	Ala	Phe	
				385					390				395			
Leu	Asn	Gly	Asp	Gln	Asn	Leu	Ile	Gly	Thr	Phe	Ala	Ser	Arg	Ile	Ser	
				405					410				415			
Gly	Ser	Gln	Asp	Ile	Tyr	Pro	His	Gly	Ser	Pro	Thr	Asn	Ser	Ile	Asn	
				420					425				430			
Tyr	Val	Ser	Cys	His	Asp	Gly	Phe	Thr	Leu	Cys	Asp	Thr	Val	Thr	Tyr	
				435					440				445			
Asn	His	Lys	His	Asn	Glu	Ala	Asn	Gly	Glu	Asp	Asn	Arg	Asp	Gly	Thr	
				450					455				460			
Asp	Ala	Asn	Tyr	Ser	Tyr	Asn	Phe	Gly	Thr	Glu	Gly	Lys	Thr	Glu	Asp	
				465					470				475			
Pro	Gly	Ile	Leu	Glu	Val	Arg	Glu	Arg	Gln	Leu	Arg	Asn	Phe	Phe	Leu	
				485					490				495			
Thr	Leu	Met	Val	Ser	Gln	Gly	Ile	Pro	Met	Ile	Gln	Ser	Gly	Asp	Glu	
				500					505				510			
Tyr	Ala	His	Thr	Ala	Glu	Gly	Asn	Asn	Asn	Arg	Trp	Ala	Leu	Asp	Ser	
				515					520				525			
Asn	Ala	Asn	Tyr	Phe	Leu	Trp	Asp	Gln	Leu	Thr	Ala	Lys	Pro	Thr	Leu	
				530					535				540			
Met	His	Phe	Leu	Cys	Asp	Leu	Ile	Ala	Phe	Arg	Lys	Lys	Tyr	Lys	Thr	
				545					550				555			
Leu	Phe	Asn	Arg	Gly	Phe	Leu	Ser	Asn	Lys	Glu	Ile	Ser	Trp	Val	Asp	
				565					570				575			
Ala	Met	Gly	Asn	Pro	Met	Thr	Trp	Arg	Pro	Gly	Asn	Phe	Leu	Ala	Phe	
				580					585				590			
Lys	Ile	Lys	Ser	Pro	Lys	Ala	His	Val	Tyr	Val	Ala	Phe	His	Val	Gly	
				595					600				605			
Ala	Gln	Asp	Gln	Leu	Ala	Thr	Leu	Pro	Lys	Ala	Ser	Ser	Asn	Phe	Leu	
				610					615				620			
Pro	Tyr	Gln	Ile	Val	Ala	Glu	Ser	Gln	Gln	Gly	Phe	Val	Pro	Gln	Asn	
				625					630				635			

Val Ala Thr Pro Thr Val Ser Leu Gln Pro His Thr Thr Leu Ile Ala
645 650 655

Ile Ser His Ala Lys Glu Val Thr
660

<210> 402

<211> 328

<212> PRT

<213> Chlamydia pneumoniae

<400> 402

Met Ala Phe Lys Glu Val Val Arg Val Ala Val Thr Gly Gly Lys Gly
5 10 15

Gln Ile Ala Tyr Asn Phe Leu Phe Ala Leu Ala His Gly Asp Val Phe
20 25 30

Gly Val Asp Arg Gly Val Asp Leu Arg Ile Tyr Asp Val Pro Gly Thr
35 40 45

Glu Arg Ala Leu Ser Gly Val Arg Met Glu Leu Asp Asp Gly Ala Tyr
50 55 60

Pro Leu Leu His Arg Leu Arg Val Thr Thr Ser Leu Asn Asp Ala Phe
65 70 75 80

Asp Gly Ile Asp Ala Ala Phe Leu Ile Gly Ala Val Pro Arg Gly Pro
85 90 95

Gly Met Glu Arg Gly Asp Leu Leu Lys Gln Asn Gly Gln Ile Phe Ser
100 105 110

Leu Gln Gly Ala Ala Leu Asn Thr Ala Ala Lys Arg Asp Ala Lys Ile
115 120 125

Phe Val Val Gly Asn Pro Val Asn Thr Asn Cys Trp Ile Ala Met Lys
130 135 140

His Ala Pro Arg Leu His Arg Lys Asn Phe His Ala Met Leu Arg Leu
145 150 155 160

Asp Gln Asn Arg Met His Ser Met Leu Ala His Arg Ala Glu Val Pro
165 170 175

Leu Glu Glu Val Ser Arg Val Val Ile Trp Gly Asn His Ser Ala Lys
180 185 190

Gln Val Pro Asp Phe Thr Gln Ala Arg Ile Ser Gly Lys Pro Ala Ala
195 200 205

Glu Val Ile Gly Asp Arg Asp Trp Leu Glu Asn Ile Leu Val His Ser
210 215 220

Val Gln Asn Arg Gly Ser Ala Val Ile Glu Ala Arg Gly Lys Ser Ser
225 230 235 240

Ala Ala Ser Ala Ser Arg Ala Leu Ala Glu Ala Ala Arg Ser Ile Phe
245 250 255

Cys Pro Lys Ser Asp Glu Trp Phe Ser Ser Gly Val Cys Ser Asp His
 260 265 270
 Asn Pro Tyr Gly Ile Pro Glu Asp Leu Ile Phe Gly Phe Pro Cys Arg
 275 280 285
 Met Leu Pro Ser Gly Asp Tyr Glu Ile Ile Pro Gly Leu Pro Trp Glu
 290 295 300
 Pro Phe Ile Arg Asn Lys Ile Gln Ile Ser Leu Asp Glu Ile Ala Gln
 305 310 315 320
 Glu Lys Ala Ser Val Ser Ser Leu
 325

<210> 403

<211> 217

<212> PRT

<213> Chlamydia pneumoniae

<400> 403

Met Lys Arg Val Ile Tyr Lys Thr Ile Phe Cys Gly Leu Thr Leu Leu
 5 10 15
 Thr Ser Leu Ser Ser Cys Ser Leu Asp Pro Lys Gly Tyr Asn Leu Glu
 20 25 30
 Thr Lys Asn Ser Arg Asp Leu Asn Gln Glu Ser Val Ile Leu Lys Glu
 35 40 45
 Asn Arg Glu Thr Pro Ser Leu Val Lys Arg Leu Ser Arg Arg Ser Arg
 50 55 60
 Arg Leu Phe Ala Arg Arg Asp Gln Thr Gln Lys Asp Thr Leu Gln Val
 65 70 75 80
 Gln Ala Asn Phe Lys Thr Tyr Ala Glu Lys Ile Ser Glu Gln Asp Glu
 85 90 95
 Arg Asp Leu Ser Phe Val Val Ser Ser Ala Ala Glu Lys Ser Ser Ile
 100 105 110
 Ser Leu Ala Leu Ser Gln Gly Glu Ile Lys Asp Ala Leu Tyr Arg Ile
 115 120 125
 Arg Glu Val His Pro Leu Ala Leu Ile Glu Ala Leu Ala Glu Asn Pro
 130 135 140
 Ala Leu Ile Glu Gly Met Lys Lys Met Gln Gly Arg Asp Trp Ile Trp
 145 150 155 160
 Asn Leu Phe Leu Thr Gln Leu Ser Glu Val Phe Ser Gln Ala Trp Ser
 165 170 175
 Gln Gly Val Ile Ser Glu Glu Asp Ile Ala Ala Phe Ala Ser Thr Leu
 180 185 190
 Gly Leu Asp Ser Gly Thr Val Ala Ser Ile Val Gln Gly Glu Arg Trp
 195 200 205

Pro Glu Leu Val Asp Ile Val Ile Thr
210 215

<210> 404

<211> 270

<212> PRT

<213> Chlamydia pneumoniae

<400> 404

Met Ile Ile Ile Lys Asn Asn Glu Leu Met Ile Arg Arg Phe Phe Lys
5 10 15

Thr Leu Phe Pro Pro Gly Pro Gln Tyr Ser Leu Cys Tyr Ala Ser Ile
20 25 30

Leu Ile Val Leu Ser Ser Leu Val Cys Val Pro Thr Phe Cys Trp Leu
35 40 45

Phe Leu Pro Glu Leu Ser Leu Ser Lys Phe Asn Pro Ser Pro Ile Arg
50 55 60

Asn Leu Phe Leu Val Ser Ser Thr Leu Ser Lys Val Pro Pro Thr Ala
65 70 75 80

Ile Ala Glu His Leu Arg Leu Ser Ala Asp Ala Pro Thr Tyr Leu His
85 90 95

Glu Phe Ser Ile Lys Glu Ala Glu Ser Ser Leu His Ala Leu Gly Ile
100 105 110

Phe Ser Ser Leu Val Ile Glu Lys Ser Pro Asp Asn Lys Gly Ile Thr
115 120 125

Ile Phe Tyr Thr Leu Gln Thr Pro Ile Ala Tyr Val Gly Asn Arg Ser
130 135 140

Asn Thr Leu Cys Asn Leu Glu Gly Ser Cys Phe Leu Gly Gln Pro Tyr
145 150 155 160

Phe Pro Ser Leu Asn Leu Pro Gln Ile Phe Phe Ser Gln Glu Asp Leu
165 170 175

Lys Met Gln Lys Leu Pro Lys Glu Lys Met Leu Phe Thr Lys Ile Leu
180 185 190

Leu Lys Glu Leu Ala Met Glu Ser Pro Lys Ile Ile Asp Leu Ser Leu
195 200 205

Ser Asp Ala Tyr Pro Gly Glu Ile Ile Val Thr Leu Ser Ser Gly Ser
210 215 220

Leu Leu Arg Leu Pro Ile Lys Thr Leu Asp Arg Ala Leu Asp Leu Tyr
225 230 235 240

Lys His Met Lys Lys Ser Pro Val Ile Glu Ser Glu Lys Gln Tyr Val
245 250 255

Tyr Asp Leu Arg Phe Pro Asn Phe Leu Leu Leu Lys Ala Leu
260 265 270

<210> 405
 <211> 651
 <212> PRT
 <213> *Chlamydia pneumoniae*

 <400> 405
 Met Val Asn Pro Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr
 5 10 15

 Pro Pro Ala Asp Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn
 20 25 30

 Lys Ser Ala Glu Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys
 35 40 45

 Glu Ser Lys Thr Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala
 50 55 60

 Val Asn Ala Leu Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser
 65 70 75 80

 Asn Ser Ser Ser Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr
 85 90 95

 Ala Thr Ala Pro Thr Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr
 100 105

 Gln Ala Gln Thr Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala
 115 120 125

 Asp Ile Gln Ala Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile
 130 135 140

 Lys Asp Thr Ala Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp
 145 150 155 160

 Glu Thr Lys Asn Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu
 165 170 175

 Leu Ala Lys Tyr Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly
 180 185 190

 Lys Leu Thr Ser Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val
 195 200 205

 Ala Asn Asn Asn Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn
 210 215 220

 Pro Val Val Pro Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp
 225 230 235 240

 Gln Thr Asp Ala Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile
 245 250 255

 Arg Asp Ala Tyr Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn
 260 265 270

 Ala Lys Ser Asn Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala
 275 280 285

Ile Ala Thr Ala Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro
 290 295 300
 Asp Ser Pro Ile Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu
 305 310 315 320
 Lys Asp Leu Lys Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn
 325 330 335
 Pro Gly Thr Thr Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly
 340 345 350
 Ser Ile Arg Val Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala
 355 360 365
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 370 375 380
 Glu Asn Pro Asp Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala
 385 390 395 400
 Arg Ala Ala Lys Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala
 405 410 415
 Asp Ala Gln Lys Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln
 420 425 430
 Gln Gly Ile Leu Asn Ala Leu Gly Gln Ile Ala Ser Ala Val Val
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 Ser Ala Gly Val Pro Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val
 450 455 460
 Lys Gln Leu Tyr Lys Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr
 465 470 475 480
 Gln Ile Ser Ala Gly Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr
 485 490 495
 Gly Arg Ala Arg Asn Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser
 500 505 510
 Thr Pro Ala Leu Thr Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg
 515 520 525
 Gly Pro Glu Lys Thr Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn
 530 535 540
 Ser Arg Thr Leu Gly Asp Val Tyr Ser Gln Val Ser Ala Leu Gln Ser
 545 550 555 560
 Val Met Gln Ile Ile Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile
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 Arg Gln Lys Leu Thr Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr
 580 585 590
 Pro Tyr Val Gln Leu Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys
 595 600 605

Leu Glu Ser Leu Phe Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys
610 615 620

Ala Leu Ser Phe Glu Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val
625 630 635 640

Asn Ile Gly Ser Leu Tyr Ser Gly Tyr Leu Gln
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<210> 406

<211> 1074

<212> DNA

<213> *Chlamydia trachomatis* serovar D

<400> 406

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<210> 407

<211> 1827

<212> DNA

<213> *Chlamydia trachomatis* serovar D

<400> 407

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<210> 408

<211> 804

<212> DNA

<213> Chlamydia trachomatis serovar D

<400> 408

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<210> 409

<211> 663

<212> DNA

<213> Chlamydia trachomatis serovar D

<400> 409

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<210> 410

<211> 1470

<212> DNA

<213> Chlamydia trachomatis serovar D

<400> 410

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<210> 411

<211> 234

<212> DNA

<213> Chlamydia trachomatis serovar D

<400> 411

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atcgtgtaaa	ttatcggtaa	agaaggacgc	actattaagg	ctatccgtac	tttattgggt	180
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<210> 412

<211> 1941

<212> DNA

<213> Chlamydia trachomatis serovar D

<400> 412

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<210> 413

<211> 693

<212> DNA

<213> *Chlamydia trachomatis* serovar D

<400> 413

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<211> 1599

<212> DNA

<213> *Chlamydia trachomatis* serovar D

<400> 414

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<210> 415
<211> 1395
<212> DNA
<213> Chlamydia trachomatis serovar D

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<210> 416
<211> 366
<212> DNA
<213> Chlamydia trachomatis serovar D

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<212> DNA
<213> Chlamydia trachomatis serovar D

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<211> 576

<212> DNA

<213> *Chlamydia trachomatis* serovar D

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<210> 419

<211> 825

<212> DNA

<213> *Chlamydia trachomatis* serovar D

<400> 419

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<210> 420

<211> 5310

<212> DNA

<213> *Chlamydia trachomatis* serovar D

<400> 420

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<211> 5253

<212> DNA

<213> Chlamydia trachomatis serovar D

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<210> 422

<211> 1980

<212> DNA

<213> *Chlamydia trachomatis* serovar D

<400> 422

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<210> 423

<211> 978

<212> DNA

<213> *Chlamydia trachomatis* serovar D

<400> 423

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<210> 424

<211> 696

<212> DNA

<213> Chlamydia trachomatis serovar D

<400> 424

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<210> 425

<211> 3756

<212> DNA

<213> Chlamydia trachomatis serovar D

<400> 425

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<210> 426

<211> 894

<212> DNA

<213> Chlamydia trachomatis serovar D

<400> 426

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<210> 427

<211> 894

<212> DNA

<213> *Chlamydia trachomatis* serovar D

<400> 427

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<210> 428

<211> 459

<212> DNA

<213> *Chlamydia trachomatis* serovar D

<400> 428

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<210> 429

<211> 1707

<212> DNA

<213> *Chlamydia trachomatis* serovar D

<400> 429

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aagaaggttt	ctctttctat	taaaagagtc	cttggtcatg	ggggagatgc	tggtcacgat	1680
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<210> 430

<211> 1998

<212> DNA

<213> *Chlamydia trachomatis* serovar D

<400> 430

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<210> 431

<211> 609

<212> PRT

<213> *Chlamydia trachomatis* serovar D

<400> 431

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Leu	Leu	Leu	Thr 20	Phe	Ser	Ser	Ala	Ile 25	His	Ser	Pro	Val	Gln 30	Gly	Glu
Ser	Leu	Val 35	Cys	Lys	Asn	Ala	Leu 40	Gln	Asp	Leu	Ser	Phe 45	Leu	Glu	His
Leu	Leu	Gln	Val	Lys	Tyr	Ala 55	Pro	Lys	Thr	Trp	Lys 60	Glu	Gln	Tyr	Leu
Gly 65	Trp	Asp	Leu	Val	Gln 70	Ser	Ser	Val	Ser	Ala 75	Gln	Gln	Lys	Leu	Arg 80
Thr	Gln	Glu	Asn 85	Ser	Thr	Ser	Phe 90	Gln	Gln	Val	Leu	Ala 95	Asp		
Phe	Ile	Gly	Gly 100	Leu	Asn	Asp	Phe 105	His	Ala	Gly	Val	Thr	Phe 110	Phe	Ala
Ile	Glu	Ser 115	Ala	Tyr	Leu	Pro	Tyr 120	Thr	Val	Gln	Lys 125	Ser	Ser	Asp	Gly
Arg	Phe 130	Tyr	Phe	Val	Asp 135	Ile	Met	Thr	Phe	Ser	Ser 140	Glu	Ile	Arg	Val
Gly 145	Asp	Glu	Leu	Leu	Glu 150	Val	Asp	Gly	Ala	Pro 155	Val	Gln	Asp	Val	Leu 160
Ala	Thr	Leu	Tyr 165	Ser	Asn	His	Lys 170	Gly	Thr	Ala	Ala	Glu	Glu 175	Ser	
Ala	Ala	Leu	Arg 180	Thr	Leu	Phe	Ser 185	Arg	Met	Ala	Ser	Leu	Gly 190	His	Lys
Val	Pro	Ser 195	Gly	Arg	Thr	Thr	Leu 200	Lys	Ile	Arg	Arg 205	Phe	Gly	Thr	
Thr	Arg 210	Glu	Val	Arg	Val	Lys 215	Trp	Arg	Tyr	Val	Pro 220	Glu	Gly	Val	Gly
Asp 225	Leu	Ala	Thr	Ile	Ala 230	Pro	Ser	Ile	Arg	Ala 235	Pro	Gln	Leu	Gln	Lys 240
Ser	Met	Arg	Ser	Phe 245	Pro	Lys	Lys	Asp 250	Asp	Ala	Phe	His	Arg 255	Ser	
Ser	Ser	Leu	Phe 260	Tyr	Ser	Pro	Met	Val 265	Pro	His	Phe	Trp	Ala 270	Glu	Leu
Arg	Asn 275	His	Tyr	Ala	Thr	Ser	Gly 280	Leu	Lys	Ser	Gly	Tyr 285	Asn	Ile	Gly
Ser	Thr 290	Asp	Gly	Phe	Leu	Pro 295	Val	Ile	Gly	Pro	Val 300	Ile	Trp	Glu	Ser
Glu 305	Gly	Leu	Phe	Arg	Ala 310	Tyr	Ile	Ser	Ser	Val 315	Thr	Asp	Gly	Asp	Gly 320
Lys	Ser	His	Lys	Val	Gly	Phe	Leu	Arg	Ile	Pro	Thr	Tyr	Ser	Trp	Gln

325										330				335			
Asp	Met	Glu	Asp	Phe	Asp	Pro	Ser	Gly	Pro	Pro	Pro	Trp	Glu	Glu	Phe		
			340					345					350				
Ala	Lys	Ile	Ile	Gln	Val	Phe	Ser	Ser	Asn	Thr	Glu	Ala	Leu	Ile	Ile		
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Asp	Gln	Thr	Asn	Asn	Pro	Gly	Gly	Ser	Val	Leu	Tyr	Leu	Tyr	Ala	Leu		
	370					375					380						
Leu	Ser	Met	Leu	Thr	Asp	Arg	Pro	Leu	Glu	Leu	Pro	Lys	His	Arg	Met		
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Ile	Leu	Thr	Gln	Asp	Glu	Val	Val	Asp	Ala	Leu	Asp	Trp	Leu	Thr	Leu		
			405						410					415			
Leu	Glu	Asn	Val	Asp	Thr	Asn	Val	Glu	Ser	Arg	Leu	Ala	Leu	Gly	Asp		
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Asn	Met	Glu	Gly	Tyr	Thr	Val	Asp	Leu	Gln	Val	Ala	Glu	Tyr	Leu	Lys		
		435					440					445					
Ser	Phe	Gly	Arg	Gln	Val	Leu	Asn	Cys	Trp	Ser	Lys	Gly	Asp	Ile	Glu		
	450					455					460						
Leu	Ser	Thr	Pro	Ile	Pro	Leu	Phe	Gly	Phe	Glu	Lys	Ile	His	Pro	His		
	465				470				475					480			
Pro	Arg	Val	Gln	Tyr	Ser	Lys	Pro	Ile	Cys	Val	Leu	Ile	Asn	Glu	Gln		
			485						490					495			
Asp	Phe	Ser	Cys	Ala	Asp	Phe	Phe	Pro	Val	Val	Leu	Lys	Asp	Asn	Asp		
			500					505					510				
Arg	Ala	Leu	Ile	Val	Gly	Thr	Arg	Thr	Ala	Gly	Ala	Gly	Gly	Phe	Val		
	515					520						525					
Phe	Asn	Val	Gln	Phe	Pro	Asn	Arg	Thr	Gly	Ile	Lys	Thr	Cys	Ser	Leu		
	530					535					540						
Thr	Gly	Ser	Leu	Ala	Val	Arg	Glu	His	Gly	Ala	Phe	Ile	Glu	Asn	Ile		
	545				550				555					560			
Gly	Val	Glu	Pro	His	Ile	Asp	Leu	Pro	Phe	Thr	Ala	Asn	Asp	Ile	Arg		
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Tyr	Lys	Gly	Tyr	Ser	Glu	Tyr	Leu	Asp	Lys	Val	Lys	Lys	Leu	Val	Cys		
			580					585					590				
Gln	Leu	Ile	Asn	Asn	Asp	Gly	Thr	Ile	Ile	Leu	Ala	Glu	Asp	Gly	Ser		
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Phe

<210> 432

<211> 268

<212> PRT

<213> Chlamydia trachomatis serovar D

<400> 432

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Phe Ala Lys Gly Pro Asn Tyr Ser Leu Tyr Ala Phe Leu Cys Ile
20 25 30

Phe Val Ser Val Leu Val Phe Leu Pro Ile Gly Leu Trp Leu Thr Leu
35 40 45

Pro Ser Phe Leu Asn Phe Lys His Ser Leu Thr Pro Ile Lys Thr Leu
50 55 60

Phe Leu Thr Cys Thr Glu Pro Pro Cys Leu Pro Glu Pro Phe Phe Ser
65 70 75 80

Asp Ile Leu His Leu Ser Ala Asp Ser Pro Pro Ala Leu Gln Thr Phe
85 90 95

Ser Thr Lys Ser Ala Glu His Phe Leu Asn Glu Leu Gly Val Phe Ser
100 105 110

Phe Ile Ser Ile Glu Lys Val Pro Asp His Lys Gly Leu Ala Ile Ser
115 120 125

Tyr Ala Leu His Thr Pro Leu Ala Phe Leu Gly Asn Gln Thr His Thr
130 135 140

Phe Ile Gly Tyr Glu Gly Gln Thr Phe Pro Ala Leu Pro Phe Phe Gln
145 150 155 160

Ser Leu Glu Leu Pro Thr Val Phe Phe Ser Gln Gln Ala Leu Ser Gln
165 170 175

Thr Arg Ile Pro His Gln Thr Leu Ser Ile Val Thr Ser Leu Ile Asp
180 185 190

Gln Leu Gln Met Asp Pro Pro Ser Ile Ile Asp Leu Ser Gln Ile Asp
195 200 205

His Tyr Pro Gly Glu Phe Val Val Ser Leu Ser Ser Gly Thr Leu Leu
210 215 220

Arg Phe Arg Lys Asp Ser Phe Leu Pro Gly Ile Gln His Tyr Gln Gln
225 230 235 240

Ala Leu Ser Leu Gly Ala Phe Ser Pro Gln Gln Ala Val Ile Cys Asp
245 250 255

Leu Arg Cys Glu Asp Tyr Leu Leu Lys Arg Lys
260 265

<210> 433

<211> 221

<212> PRT

<213> Chlamydia trachomatis serovar D

<400> 433

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 Ser Gly Leu Ser Gly Leu Ser Ser Cys Cys Ala Asn Ser Tyr Gly Ser
 20 25 30
 Thr Leu Ala Lys Asn Thr Ala Glu Ile Lys Glu Glu Ser Val Thr Leu
 35 40 45
 Arg Glu Lys Pro Asp Ala Gly Cys Lys Lys Lys Ser Ser Cys Tyr Leu
 50 55 60
 Arg Lys Phe Phe Ser Arg Lys Lys Pro Lys Glu Lys Thr Glu Pro Val
 65 70 75 80
 Leu Pro Asn Phe Lys Ser Tyr Ala Asp Pro Met Thr Asp Ser Glu Arg
 85 90 95
 Lys Asp Leu Ser Phe Val Val Ser Ala Ala Asp Lys Ser Ser Ile
 100 105 110
 Ala Leu Ala Met Ala Gln Gly Glu Ile Lys Gly Ala Leu Ser Arg Ile
 115 120 125
 Arg Glu Ile His Pro Leu Ala Leu Leu Gln Ala Leu Ala Glu Asp Pro
 130 135 140
 Ala Leu Ile Ala Gly Met Lys Lys Met Gln Gly Arg Asp Trp Val Trp
 145 150 155 160
 Asn Ile Phe Ile Thr Glu Leu Ser Lys Val Phe Ser Gln Ala Ala Ser
 165 170 175
 Leu Gly Ala Phe Ser Val Ala Asp Val Ala Ala Phe Ala Ser Thr Leu
 180 185 190
 Gly Leu Asp Ser Gly Thr Val Thr Ser Ile Val Asp Gly Glu Arg Trp
 195 200 205
 Ala Glu Leu Ile Asp Val Val Ile Gln Asn Pro Ala Ile
 210 215 220

<210> 434
 <211> 490
 <212> PRT
 <213> Chlamydia trachomatis serovar D

<400> 434
 Met Ser Asp Leu Ser Asp Leu Phe Lys Thr His Phe Thr Gln Tyr Ala
 5 10 15
 Ser Tyr Val Ile Leu Glu Arg Ala Ile Pro His Val Leu Asp Gly Leu
 20 25 30
 Lys Pro Val Gln Arg Arg Leu Leu Trp Thr Leu Phe Arg Met Asp Asp
 35 40 45
 Gly Lys Met His Lys Val Ala Asn Ile Ala Gly Arg Thr Met Ala Leu
 50 55 60
 His Pro His Gly Asp Ala Pro Ile Val Glu Ala Leu Val Val Leu Ala

65		70		75		80
Asn Lys Gly Phe Leu	Ile Glu Thr Gln Gly	Asn Phe Gly Asn Pro Leu				
	85		90		95	
Thr Gly Asp Pro His	Ala Ala Ala Arg	Tyr Ile Glu Ala Arg Leu Ser				
	100	105	110			
Pro Leu Ala Lys Glu	Val Leu Phe Asn Thr	Asp Leu Met Thr Phe His				
	115	120	125			
Asp Ser Tyr Asp Gly	Arg Glu Gln Glu	Pro Asp Ile Leu Ala Ala Lys				
	130	135	140			
Ile Pro Leu Leu Leu	Leu His Gly Val Asp	Gly Ile Ala Val Gly Met				
	145	150	155			160
Thr Thr Lys Ile Phe	Pro His Asn Phe Cys	Asp Leu Leu Glu Ala Gln				
	165	170	175			
Ile Ala Ile Leu Asn	Asp Gln Pro Phe Ser	Leu Leu Pro Asp Phe Pro				
	180	185	190			
Pro Gly Gly Thr Met	Asp Ala Ser Asp Tyr	Gln Asp Gly Leu Gly Ser				
	195	200	205			
Ile Val Leu Arg Ala	Thr Ile Asp Ile Ile	Asn Asp Lys Thr Leu Leu				
	210	215	220			
Ile Lys Glu Ile Cys	Pro Ser Thr Thr Thr	Glu Thr Leu Ile Arg Ser				
	225	230	235			240
Ile Glu Asn Ala Ala	Lys Arg Gly Ile Ile	Lys Ile Asp Ser Ile Gln				
	245	250	255			
Asp Phe Ser Thr Asp	Leu Pro His Ile Glu	Ile Lys Leu Pro Lys Gly				
	260	265	270			
Ile Tyr Ala Lys Asp	Leu Leu Arg Pro Leu	Tyr Thr His Thr Glu Cys				
	275	280	285			
Gln Val Ile Leu Thr	Ser Arg Pro Thr Ala	Ile Tyr Gln Gly Lys Pro				
	290	295	300			
Trp Glu Thr Thr Ile	Ser Glu Ile Leu Arg	Leu Gln Thr Lys Thr Leu				
	305	310	315			320
Gln Asn Tyr Leu Lys	Lys Glu Leu Leu Ile	Leu Glu Asp Ser Leu Ser				
	325	330	335			
Arg Glu Leu Tyr His	Lys Thr Leu Glu Tyr	Leu Phe Ile Lys His Lys				
	340	345	350			
Leu Tyr Asp Thr Val	Arg Ser Met Leu Ser	Lys Arg Lys Thr Ser Pro				
	355	360	365			
Ser Ser Ser Thr Ile	His Asn Ala Val Leu	Glu Ala Leu Thr Pro Phe				
	370	375	380			
Leu Asp Thr Leu Pro	Ala Pro Asp Lys Gln	Ala Thr Ala Gln Leu Ala				
	385	390	395			400

Ala Leu Thr Ile Lys Lys Ile Leu Cys Phe Asp Glu Asn Ser Tyr Glu
 405 410 415

Lys Glu Leu Ala Cys Leu Glu Lys Lys Arg Ser Ser Val Gln Lys Asp
 420 425 430

Leu Ser Gln Leu Lys Lys Tyr Thr Val Leu Tyr Ile Lys Lys Leu Leu
 435 440 445

Glu Thr Tyr Arg Gln Leu Gly His Arg Lys Thr Lys Ile Ala Lys Phe
 450 455 460

Asp Asp Leu Pro Thr Glu Arg Val Ser Ala His Lys Lys Ala Lys Glu
 465 470 475 480

Leu Ala Ala Leu Asp Gln Glu Glu Asn Phe
 485 490

<210> 435

<211> 78

<212> PRT

<213> Chlamydia trachomatis serovar D

<400> 435

Met Lys Glu Phe Leu Ala Tyr Ile Val Lys Asn Leu Val Asp Lys Pro
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Glu Glu Val His Leu Lys Glu Val Gln Gly Thr Asn Thr Ile Ile Tyr
 20 25 30

Glu Leu Thr Val Ala Lys Gly Asp Ile Gly Lys Ile Ile Gly Lys Glu
 35 40 45

Gly Arg Thr Ile Lys Ala Ile Arg Thr Leu Leu Val Ser Val Ala Ser
 50 55 60

Arg Asp Asn Val Lys Val Ser Leu Glu Ile Met Glu Glu Arg
 65 70 75

<210> 436

<211> 647

<212> PRT

<213> Chlamydia trachomatis serovar D

<400> 436

Met Glu Ser Gly Pro Glu Ser Val Ser Ser Asn Gln Ser Ser Met Asn
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Pro Ile Ile Asn Gly Gln Ile Ala Ser Asn Ser Glu Thr Lys Glu Ser
 20 25 30

Thr Lys Glu Ser Glu Ala Ser Pro Ser Ala Ser Ser Val Ser Ser
 35 40 45

Trp Ser Phe Leu Ser Ser Ala Lys His Ala Leu Ile Ser Leu Arg Asp
 50 55 60

Ala Ile Leu Asn Lys Asn Ser Ser Pro Thr Asp Ser Leu Ser Gln Leu

65		70		75		80
Glu Ala Ser Thr Ser	Thr Ser Thr Val Thr	Arg Val Ala Ala Arg Asp				
	85	90			95	
Tyr Asn Glu Ala Lys	Ser Asn Phe Asp Thr	Ala Lys Ser Gly Leu Glu				
	100	105			110	
Asn Ala Thr Thr Leu	Ala Glu Tyr Glu Thr	Lys Met Ala Asp Leu Met				
	115	120			125	
Ala Ala Leu Gln Asp	Met Glu Arg Leu Ala	Lys Gln Lys Ala Glu Val				
	130	135			140	
Thr Arg Ile Lys Glu	Ala Leu Gln Glu Lys	Gln Glu Val Ile Asp Lys				
	145	150			155	
Leu Asn Gln Leu Val	Lys Leu Glu Lys Gln	Asn Gln Thr Leu Lys Glu				
	165	170			175	
Thr Leu Thr Thr Thr	Asp Ser Ala Asp Gln	Ile Pro Ala Ile Asn Ser				
	180	185			190	
Gln Leu Glu Glu Ile	Asn Lys Asn Ser Ala	Asp Gln Ile Ile Lys Asp Leu				
	195	200			205	
Glu Gly Gln Asn Ile	Ser Tyr Glu Ala Val	Leu Thr Asn Ala Gly Glu				
	210	215			220	
Val Ile Lys Ala Ser	Ser Glu Ala Gly Ile	Lys Leu Gly Gln Ala Leu				
	225	230			235	
Gln Ser Ile Val Asp	Ala Gly Asp Gln Ser	Gln Ala Ala Val Leu Gln				
	245	250			255	
Ala Gln Gln Asn Asn	Ser Pro Asp Asn Ile	Ala Ala Thr Lys Lys Leu				
	260	265			270	
Ile Asp Ala Ala Glu	Thr Lys Val Asn Glu	Leu Lys Gln Glu His Thr				
	275	280			285	
Gly Leu Thr Asp Ser	Pro Leu Val Lys Lys	Ala Glu Glu Gln Ile Ser				
	290	295			300	
Gln Ala Gln Lys Asp	Ile Gln Glu Ile Lys	Pro Ser Gly Ser Asp Ile				
	305	310			315	
Pro Ile Val Gly Pro	Ser Gly Ser Ala Ala	Ser Ala Gly Ser Ala Val				
	325	330			335	
Gly Ala Leu Lys Ser	Ser Asn Asn Ser Gly	Arg Ile Ser Leu Leu Leu				
	340	345			350	
Asp Asp Val Asp Asn	Glu Met Ala Ala Ile	Ala Met Gln Gly Phe Arg				
	355	360			365	
Ser Met Ile Glu Gln	Phe Asn Val Asn Asn	Pro Ala Thr Ala Lys Glu				
	370	375			380	
Leu Gln Ala Met Glu	Ala Gln Leu Thr Ala	Met Ser Asp Gln Leu Val				
	385	390			395	
					400	

Gly Ala Asp Gly Glu Leu Pro Ala Glu Ile Gln Ala Ile Lys Asp Ala
 405 410 415
 Leu Ala Gln Ala Leu Lys Gln Pro Ser Thr Asp Gly Leu Ala Thr Ala
 420 425 430
 Met Gly Gln Val Ala Phe Ala Ala Lys Val Gly Gly Gly Ser Ala
 435 440 445
 Gly Thr Ala Gly Thr Val Gln Met Asn Val Lys Gln Leu Tyr Lys Thr
 450 455 460
 Ala Phe Ser Ser Thr Ser Ser Ser Tyr Ala Ala Leu Ser Asp
 465 470 475 480
 Gly Tyr Ser Ala Tyr Lys Thr Leu Asn Ser Leu Tyr Ser Glu Ser Arg
 485 490 495
 Ser Gly Val Gln Ser Ala Ile Ser Gln Thr Ala Asn Pro Ala Leu Ser
 500 505 510
 Arg Ser Val Ser Arg Ser Gly Ile Glu Ser Gln Gly Arg Ser Ala Asp
 515 520 525
 Ala Ser Gln Arg Ala Ala Glu Thr Ile Val Arg Asp Ser Gln Thr Leu
 530 535 540
 Gly Asp Val Tyr Ser Arg Leu Gln Val Leu Asp Ser Leu Met Ser Thr
 545 550 555 560
 Ile Val Ser Asn Pro Gln Val Asn Gln Glu Glu Ile Met Gln Lys Leu
 565 570 575
 Thr Ala Ser Ile Ser Lys Ala Pro Gln Phe Gly Tyr Pro Ala Val Gln
 580 585 590
 Asn Ser Ala Asp Ser Leu Gln Lys Phe Ala Ala Gln Leu Glu Arg Glu
 595 600 605
 Phe Val Asp Gly Glu Arg Ser Leu Ala Glu Ser Arg Glu Asn Ala Phe
 610 615 620
 Arg Lys Gln Pro Ala Phe Ile Gln Gln Val Leu Val Asn Ile Ala Ser
 625 630 635 640
 Leu Phe Ser Gly Tyr Leu Ser
 645

<210> 437
 <211> 231
 <212> PRT
 <213> Chlamydia trachomatis serovar D

<400> 437
 Met Met Glu Val Phe Met Asn Phe Leu Asp Gln Leu Asp Leu Ile Ile
 5 10 15
 Gln Asn Lys His Met Leu Glu His Thr Phe Tyr Val Lys Trp Ser Lys
 20 25 30

Gly	Leu	Thr	Lys	Glu	Gln	Leu	Gln	Ala	Tyr	Ala	Lys	Asp	Tyr	Tyr	
	35					40					45				
Leu	His	Ile	Lys	Ala	Phe	Pro	Lys	Tyr	Leu	Ser	Ala	Ile	His	Ser	Arg
	50					55					60				
Cys	Asp	Asp	Leu	Glu	Ala	Arg	Lys	Leu	Leu	Leu	Asp	Asn	Leu	Met	Asp
	65				70					75					80
Glu	Glu	Asn	Gly	Tyr	Pro	Asn	His	Ile	Asp	Leu	Trp	Lys	Gln	Phe	Val
				85					90					95	
Phe	Ala	Leu	Gly	Val	Thr	Pro	Glu	Glu	Leu	Glu	Ala	His	Glu	Pro	Ser
			100					105					110		
Glu	Ala	Ala	Lys	Ala	Lys	Val	Ala	Thr	Phe	Met	Arg	Trp	Cys	Thr	Gly
		115					120					125			
Asp	Ser	Leu	Ala	Ala	Gly	Val	Ala	Ala	Leu	Tyr	Ser	Tyr	Glu	Ser	Gln
	130					135					140				
Ile	Pro	Arg	Ile	Ala	Arg	Glu	Lys	Ile	Arg	Gly	Leu	Thr	Glu	Tyr	Phe
	145				150					155					160
Gly	Phe	Ser	Asn	Pro	Glu	Asp	Tyr	Ala	Tyr	Phe	Thr	Glu	His	Glu	Glu
				165					170					175	
Ala	Asp	Val	Arg	His	Ala	Arg	Glu	Glu	Lys	Ala	Leu	Ile	Glu	Met	Leu
			180					185					190		
Leu	Lys	Asp	Asp	Ala	Asp	Lys	Val	Leu	Glu	Ala	Ser	Gln	Glu	Val	Thr
	195						200					205			
Gln	Ser	Leu	Tyr	Gly	Phe	Leu	Asp	Ser	Phe	Leu	Asp	Pro	Gly	Thr	Cys
	210					215					220				
Cys	Ser	Cys	His	Gln	Ser	Tyr									
	225				230										
<210> 438															
<211> 533															
<212> PRT															
<213> Chlamydia trachomatis serovar D															
<400> 438															
Met	Ser	Asn	Ser	Phe	Arg	Asp	Gln	Glu	Gln	Gly	Leu	Gln	Ala	Val	Phe
				5					10					15	
Arg	Ala	Ala	Arg	Val	Ile	Ser	His	Met	Phe	Ser	Gln	Thr	Ile	Gly	Pro
			20					25					30		
Tyr	Gly	Phe	Ser	Thr	Ile	Val	His	Asn	Val	Gln	Asp	Thr	Arg	Thr	Thr
	35						40					45			
Gln	Asp	Ser	Gln	Ser	Met	Leu	Lys	Asp	Ile	Leu	Phe	Pro	Asp	Val	Phe
	50					55					60				
Glu	Asn	Ile	Gly	Met	Lys	Leu	Ile	Arg	Asp	Thr	Ala	Leu	Arg	Thr	Arg
	65				70				7						

Met Arg Phe Gly Asp Gly Ala Lys Thr Thr Ala Leu Leu Ile Glu Ala
85 90 95

Leu Leu Ala Glu Gly Met Thr Gly Ile Gln Lys Gly Leu Asp Pro His
100 105 110

Glu Ile His Arg Gly Met Leu Leu Ala Glu Lys Lys Ile Gln Glu Val
115 120 125

Phe Tyr Arg Glu Thr Phe Pro Leu Ser Asp Leu Glu His Thr Val Tyr
130 135 140

Val Ser Ser Ile Ala Arg Cys Asn Ser Glu Ile Ala Ser Val Leu
145 150 155 160

Ser Ser Ala Val Gly Tyr Gly Gly Lys Asn Gly Tyr Tyr Ile Val Glu
165 170 175

Glu His Glu Glu His Glu Thr Tyr Trp His Ala Glu Glu His Ala Val
180 185 190

Trp Asp Phe Gly Tyr Ala Ser Pro Tyr Phe Ile Thr His Ala Glu Thr
195 200 205

Gly Thr Val Glu Tyr Ser Gln Val Tyr Ile Leu Val Ser Glu Gln Pro
210 215 220

Leu His Tyr Ser Asn Pro Ser Phe Leu Thr Phe Leu Gln Ser Val Val
225 230 235 240

Gln Ala Gly Lys Thr Pro Leu Val Ile Leu Ala Glu Ala Phe Asp Lys
245 250 255

Glu Leu Leu Ala Met Leu Glu Met Asn Gln Ile Glu Arg Val Phe Pro
260 265 270

Val Cys Ala Val Lys Val Ser Gly Lys His Ala Arg Glu Ser Leu Glu
275 280 285

Asp Ile Ala Val Leu Thr Gly Ala Thr Leu Leu Ser Glu Met Asp Phe
290 295 300

Glu Asp Ser Glu Glu Glu Arg Ile Thr Asn Arg Leu Gly Phe Val Ala
305 310 315 320

Gly Ile Cys Val Ser Ser Thr Ser Leu Cys Val Pro Arg Glu Thr Asp
325 330 335

Asn Lys Gln Arg Met Ala Glu His Cys Ala Phe Leu Gln Asp Lys Leu
340 345 350

Ser Phe Ser Ser Gln Glu Glu Glu Ala Ser Ala Arg Leu Arg Arg Leu
355 360 365

Ala Arg Leu Ser Ser Gly Glu Val Cys Ile His Ile Ala Ala Asp Cys
370 375 380

Ile Pro Gln Glu Glu Ile Gly Tyr Ile Thr Ser Ser Ile Arg Ala Met
385 390 395 400

Thr Glu Ser Leu Arg Ser Gly Cys Leu Pro Gly Gly Gly Cys Ala Phe
 405 410 415
 Ile Arg Ala Ala Arg Glu Ile Ser Val Pro Leu Ala Leu Ser Pro Ser
 420 425 430
 Glu Arg Phe Gly Phe Leu Ala Val Leu Ser Ala Ala Glu Lys Pro Phe
 435 440 445
 Arg Ala Ile Val Thr Arg Ser Arg Arg Val Glu Glu Glu Val Phe Ser
 450 455 460
 Glu Val Phe Ser Gln Ala Asp Trp Arg Val Gly Phe Asn Gly Val Ser
 465 470 475 480
 Gly Phe Val Glu Asp Ile Val Ser Gln Gly Ile Cys Asp Gly Ala Ser
 485 490 495
 Cys Ile Gln Tyr Ala Leu Ser His Ala Val Gly Thr Thr Gly Leu Leu
 500 505 510
 Leu Thr Ser Ala Leu Phe Ile Ala Ser Gln Glu Pro Met Leu Arg Glu
 515 520 525
 Glu Asn Ser Glu Glu
 530

<210> 439

<211> 465

<212> PRT

<213> Chlamydia trachomatis serovar D

<400> 439

Met Asn Glu Ala Phe Asp Cys Val Val Ile Gly Ala Gly Pro Gly Gly
 5 10 15
 Tyr Val Ala Ala Ile Thr Ala Ala Gln Ala Gly Leu Lys Thr Ala Leu
 20 25 30
 Ile Glu Lys Arg Glu Ala Gly Gly Thr Cys Leu Asn Arg Gly Cys Ile
 35 40 45
 Pro Ser Lys Ala Leu Leu Ala Gly Ala Glu Val Val Thr Gln Ile Arg
 50 55 60
 His Ala Asp Gln Phe Gly Ile His Val Glu Gly Phe Ser Ile Asn Tyr
 65 70 75 80
 Pro Ala Met Val Gln Arg Lys Asp Ser Val Val Arg Ser Ile Arg Asp
 85 90 95
 Gly Leu Asn Gly Leu Ile Arg Ser Asn Lys Ile Thr Val Phe Ser Gly
 100 105 110
 Arg Gly Ser Leu Ile Ser Ser Thr Glu Val Lys Ile Leu Gly Glu Asn
 115 120 125
 Pro Ser Val Ile Lys Ala His Ser Ile Ile Leu Ala Thr Gly Ser Glu
 130 135 140

Pro Arg Ala Phe Pro Gly Ile Pro Phe Ser Ala Glu Ser Pro Arg Ile
 145 150 155 160
 Leu Cys Ser Thr Gly Val Leu Asn Leu Lys Glu Ile Pro Gln Lys Met
 165 170 175
 Ala Ile Ile Gly Gly Gly Val Ile Gly Cys Glu Phe Ala Ser Leu Phe
 180 185 190
 His Thr Leu Gly Ser Glu Val Ser Val Ile Glu Ala Ser Ser Gln Ile
 195 200 205
 Leu Ala Leu Asn Asn Pro Asp Ile Ser Lys Thr Met Phe Asp Lys Phe
 210 215 220
 Thr Arg Gln Gly Leu Arg Phe Val Leu Glu Ala Ser Val Ser Asn Ile
 225 230 235 240
 Glu Asp Ile Gly Asp Arg Val Arg Leu Thr Ile Asn Gly Asn Val Glu
 245 250 255
 Glu Tyr Asp Tyr Val Leu Val Ser Ile Gly Arg Arg Leu Asn Thr Glu
 260 265 270
 Asn Ile Gly Leu Asp Lys Ala Gly Val Ile Cys Asp Glu Arg Gly Val
 275 280 285
 Ile Pro Thr Asp Ala Thr Met Arg Thr Asn Val Pro Asn Ile Tyr Ala
 290 295 300
 Ile Gly Asp Ile Thr Gly Lys Trp Gln Leu Ala His Val Ala Ser His
 305 310 315 320
 Gln Gly Ile Ile Ala Ala Arg Asn Ile Ala Gly His Lys Glu Glu Ile
 325 330 335
 Asp Tyr Ser Ala Val Pro Ser Val Ile Phe Thr Phe Pro Glu Val Ala
 340 345 350
 Ser Val Gly Leu Ser Pro Thr Ala Ala Gln Gln Gln Lys Ile Pro Val
 355 360 365
 Lys Val Thr Lys Phe Pro Phe Arg Ala Ile Gly Lys Ala Val Ala Met
 370 375 380
 Gly Glu Ala Asp Gly Phe Ala Ala Ile Ile Ser His Glu Thr Thr Gln
 385 390 395 400
 Gln Ile Leu Gly Ala Tyr Val Ile Gly Pro His Ala Ser Ser Leu Ile
 405 410 415
 Ser Glu Ile Thr Leu Ala Val Arg Asn Glu Leu Thr Leu Pro Cys Ile
 420 425 430
 Tyr Glu Thr Ile His Ala His Pro Thr Leu Ala Glu Val Trp Ala Glu
 435 440 445
 Ser Ala Leu Leu Ala Val Asp Thr Pro Leu His Met Pro Pro Ala Lys
 450 455 460

Lys

465

<210> 440

$\langle 211 \rangle$ 122

<212> PRT

<213> Chlamydia trachomatis serovar D

 $\langle 400 \rangle$ 440

Met Pro Arg Ile Ile Gly Ile Asp Ile Pro Ala Lys Lys Lys Leu Lys

Ile Ser Leu Thr Tyr Ile Tyr Gly Ile Gly Pro Ala Leu Ser Lys Glu
20 25 30

Ile Ile Ala Arg Leu Gln Leu Asn Pro Glu Ala Arg Ala Ala Glu Leu
35 40 45

Thr Glu Glu Glu Val Gly Arg Leu Asn Ala Leu Leu Gln Ser Asp Tyr
50 55 60

Val Val Glu Gly Asp Leu Arg Arg Arg Val Gln Ser Asp Ile Lys Arg
65 70 75 80

Leu Ile Thr Ile His Ala Tyr Arg Gly Gln Arg His Arg Leu Ser Leu
85 90 95

Pro Val Arg Gly Gln Arg Thr Lys Thr Asn Ser Arg Thr Arg Lys Gly
100 105 110

Lys Arg Lys Thr Val Ala Gly Lys Lys Lys
115 120

<210> 441

<211> 553

<212> PRT

<213> Chlamydia trachomatis serovar D

<400> 441

Met Arg Ile Gly Asp Pro Met Asn Lys Leu Ile Arg Arg Ala Val Thr
5 10 15

Ile Phe Ala Val Thr Ser Val Ala Ser Leu Phe Ala Ser Gly Val Leu
20 25 30

Glu Thr Ser Met Ala Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala
35 40 45

Asp Thr Lys Ala Lys Asp Asn Thr Ser His Lys Ser Lys Lys Ala Arg
50 55 60

Lys Asn His Ser Lys Glu Thr Pro Val Asp Arg Lys Glu Val Ala Pro
65 70 75 80

Val His Glu Ser Lys Ala Thr Gly Pro Lys Gln Asp Ser Cys Phe Gly
85 90 95

Arg Met Tyr Thr Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile Thr
100 105 110

Gln Ala Val Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile Glu
 115 120 125
 Ile Thr Ala Thr Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln
 130 135 140
 Gln Leu Pro Cys Glu Ala Glu Phe Val Arg Ser Asp Pro Ala Thr Thr
 145 150 155 160
 Pro Thr Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln
 165 170 175
 Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly
 180 185 190
 Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg Ser
 195 200 205
 Val Thr Lys Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly Pro
 210 215 220
 Glu Asn Ala Cys Leu Arg Cys Pro Val Val Tyr Lys Ile Asn Ile Val
 225 230 235 240
 Asn Gln Gly Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro Val
 245 250 255
 Pro Asp Gly Tyr Ala His Ser Ser Gly Gln Arg Val Leu Thr Phe Thr
 260 265 270
 Leu Gly Asp Met Gln Pro Gly Glu His Arg Thr Ile Thr Val Glu Phe
 275 280 285
 Cys Pro Leu Lys Arg Gly Arg Ala Thr Asn Ile Ala Thr Val Ser Tyr
 290 295 300
 Cys Gly Gly His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn Glu
 305 310 315 320
 Pro Cys Val Gln Val Ser Ile Ala Gly Ala Asp Trp Ser Tyr Val Cys
 325 330 335
 Lys Pro Val Glu Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu Val
 340 345 350
 Leu Arg Asp Val Val Val Glu Asp Thr Leu Ser Pro Gly Val Thr Val
 355 360 365
 Leu Glu Ala Ala Gly Ala Gln Ile Ser Cys Asn Lys Val Val Trp Thr
 370 375 380
 Val Lys Glu Leu Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu Val
 385 390 395 400
 Arg Ala Gln Thr Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys Ser
 405 410 415
 Cys Ser Asp Cys Gly Thr Cys Thr Ser Cys Ala Glu Ala Thr Thr Tyr
 420 425 430
 Trp Lys Gly Val Ala Ala Thr His Met Cys Val Val Asp Thr Cys Asp

435 440 445
 Pro Val Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr Asn
 450 455 460
 Arg Gly Ser Ala Glu Asp Thr Asn Val Ser Leu Met Leu Lys Phe Ser
 465 470 475 480
 Lys Glu Leu Gln Pro Val Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile
 485 490 495
 Thr Gly Asn Thr Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys
 500 505 510
 Glu Thr Val Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly Asp
 515 520 525
 Ala Arg Gly Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro Val
 530 535 540
 Ser Asp Thr Glu Asn Thr His Ile Tyr
 545 550

 <210> 442
 <211> 192
 <212> PRT
 <213> Chlamydia trachomatis serovar D

 <400> 442
 Met Pro Glu Gly Glu Met Met His Lys Leu Gln Asp Val Ile Asp Arg
 5 10 15
 Lys Leu Leu Asp Ser Arg Arg Ile Phe Phe Ser Glu Pro Val Thr Glu
 20 25 30
 Lys Ser Ala Thr Glu Ala Ile Lys Lys Leu Trp Tyr Leu Glu Leu Thr
 35 40 45
 Asn Pro Gly Gln Pro Ile Val Phe Val Ile Asn Ser Pro Gly Gly Ser
 50 55 60
 Val Asp Ala Gly Phe Ala Val Trp Asp Gln Ile Lys Met Ile Ser Ser
 65 70 75 80
 Pro Leu Thr Thr Val Val Thr Gly Leu Ala Ala Ser Met Gly Ser Val
 85 90 95
 Leu Ser Leu Cys Ala Val Pro Gly Arg Arg Phe Ala Thr Pro His Ala
 100 105 110
 Arg Ile Met Ile His Gln Pro Ser Ile Gly Gly Thr Ile Thr Gly Gln
 115 120 125
 Ala Thr Asp Leu Asp Ile His Ala Arg Glu Ile Leu Lys Thr Lys Ala
 130 135 140
 Arg Ile Ile Asp Val Tyr Val Glu Ala Thr Gly Gln Ser Arg Glu Val
 145 150 155 160
 Ile Glu Lys Ala Ile Asp Arg Asp Met Trp Met Ser Ala Asn Glu Ala

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                                165                170                175
Met Glu Phe Gly Leu Leu Asp Gly Ile Leu Phe Ser Phe Asn Asp Leu
      180                185                190

<210> 443
<211> 275
<212> FRT
<213> Chlamydia trachomatis serovar D

<400> 443
Met Gly Phe Ser Ser Leu Leu Thr Thr Cys Arg Tyr Leu Leu Tyr Ser
      5                                10                15

Gly Ala Gly Asn Ser Phe Ile Leu Gly Glu Ser Met Pro Ser Leu Glu
      20                25                30

Asp Val Leu Phe Leu Cys Gln Glu Glu Met Val Asp Gly Phe Leu Cys
      35                40                45

Val Glu Ser Ser Glu Ile Ala Asp Ala Lys Leu Thr Val Phe Asn Ser
      50                55                60

Asp Gly Ser Ile Ala Ser Met Cys Gly Asn Gly Leu Arg Cys Ala Met
      65                70                75                80

Ala His Val Ala Gln Cys Phe Gly Leu Glu Asp Val Ser Ile Glu Thr
      85                90                95

Glu Arg Gly Val Tyr Gln Gly Lys Phe Phe Ser Met Asn Arg Val Leu
      100                105                110

Val Asp Met Thr Leu Pro Asp Trp Lys Lys Ala Glu Arg Lys Leu Thr
      115                120                125

His Val Leu Pro Gly Met Pro Glu Gln Val Phe Phe Ile Asp Thr Gly
      130                135                140

Val Pro His Val Val Val Phe Val Ser Asp Leu Ser Lys Val Pro Val
      145                150                155                160

Gln Glu Trp Gly Ser Phe Leu Arg Tyr His Glu Asp Phe Ala Pro Glu
      165                170                175

Gly Val Asn Val Asp Phe Val Gln Arg Lys Lys Asp Asp Leu Leu Leu
      180                185                190

Val Tyr Thr Tyr Glu Arg Gly Cys Glu Arg Glu Thr Leu Ser Cys Gly
      195                200                205

Thr Gly Met Leu Ala Ser Ala Leu Val Ala Ala Asp Ile Phe Ser Leu
      210                215                220

Gly Gln Asp Phe Ser Ile Ala Val Cys Ser Arg Ser Arg Asn Leu Ile
      225                230                235                240

Lys Ile Phe Ser Glu Lys Gly Lys Val Phe Leu Glu Gly Pro Val Ser
      245                250                255

Leu Leu Asn Arg Ser Glu Asn Phe Gly Trp Leu Glu Pro Lys Ser Arg

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260 265 270

Arg Phe Gly
275

<210> 444
<211> 1770
<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 444

Met Lys Phe Met Ser Ala Thr Ala Val Phe Ala Ala Ala Leu Ser Ser
5 10 15

Val Thr Glu Ala Ser Ser Ile Gln Asp Gln Ile Lys Asn Thr Asp Cys
20 25 30

Asn Val Ser Lys Leu Gly Tyr Ser Thr Ser Gln Ala Phe Thr Asp Met
35 40 45

Met Leu Ala Asp Asn Thr Glu Tyr Arg Ala Ala Asp Ser Val Ser Phe
50 55 60

Tyr Asp Phe Ser Thr Ser Ser Arg Leu Pro Arg Lys His Leu Ser Ser
65 70 75 80

Ser Ser Glu Ala Ser Pro Thr Thr Glu Gly Val Ser Ser Ser Ser Ser
85 90 95

Gly Glu Thr Asp Glu Lys Thr Glu Glu Glu Leu Asp Asn Gly Gly Ile
100 105 110

Ile Tyr Ala Arg Glu Lys Leu Thr Ile Ser Glu Ser Gln Asp Ser Leu
115 120 125

Ser Asn Gln Ser Ile Glu Leu His Asp Asn Ser Ile Phe Phe Gly Glu
130 135 140

Gly Glu Val Ile Phe Asp His Arg Val Ala Leu Lys Asn Gly Gly Ala
145 150 155 160

Ile Tyr Gly Glu Lys Glu Val Val Phe Glu Asn Ile Lys Ser Leu Leu
165 170 175

Val Glu Val Asn Ile Ala Val Glu Lys Gly Gly Ser Val Tyr Ala Lys
180 185 190

Glu Arg Val Ser Leu Glu Asn Val Thr Glu Ala Thr Phe Ser Ser Asn
195 200 205

Gly Gly Glu Gln Gly Gly Gly Ile Tyr Ser Glu Gln Asp Met Leu
210 215 220

Ile Ser Asp Cys Asn Asn Val His Phe Gln Gly Asn Ala Ala Gly Ala
225 230 235 240

Thr Ala Val Lys Gln Cys Leu Asp Glu Glu Met Ile Val Leu Leu Ala
245 250 255

Glu Cys Val Asp Ser Leu Ser Glu Asp Thr Leu Asp Ser Thr Pro Glu

260										265					270				
Thr	Glu	Gln	Thr	Glu	Ser	Asn	Gly	Asn	Gln	Asp	Gly	Ser	Ser	Glu	Thr				
275										280					285				
Glu	Asp	Thr	Gln	Val	Ser	Glu	Ser	Pro	Glu	Ser	Thr	Pro	Ser	Pro	Asp				
290										295					300				
Asp	Val	Leu	Gly	Lys	Gly	Gly	Gly	Ile	Tyr	Thr	Glu	Lys	Ser	Leu	Thr				
305										310					315				
Ile	Thr	Gly	Ile	Thr	Gly	Thr	Ile	Asp	Phe	Val	Ser	Asn	Ile	Ala	Thr				
320										325					330				
Asp	Ser	Gly	Ala	Gly	Val	Phe	Thr	Lys	Glu	Asn	Leu	Ser	Cys	Thr	Asn				
335										340					345				
Thr	Asn	Ser	Leu	Gln	Phe	Leu	Lys	Asn	Ser	Ala	Gly	Gln	His	Gly	Gly				
350										355					360				
Gly	Ala	Tyr	Val	Thr	Gln	Thr	Met	Ser	Val	Thr	Asn	Thr	Thr	Ser	Glu				
365										370					375				
Ser	Ile	Thr	Thr	Pro	Pro	Leu	Ile	Gly	Glu	Val	Ile	Phe	Ser	Glu	Asn				
380										385					390				
Thr	Ala	Lys	Gly	His	Gly	Gly	Gly	Ile	Cys	Thr	Asn	Lys	Leu	Ser	Leu				
395										400					405				
Ser	Asn	Leu	Lys	Thr	Val	Thr	Leu	Thr	Lys	Asn	Ser	Ala	Lys	Glu	Ser				
410										415					420				
Gly	Gly	Ala	Ile	Phe	Thr	Asp	Leu	Ala	Ser	Ile	Pro	Ile	Thr	Asp	Thr				
425										430					435				
Pro	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Ser	Ser	Pro	Ala	Ser	Thr	Pro	Glu				
440										445					450				
Val	Val	Ala	Ser	Ala	Lys	Ile	Asn	Arg	Phe	Phe	Ala	Ser	Thr	Ala	Lys				
455										460					465				
Pro	Ala	Ala	Pro	Ser	Leu	Thr	Glu	Ala	Glu	Ser	Asp	Gln	Thr	Asp	Gln				
470										475					480				
Thr	Glu	Thr	Ser	Asp	Thr	Asn	Ser	Asp	Ile	Asp	Val	Ser	Ile	Glu	Asn				
485										490					495				
Ile	Leu	Asn	Val	Ala	Ile	Asn	Gln	Asn	Thr	Ser	Ala	Lys	Lys	Gly	Gly				
500										505					510				
Ala	Ile	Tyr	Gly	Lys	Lys	Ala	Lys	Leu	Ser	Arg	Ile	Asn	Asn	Leu	Glu				
515										520					525				
Leu	Ser	Gly	Asn	Ser	Ser	Gln	Asp	Val	Gly	Gly	Gly	Leu	Cys	Leu	Thr				
530										535					540				
Glu	Ser	Val	Glu	Phe	Asp	Ala	Ile	Gly	Ser	Leu	Leu	Ser	His	Tyr	Asn				
545										550					555				
Ser	Ala	Ala	Lys	Glu	Gly	Gly	Ala	Ile	His	Ser	Lys	Thr	Val	Thr	Leu				
560										565					570				
575										580					585				

Ser Asn Leu Lys Ser Thr Phe Thr Phe Ala Asp Asn Thr Val Lys Ala
 595 600 605
 Ile Val Glu Ser Thr Pro Glu Ala Pro Glu Glu Ile Pro Pro Val Glu
 610 615 620
 Gly Glu Glu Ser Thr Ala Thr Glu Asp Pro Asn Ser Asn Thr Glu Gly
 625 630 635 640
 Ser Ser Ala Asn Thr Asn Leu Glu Gly Ser Gln Gly Asp Thr Ala Asp
 645 650 655
 Thr Gly Thr Gly Asp Val Asn Asn Glu Ser Gln Asp Thr Ser Asp Thr
 660 665 670
 Gly Asn Ala Glu Ser Glu Glu Gln Leu Gln Asp Ser Thr Gln Ser Asn
 675 680 685
 Glu Glu Asn Thr Leu Pro Asn Ser Asn Ile Asp Gln Ser Asn Glu Asn
 690 695 700
 Thr Asp Glu Ser Ser Asp Ser His Thr Glu Glu Ile Thr Asp Glu Ser
 705 710 715 720
 Val Ser Ser Ser Ser Glu Ser Gly Ser Ser Thr Pro Gln Asp Gly Gly
 725 730 735
 Ala Ala Ser Ser Gly Ala Pro Ser Gly Asp Gln Ser Ile Ser Ala Asn
 740 745 750
 Ala Cys Leu Ala Lys Ser Tyr Ala Ala Ser Thr Asp Ser Ser Pro Val
 755 760 765
 Ser Asn Ser Ser Gly Ser Glu Glu Pro Val Thr Ser Ser Ser Asp Ser
 770 775 780
 Asp Val Thr Ala Ser Ser Asp Asn Pro Asp Ser Ser Ser Ser Gly Asp
 785 790 795 800
 Ser Ala Gly Asp Ser Glu Glu Pro Thr Glu Pro Glu Ala Gly Ser Thr
 805 810 815
 Thr Glu Thr Leu Thr Leu Ile Gly Gly Gly Ala Ile Tyr Gly Glu Thr
 820 825 830
 Val Lys Ile Glu Asn Phe Ser Gly Gln Gly Ile Phe Ser Gly Asn Lys
 835 840 845
 Ala Ile Asp Asn Thr Thr Glu Gly Ser Ser Ser Lys Ser Asp Val Leu
 850 855 860
 Gly Gly Ala Val Tyr Ala Lys Thr Leu Phe Asn Leu Asp Ser Gly Ser
 865 870 875 880
 Ser Arg Arg Thr Val Thr Phe Ser Gly Asn Thr Val Ser Ser Gln Ser
 885 890 895
 Thr Thr Gly Gln Val Ala Gly Gly Ala Ile Tyr Ser Pro Thr Val Thr
 900 905 910

Ile Ala Thr Pro Val Val Phe Ser Lys Asn Ser Ala Thr Asn Asn Ala
 915 920 925
 Asn Asn Thr Thr Asp Thr Gln Arg Lys Asp Thr Phe Gly Gly Ala Ile
 930 935 940
 Gly Ala Thr Ser Ala Val Ser Leu Ser Gly Gly Ala His Phe Leu Glu
 945 950 955 960
 Asn Val Ala Asp Leu Gly Ser Ala Ile Gly Leu Val Pro Gly Thr Gln
 965 970 975
 Asn Thr Glu Thr Val Lys Leu Glu Ser Gly Ser Tyr Tyr Phe Glu Lys
 980 985 990
 Asn Lys Ala Leu Lys Arg Ala Thr Ile Tyr Ala Pro Val Val Ser Ile
 995 1000 1005
 Lys Ala Tyr Thr Ala Thr Phe Asn Gln Asn Arg Ser Leu Glu Glu Gly
 1010 1015 1020
 Ser Ala Ile Tyr Phe Thr Lys Glu Ala Ser Ile Glu Ser Leu Gly Ser
 1025 1030 1035 1040
 Val Leu Phe Thr Gly Asn Leu Val Thr Leu Thr Leu Ser Thr Thr Thr
 1045 1050 1055
 Glu Gly Thr Pro Ala Thr Thr Ser Gly Asp Val Thr Lys Tyr Gly Ala
 1060 1065 1070
 Ala Ile Phe Gly Gln Ile Ala Ser Ser Asn Gly Ser Gln Thr Asp Asn
 1075 1080 1085
 Leu Pro Leu Lys Leu Ile Ala Ser Gly Gly Asn Ile Cys Phe Arg Asn
 1090 1095 1100
 Asn Glu Tyr Arg Pro Thr Ser Ser Asp Thr Gly Thr Ser Thr Phe Cys
 1105 1110 1115 1120
 Ser Ile Ala Gly Asp Val Lys Leu Thr Met Gln Ala Ala Lys Gly Lys
 1125 1130 1135
 Thr Ile Ser Phe Phe Asp Ala Ile Arg Thr Ser Thr Lys Lys Thr Gly
 1140 1145 1150
 Thr Gln Ala Thr Ala Tyr Asp Thr Leu Asp Ile Asn Lys Ser Glu Asp
 1155 1160 1165
 Ser Glu Thr Val Asn Ser Ala Phe Thr Gly Thr Ile Leu Phe Ser Ser
 1170 1175 1180
 Glu Leu His Glu Asn Lys Ser Tyr Ile Pro Gln Asn Val Val Leu His
 1185 1190 1195 1200
 Ser Gly Ser Leu Val Leu Lys Pro Asn Thr Glu Leu His Val Ile Ser
 1205 1210 1215
 Phe Glu Gln Lys Glu Gly Ser Ser Leu Val Met Thr Pro Gly Ser Val
 1220 1225 1230
 Leu Ser Asn Gln Thr Val Ala Asp Gly Ala Leu Val Ile Asn Asn Met

1235	1240	1245
Thr Ile Asp Leu Ser Ser Val Glu Lys Asn Gly Ile Ala Glu Gly Asn 1250 1255 1260		
Ile Phe Thr Pro Pro Glu Leu Arg Ile Ile Asp Thr Thr Thr Gly Gly 1265 1270 1275 1280		
Ser Gly Gly Thr Pro Ser Thr Asp Ser Glu Ser Asn Gln Asn Ser Asp 1285 1290 1295		
Asp Thr Glu Glu Gln Asn Asn Asn Asp Ala Ser Asn Gln Gly Glu Ser 1300 1305 1310		
Ala Asn Gly Ser Ser Ser Pro Ala Val Ala Ala Ala His Thr Ser Arg 1315 1320 1325		
Thr Arg Asn Phe Ala Ala Ala Ala Thr Ala Thr Pro Thr Thr Thr Pro 1330 1335 1340		
Thr Ala Thr Thr Thr Thr Ser Asn Gln Val Ile Leu Gly Gly Glu Ile 1345 1350 1355 1360		
Lys Leu Ile Asp Pro Asn Gly Thr Phe Phe Gln Asn Pro Ala Leu Arg 1365 1370 1375		
Ser Asp Gln Gln Ile Ser Leu Leu Val Leu Pro Thr Asp Ser Ser Lys 1380 1385 1390		
Met Gln Ala Gln Lys Ile Val Leu Thr Gly Asp Ile Ala Pro Gln Lys 1395 1400 1405		
Gly Tyr Thr Gly Thr Leu Thr Leu Asp Pro Asp Gln Leu Asn Gly 1410 1415 1420		
Thr Ile Ser Val Leu Trp Lys Phe Asp Ser Tyr Arg Gln Trp Ala Tyr 1425 1430 1435 1440		
Val Pro Arg Asp Asn His Phe Tyr Ala Asn Ser Ile Leu Gly Ser Gln 1445 1450 1455		
Met Leu Met Val Thr Val Lys Gln Gly Leu Leu Asn Asp Lys Met Asn 1460 1465 1470		
Leu Ala Arg Phe Glu Glu Val Ser Tyr Asn Asn Leu Trp Ile Ser Gly 1475 1480 1485		
Leu Gly Thr Met Leu Ser Gln Val Gly Thr Pro Thr Ser Glu Glu Phe 1490 1495 1500		
Thr Tyr Tyr Ser Arg Gly Ala Ser Val Ala Leu Asp Ala Lys Pro Ala 1505 1510 1515 1520		
His Asp Val Ile Val Gly Ala Ala Phe Ser Lys Met Ile Gly Lys Thr 1525 1530 1535		
Lys Ser Leu Lys Arg Glu Asn Asn Tyr Thr His Lys Gly Ser Glu Tyr 1540 1545 1550		
Ser Tyr Gln Ala Ser Val Tyr Gly Gly Lys Pro Phe His Phe Val Ile 1555 1560 1565		

Asn Lys Lys Thr Glu Lys Ser Leu Pro Leu Leu Leu Gln Gly Val Ile
 1570 1575 1580
 Ser Tyr Gly Tyr Ile Lys His Asp Thr Val Thr His Tyr Pro Thr Ile
 1585 1590 1595 1600
 Arg Glu Arg Asn Lys Gly Glu Trp Glu Asp Leu Gly Trp Leu Thr Ala
 1605 1610 1615
 Leu Arg Val Ser Ser Val Leu Arg Thr Pro Ala Gln Gly Asp Thr Lys
 1620 1625 1630
 Arg Ile Thr Val Tyr Gly Glu Leu Glu Tyr Ser Ser Ile Arg Gln Lys
 1635 1640 1645
 Gln Phe Thr Glu Thr Glu Tyr Asp Pro Arg Tyr Phe Asp Asn Cys Thr
 1650 1655 1660
 Tyr Arg Asn Leu Ala Ile Pro Met Gly Leu Ala Phe Glu Gly Glu Leu
 1665 1670 1675 1680
 Ser Gly Asn Asp Ile Leu Met Tyr Asn Arg Phe Ser Val Ala Tyr Met
 1685 1690 1695
 Leu Ser Ile Tyr Arg Asn Ser Pro Thr Cys Lys Tyr Gln Val Leu Ser
 1700 1705 1710
 Ser Gly Glu Gly Glu Ile Ile Cys Gly Val Pro Thr Arg Asn Ser
 1715 1720 1725
 Ala Arg Gly Glu Tyr Ser Thr Gln Leu Tyr Leu Gly Pro Leu Trp Thr
 1730 1735 1740
 Leu Tyr Gly Ser Tyr Thr Ile Glu Ala Asp Ala His Thr Leu Ala His
 1745 1750 1755 1760
 Met Met Asn Cys Gly Ala Arg Met Thr Phe
 1765 1770

<210> 445
 <211> 1751
 <212> PRT
 <213> Chlamydia trachomatis serovar D

<400> 445
 Met Lys Trp Leu Ser Ala Thr Ala Val Phe Ala Ala Val Leu Pro Ser
 5 10 15
 Val Ser Gly Phe Cys Phe Pro Glu Pro Lys Glu Leu Asn Phe Ser Arg
 20 25 30
 Val Gly Thr Ser Ser Ser Thr Thr Phe Thr Glu Thr Val Gly Glu Ala
 35 40 45
 Gly Ala Glu Tyr Ile Val Ser Gly Asn Ala Ser Phe Thr Lys Phe Thr
 50 55 60
 Asn Ile Pro Thr Thr Asp Thr Thr Thr Pro Thr Asn Ser Asn Ser Ser
 65 70 75 80

Ser Ser Asn Gly Glu Thr Ala Ser Val Ser Glu Asp Ser Asp Ser Thr
 85 90 95
 Thr Thr Thr Pro Asp Pro Lys Gly Gly Ala Phe Tyr Asn Ala His
 100 105 110
 Ser Gly Val Leu Ser Phe Met Thr Arg Ser Gly Thr Glu Gly Ser Leu
 115 120 125
 Thr Leu Ser Glu Ile Lys Ile Thr Gly Glu Gly Ala Ile Phe Ser
 130 135 140
 Gln Gly Glu Leu Leu Phe Thr Asp Leu Thr Gly Leu Thr Ile Gln Asn
 145 150 155 160
 Asn Leu Ser Gln Leu Ser Gly Gly Ala Ile Phe Gly Glu Ser Thr Ile
 165 170 175
 Ser Leu Ser Gly Ile Thr Lys Ala Thr Phe Ser Ser Asn Ser Ala Glu
 180 185 190
 Val Pro Ala Pro Val Lys Lys Pro Thr Glu Pro Lys Ala Gln Thr Ala
 195 200 205
 Ser Glu Thr Ser Gly Ser Ser Ser Ser Ser Gly Asn Asp Ser Val Ser
 210 215 220
 Ser Pro Ser Ser Ser Arg Ala Glu Pro Ala Ala Asn Leu Gln Ser
 225 230 235 240
 His Phe Ile Cys Ala Thr Ala Thr Pro Ala Ala Gln Thr Asp Thr Glu
 245 250 255
 Thr Ser Thr Pro Ser His Lys Pro Gly Ser Gly Gly Ala Ile Tyr Ala
 260 265 270
 Lys Gly Asp Leu Thr Ile Ala Asp Ser Gln Glu Val Leu Phe Ser Ile
 275 280 285
 Asn Lys Ala Thr Lys Asp Gly Gly Ala Ile Phe Ala Glu Lys Asp Val
 290 295 300
 Ser Phe Glu Asn Ile Thr Ser Leu Lys Val Gln Thr Asn Gly Ala Glu
 305 310 315 320
 Glu Lys Gly Gly Ala Ile Tyr Ala Lys Gly Asp Leu Ser Ile Gln Ser
 325 330 335
 Ser Lys Gln Ser Leu Phe Asn Ser Asn Tyr Ser Lys Gln Gly Gly Gly
 340 345 350
 Ala Leu Tyr Val Glu Gly Asp Ile Asn Phe Gln Asp Leu Glu Glu Ile
 355 360 365
 Arg Ile Lys Tyr Asn Lys Ala Gly Thr Phe Glu Thr Lys Lys Ile Thr
 370 375 380
 Leu Pro Lys Ala Gln Ala Ser Ala Gly Asn Ala Asp Ala Trp Ala Ser
 385 390 395 400

Ser Ser Pro Gln Ser Gly Ser Gly Ala Thr Thr Val Ser Asn Ser Gly
 405 410 415
 Asp Ser Ser Ser Gly Ser Asp Ser Asp Thr Ser Glu Thr Val Pro Ala
 420 425 430
 Thr Ala Lys Gly Gly Gly Leu Tyr Thr Asp Lys Asn Leu Ser Ile Thr
 435 440 445
 Asn Ile Thr Gly Ile Ile Glu Ile Ala Asn Asn Lys Ala Thr Asp Val
 450 455 460
 Gly Gly Gly Ala Tyr Val Lys Gly Thr Leu Thr Cys Glu Asn Ser His
 465 470 475 480
 Arg Leu Gln Phe Leu Lys Asn Ser Ser Asp Lys Gln Gly Gly Gly Ile
 485 490 495
 Tyr Gly Glu Asp Asn Ile Thr Leu Ser Asn Leu Thr Gly Lys Thr Leu
 500 505 510
 Phe Gln Glu Asn Thr Ala Lys Glu Glu Gly Gly Gly Leu Phe Ile Lys
 515 520 525
 Gly Thr Asp Lys Ala Leu Thr Met Thr Gly Leu Asp Ser Phe Cys Leu
 530 535 540
 Ile Asn Asn Thr Ser Glu Lys His Gly Gly Gly Ala Phe Val Thr Lys
 545 550 555 560
 Glu Ile Ser Gln Thr Tyr Thr Ser Asp Val Glu Thr Ile Pro Gly Ile
 565 570 575
 Thr Pro Val His Gly Glu Thr Val Ile Thr Gly Asn Lys Ser Thr Gly
 580 585 590
 Gly Asn Gly Gly Gly Val Cys Thr Lys Arg Leu Ala Leu Ser Asn Leu
 595 600 605
 Gln Ser Ile Ser Ile Ser Gly Asn Ser Ala Ala Glu Asn Gly Gly Gly
 610 615 620
 Ala His Thr Cys Pro Asp Ser Phe Pro Thr Ala Asp Thr Ala Glu Gln
 625 630 635 640
 Pro Ala Ala Ala Ser Ala Ala Thr Ser Thr Pro Glu Ser Ala Pro Val
 645 650 655
 Val Ser Thr Ala Leu Ser Thr Pro Ser Ser Thr Val Ser Ser Leu
 660 665 670
 Thr Leu Leu Ala Ala Ser Ser Gln Ala Ser Pro Ala Thr Ser Asn Lys
 675 680 685
 Glu Thr Gln Asp Pro Asn Ala Asp Thr Asp Leu Leu Ile Asp Tyr Val
 690 695 700
 Val Asp Thr Thr Ile Ser Lys Asn Thr Ala Lys Lys Gly Gly Gly Ile
 705 710 715 720
 Tyr Ala Lys Lys Ala Lys Met Ser Arg Ile Asp Gln Leu Asn Ile Ser

725										730					735				
Glu	Asn	Ser	Ala	Thr	Glu	Ile	Gly	Gly	Gly	Ile	Cys	Cys	Lys	Glu	Ser				
			740				745						750						
Leu	Glu	Leu	Asp	Ala	Leu	Val	Ser	Leu	Ser	Val	Thr	Glu	Asn	Leu	Val				
			755				760						765						
Gly	Lys	Glu	Gly	Gly	Gly	Leu	His	Ala	Lys	Thr	Val	Asn	Ile	Ser	Asn				
			770				775						780						
Leu	Lys	Ser	Gly	Phe	Ser	Phe	Ser	Asn	Asn	Lys	Ala	Asn	Ser	Ser	Ser				
			785				790						795			800			
Thr	Gly	Val	Ala	Thr	Thr	Ala	Ser	Ala	Pro	Ala	Ala	Ala	Ala	Ala	Ser				
			805				810						815						
Leu	Gln	Ala	Ala	Ala	Ala	Ala	Val	Pro	Ser	Ser	Pro	Ala	Thr	Pro	Thr				
			820				825						830						
Tyr	Ser	Gly	Val	Val	Gly	Gly	Ala	Ile	Tyr	Gly	Glu	Lys	Val	Thr	Phe				
			835				840						845						
Ser	Gln	Cys	Ser	Gly	Thr	Cys	Gln	Phe	Ser	Gly	Asn	Gln	Ala	Ile	Asp				
			850				855						860						
Asn	Asn	Pro	Ser	Gln	Ser	Ser	Leu	Asn	Val	Gln	Gly	Gly	Ala	Ile	Tyr				
			865				870						875			880			
Ala	Lys	Thr	Ser	Leu	Ser	Ile	Gly	Ser	Ser	Asp	Ala	Gly	Thr	Ser	Tyr				
			885				890						895						
Ile	Phe	Ser	Gly	Asn	Ser	Val	Ser	Thr	Gly	Lys	Ser	Gln	Thr	Thr	Gly				
			900				905						910						
Gln	Ile	Ala	Gly	Gly	Ala	Ile	Tyr	Ser	Pro	Thr	Val	Thr	Leu	Asn	Cys				
			915				920						925						
Pro	Ala	Thr	Phe	Ser	Asn	Asn	Thr	Ala	Ser	Met	Ala	Thr	Pro	Lys	Thr				
			930				935						940						
Ser	Ser	Glu	Asp	Gly	Ser	Ser	Gly	Asn	Ser	Ile	Lys	Asp	Thr	Ile	Gly				
			945				950						955			960			
Gly	Ala	Ile	Ala	Gly	Thr	Ala	Ile	Thr	Leu	Ser	Gly	Val	Ser	Arg	Phe				
			965				970						975						
Ser	Gly	Asn	Thr	Ala	Asp	Leu	Gly	Ala	Ala	Ile	Gly	Thr	Leu	Ala	Asn				
			980				985						990						
Ala	Asn	Thr	Pro	Ser	Ala	Thr	Ser	Gly	Ser	Gln	Asn	Ser	Ile	Thr	Glu				
			995				1000						1005						
Lys	Ile	Thr	Leu	Glu	Asn	Gly	Ser	Phe	Ile	Phe	Glu	Arg	Asn	Gln	Ala				
			1010				1015						1020						
Asn	Lys	Arg	Gly	Ala	Ile	Tyr	Ser	Pro	Ser	Val	Ser	Ile	Lys	Gly	Asn				
			1025				1030						1035			1040			
Asn	Ile	Thr	Phe	Asn	Gln	Asn	Thr	Ser	Thr	His	Asp	Gly	Ser	Ala	Ile				
			1045				1050						1055						

Tyr Phe Thr Lys Asp Ala Thr Ile Glu Ser Leu Gly Ser Val Leu Phe
 1060 1065 1070
 Thr Gly Asn Asn Val Thr Ala Thr Gln Ala Ser Ser Ala Thr Ser Gly
 1075 1080 1085
 Gln Asn Thr Asn Thr Ala Asn Tyr Gly Ala Ala Ile Phe Gly Asp Pro
 1090 1095 1100
 Gly Thr Thr Gln Ser Ser Gln Thr Asp Ala Ile Leu Thr Leu Leu Ala
 1105 1110 1115 1120
 Ser Ser Gly Asn Ile Thr Phe Ser Asn Asn Ser Leu Gln Asn Asn Gln
 1125 1130 1135
 Gly Asp Thr Pro Ala Ser Lys Phe Cys Ser Ile Ala Gly Tyr Val Lys
 1140 1145 1150
 Leu Ser Leu Gln Ala Ala Lys Gly Lys Thr Ile Ser Phe Phe Asp Cys
 1155 1160 1165
 Val His Thr Ser Thr Lys Lys Ile Gly Ser Thr Gln Asn Val Tyr Glu
 1170 1175 1180
 Thr Leu Asp Ile Asn Lys Glu Glu Asn Ser Asn Pro Tyr Thr Gly Thr
 1185 1190 1195 1200
 Ile Val Phe Ser Ser Glu Leu His Glu Asn Lys Ser Tyr Ile Pro Gln
 1205 1210 1215
 Asn Ala Ile Leu His Asn Gly Thr Leu Val Leu Lys Glu Lys Thr Glu
 1220 1225 1230
 Leu His Val Val Ser Phe Glu Gln Lys Glu Gly Ser Lys Leu Ile Met
 1235 1240 1245
 Lys Pro Gly Ala Val Leu Ser Asn Gln Asn Ile Ala Asn Gly Ala Leu
 1250 1255 1260
 Val Ile Asn Gly Leu Thr Ile Asp Leu Ser Ser Met Gly Thr Pro Gln
 1265 1270 1275 1280
 Ala Gly Glu Ile Phe Ser Pro Pro Glu Leu Arg Ile Val Ala Thr Thr
 1285 1290 1295
 Ser Ser Ala Ser Gly Gly Ser Gly Val Ser Ser Ser Ile Pro Thr Asn
 1300 1305 1310
 Pro Lys Arg Ile Ser Ala Ala Ala Pro Ser Gly Ser Ala Ala Thr Thr
 1315 1320 1325
 Pro Thr Met Ser Glu Asn Lys Val Phe Leu Thr Gly Asp Leu Thr Leu
 1330 1335 1340
 Ile Asp Pro Asn Gly Asn Phe Tyr Gln Asn Pro Met Leu Gly Ser Asp
 1345 1350 1355 1360
 Leu Asp Val Pro Leu Ile Lys Leu Pro Thr Asn Thr Ser Asp Val Gln
 1365 1370 1375

Val Tyr Asp Leu Thr Leu Ser Gly Asp Leu Phe Pro Gln Lys Gly Tyr
 1380 1385 1390
 Met Gly Thr Trp Thr Leu Asp Ser Asn Pro Gln Thr Gly Lys Leu Gln
 1395 1400 1405
 Ala Arg Trp Thr Phe Asp Thr Tyr Arg Arg Trp Val Tyr Ile Pro Arg
 1410 1415 1420
 Asp Asn His Phe Tyr Ala Asn Ser Ile Leu Gly Ser Gln Asn Ser Met
 1425 1430 1435 1440
 Ile Val Val Lys Gln Gly Leu Ile Asn Asn Met Leu Asn Asn Ala Arg
 1445 1450 1455
 Phe Asp Asp Ile Ala Tyr Asn Asn Phe Trp Val Ser Gly Val Gly Thr
 1460 1465 1470
 Phe Leu Ala Gln Gln Gly Thr Pro Leu Ser Glu Glu Phe Ser Tyr Tyr
 1475 1480 1485
 Ser Arg Gly Thr Ser Val Ala Ile Asp Ala Lys Pro Arg Gln Asp Phe
 1490 1495 1500
 Ile Leu Gly Ala Ala Phe Ser Lys Met Val Gly Lys Thr Lys Ala Ile
 1505 1510 1515 1520
 Lys Lys Met His Asn Tyr Phe His Lys Gly Ser Glu Tyr Ser Tyr Gln
 1525 1530 1535
 Ala Ser Val Tyr Gly Gly Lys Phe Leu Tyr Phe Leu Leu Asn Lys Gln
 1540 1545 1550
 His Gly Trp Ala Leu Pro Phe Leu Ile Gln Gly Val Val Ser Tyr Gly
 1555 1560 1565
 His Ile Lys His Asp Thr Thr Thr Leu Tyr Pro Ser Ile His Glu Arg
 1570 1575 1580
 Asn Lys Gly Asp Trp Glu Asp Leu Gly Trp Leu Ala Asp Leu Arg Ile
 1585 1590 1595 1600
 Ser Met Asp Leu Lys Glu Pro Ser Lys Asp Ser Ser Lys Arg Ile Thr
 1605 1610 1615
 Val Tyr Gly Glu Leu Glu Tyr Ser Ser Ile Arg Gln Lys Gln Phe Thr
 1620 1625 1630
 Glu Ile Asp Tyr Asp Pro Arg His Phe Asp Asp Cys Ala Tyr Arg Asn
 1635 1640 1645
 Leu Ser Leu Pro Val Gly Cys Ala Val Glu Gly Ala Ile Met Asn Cys
 1650 1655 1660
 Asn Ile Leu Met Tyr Asn Lys Leu Ala Leu Ala Tyr Met Pro Ser Ile
 1665 1670 1675 1680
 Tyr Arg Asn Asn Pro Val Cys Lys Tyr Arg Val Leu Ser Ser Asn Glu
 1685 1690 1695
 Ala Gly Gln Val Ile Cys Gly Val Pro Thr Arg Thr Ser Ala Arg 'Ala

1700					1705					1710					
Glu	Tyr	Ser	Thr	Gln	Leu	Tyr	Leu	Gly	Pro	Phe	Trp	Thr	Leu	Tyr	Gly
1715					1720					1725					
Asn	Tyr	Thr	Ile	Asp	Val	Gly	Met	Tyr	Thr	Leu	Ser	Gln	Met	Thr	Ser
1730					1735					1740					
Cys	Gly	Ala	Arg	Met	Ile	Phe									
1745					1750										
<p><210> 446</p> <p><211> 660</p> <p><212> PRT</p> <p><213> Chlamydia trachomatis serovar D</p> <p><400> 446</p>															
Met	Ser	Glu	Lys	Arg	Lys	Ser	Asn	Lys	Ile	Ile	Gly	Ile	Asp	Leu	Gly
5					10					15					
Thr	Thr	Asn	Ser	Cys	Val	Ser	Val	Met	Glu	Gly	Gly	Gln	Pro	Lys	Val
20					25					30					
Ile	Ala	Ser	Ser	Glu	Gly	Thr	Arg	Thr	Thr	Pro	Ser	Ile	Val	Ala	Phe
35					40					45					
Lys	Gly	Gly	Glu	Thr	Leu	Val	Gly	Ile	Pro	Ala	Lys	Arg	Gln	Ala	Val
50					55					60					
Thr	Asn	Pro	Glu	Lys	Thr	Leu	Ala	Ser	Thr	Lys	Arg	Phe	Ile	Gly	Arg
65					70					75					
Lys	Phe	Ser	Glu	Val	Glu	Ser	Glu	Ile	Lys	Thr	Val	Pro	Tyr	Lys	Val
85					90					95					
Ala	Pro	Asn	Ser	Lys	Gly	Asp	Ala	Val	Phe	Asp	Val	Glu	Gln	Lys	Leu
100					105					110					
Tyr	Thr	Pro	Glu	Glu	Ile	Gly	Ala	Gln	Ile	Leu	Met	Lys	Met	Lys	Glu
115					120					125					
Thr	Ala	Glu	Ala	Tyr	Leu	Gly	Glu	Thr	Val	Thr	Glu	Ala	Val	Ile	Thr
130					135					140					
Val	Pro	Ala	Tyr	Phe	Asn	Asp	Ser	Gln	Arg	Ala	Ser	Thr	Lys	Asp	Ala
145					150					155					
Gly	Arg	Ile	Ala	Gly	Leu	Asp	Val	Lys	Arg	Ile	Ile	Pro	Glu	Pro	Thr
165					170					175					
Ala	Ala	Ala	Leu	Ala	Tyr	Gly	Ile	Asp	Lys	Glu	Gly	Asp	Lys	Lys	Ile
180					185					190					
Ala	Val	Phe	Asp	Leu	Gly	Gly	Gly	Thr	Phe	Asp	Ile	Ser	Ile	Leu	Glu
195					200					205					
Ile	Gly	Asp	Gly	Val	Phe	Glu	Val	Leu	Ser	Thr	Asn	Gly	Asp	Thr	His
210					215					220					
Leu	Gly	Gly	Asp	Asp	Phe	Asp	Gly	Val	Ile	Ile	Asn	Trp	Met	Leu	Asp

225		230		235		240
Glu Phe Lys Lys Gln Glu Gly Ile Asp Leu Ser Lys Asp Asn Met Ala						
		245		250		255
Leu Gln Arg Leu Lys Asp Ala Ala Glu Lys Ala Lys Ile Glu Leu Ser						
		260		265		270
Gly Val Ser Ser Thr Glu Ile Asn Gln Pro Phe Ile Thr Ile Asp Ala						
		275		280		285
Asn Gly Pro Lys His Leu Ala Leu Thr Leu Thr Arg Ala Gln Phe Glu						
		290		295		300
His Leu Ala Ser Ser Leu Ile Glu Arg Thr Lys Gln Pro Cys Ala Gln						
		305		310		315
Ala Leu Lys Asp Ala Lys Leu Ser Ala Ser Asp Ile Asp Asp Val Leu						
		325		330		335
Leu Val Gly Gly Met Ser Arg Met Pro Ala Val Gln Ala Val Val Lys						
		340		345		350
Glu Ile Phe Gly Lys Glu Pro Asn Lys Gly Val Asn Pro Asp Glu Val						
		355		360		365
Val Ala Ile Gly Ala Ala Ile Gln Gly Gly Val Leu Gly Gly Glu Val						
		370		375		380
Lys Asp Val Leu Leu Leu Asp Val Ile Pro Leu Ser Leu Gly Ile Glu						
		385		390		395
Thr Leu Gly Gly Val Met Thr Pro Leu Val Glu Arg Asn Thr Thr Ile						
		405		410		415
Pro Thr Gln Lys Lys Gln Ile Phe Ser Thr Ala Ala Asp Asn Gln Pro						
		420		425		430
Ala Val Thr Ile Val Val Leu Gln Gly Glu Arg Pro Met Ala Lys Asp						
		435		440		445
Asn Lys Glu Ile Gly Arg Phe Asp Leu Thr Asp Ile Pro Pro Ala Pro						
		450		455		460
Arg Gly His Pro Gln Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly						
		465		470		475
Ile Leu His Val Ser Ala Lys Asp Ala Ala Ser Gly Arg Glu Gln Lys						
		485		490		495
Ile Arg Ile Glu Ala Ser Ser Gly Leu Lys Glu Asp Glu Ile Gln Gln						
		500		505		510
Met Ile Arg Asp Ala Glu Leu His Lys Glu Glu Asp Lys Gln Arg Lys						
		515		520		525
Glu Ala Ser Asp Val Lys Asn Glu Ala Asp Gly Met Ile Phe Arg Ala						
		530		535		540
Glu Lys Ala Val Lys Asp Tyr His Asp Lys Ile Pro Ala Glu Leu Val						
		545		550		555
						560

[illegible]

<210> 447

<211> 326

<212> PRT

<213> Chlamydia trachomatis serovar D

<400> 447

Met	Val	Ser	Gln	Thr	Val	Ser	Val	Ala	Val	Thr	Gly	Gly	Thr	Gly	Gln
			5						10					15	
Ile	Ala	Tyr	Ser	Phe	Leu	Phe	Ser	Leu	Ala	His	Gly	Asp	Val	Phe	Gly
			20					25					30		
Leu	Asp	Cys	Gly	Ile	Asp	Leu	Arg	Ile	Tyr	Asp	Ile	Pro	Gly	Thr	Glu
		35					40					45			
Arg	Ala	Leu	Ser	Gly	Val	Arg	Met	Glu	Leu	Asp	Asp	Gly	Ala	Phe	Pro
		50				55					60				
Leu	Leu	Gln	Arg	Val	Gln	Val	Thr	Thr	Ser	Leu	His	Asp	Ala	Phe	Asp
					70						75				80
Gly	Ile	Asp	Ala	Ala	Phe	Leu	Ile	Gly	Ser	Val	Pro	Arg	Gly	Pro	Gly
			85						90					95	
Met	Glu	Arg	Arg	Asp	Leu	Leu	Lys	Lys	Asn	Gly	Glu	Ile	Phe	Ala	Thr
			100					105					110		
Gln	Gly	Lys	Ala	Leu	Asn	Thr	Thr	Ala	Lys	Arg	Asp	Ala	Lys	Ile	Phe
			115				120					125			
Val	Val	Gly	Asn	Pro	Val	Asn	Thr	Asn	Cys	Trp	Ile	Ala	Met	Asn	His
		130				135					140				
Ala	Pro	Arg	Leu	Leu	Arg	Lys	Asn	Phe	His	Ala	Met	Leu	Arg	Leu	Asp
					150					155					160
Gln	Asn	Arg	Met	His	Ser	Met	Leu	Ser	His	Arg	Ala	Glu	Val	Pro	Leu
				165					170					175	

Ser Ala Val Ser Gln Val Val Val Trp Gly Asn His Ser Ala Lys Gln
 180 185 190
 Val Pro Asp Phe Thr Gln Ala Leu Ile Asn Asp Arg Pro Ile Ala Glu
 195 200 205
 Thr Ile Ala Asp Arg Asp Trp Leu Glu Asn Ile Met Val Pro Ser Val
 210 215 220
 Gln Ser Arg Gly Ser Ala Val Ile Glu Ala Arg Gly Lys Ser Ser Ala
 225 230 235 240
 Ala Ser Ala Ala Arg Ala Leu Ala Glu Ala Ala Arg Ser Ile Tyr Gln
 245 250 255
 Pro Lys Glu Gly Glu Trp Phe Ser Ser Gly Val Cys Ser Asp His Asn
 260 265 270
 Pro Tyr Gly Leu Pro Glu Asp Leu Ile Phe Gly Phe Pro Cys Arg Met
 275 280 285
 Leu Ala Thr Gly Glu Tyr Glu Val Ile Pro Arg Leu Pro Trp Asp Ala
 290 295 300
 Phe Ile Arg Gly Lys Met Gln Ile Ser Leu Asp Glu Ile Leu Gln Glu
 305 310 315 320
 Lys Ala Ser Val Ser Leu
 325

<210> 448
 <211> 232
 <212> PRT
 <213> Chlamydia trachomatis serovar D

<400> 448
 Met Thr Lys His Gly Lys Arg Ile Arg Gly Ile Gln Glu Thr Tyr Asp
 5 10 15
 Leu Ala Lys Ser Tyr Ser Leu Gly Glu Ala Ile Asp Ile Leu Lys Gln
 20 25 30
 Cys Pro Thr Val Arg Phe Asp Gln Thr Val Asp Val Ser Val Lys Leu
 35 40 45
 Gly Ile Asp Pro Arg Lys Ser Asp Gln Gln Ile Arg Gly Ser Val Ser
 50 55 60
 Leu Pro His Gly Thr Gly Lys Val Leu Arg Ile Leu Val Phe Ala Ala
 65 70 75 80
 Gly Asp Lys Ala Ala Glu Ala Ile Glu Ala Gly Ala Asp Phe Val Gly
 85 90 95
 Ser Asp Asp Leu Val Glu Lys Ile Lys Gly Gly Trp Val Asp Phe Asp
 100 105 110
 Val Ala Val Ala Thr Pro Asp Met Met Arg Glu Val Gly Lys Leu Gly
 115 120 125

Lys Val Leu Gly Pro Arg Asn Leu Met Pro Thr Pro Lys Ala Gly Thr
 130 135 140
 Val Thr Thr Asp Val Val Lys Thr Val Ala Glu Leu Arg Lys Gly Lys
 145 150 155 160
 Ile Glu Phe Lys Ala Asp Arg Ala Gly Val Cys Asn Val Gly Val Ala
 165 170 175
 Lys Leu Ser Phe Asp Ser Ala Gln Ile Lys Glu Asn Val Glu Ala Leu
 180 185 190
 Cys Ala Ala Leu Val Lys Ala Lys Pro Ala Thr Ala Lys Gly Gln Tyr
 195 200 205
 Leu Val Asn Phe Thr Ile Ser Ser Thr Met Gly Pro Gly Val Thr Val
 210 215 220
 Asp Thr Arg Glu Leu Ile Ala Leu
 225 230

<210> 449

<211> 1252

<212> PRT

<213> Chlamydia trachomatis serovar D

<400> 449

Met Phe Lys Cys Pro Glu Arg Val Ser Ile Lys Lys Lys Glu Asp Ile
 5 10 15
 Leu Asp Leu Pro Asn Leu Val Glu Val Gln Ile Lys Ser Tyr Lys Gln
 20 25 30
 Phe Leu Gln Ile Gly Lys Leu Ala Glu Glu Arg Glu Asn Ile Gly Leu
 35 40 45
 Glu Glu Val Phe Arg Glu Ile Phe Pro Ile Lys Ser Tyr Asn Glu Ala
 50 55 60
 Thr Ile Leu Glu Tyr Leu Ser Tyr Asn Leu Gly Val Pro Lys Tyr Ser
 65 70 75 80
 Pro Glu Glu Cys Ile Arg Arg Gly Ile Thr Tyr Ser Val Thr Leu Lys
 85 90 95
 Val Arg Phe Arg Leu Thr Asp Glu Thr Gly Ile Lys Glu Glu Glu Val
 100 105 110
 Tyr Met Gly Thr Ile Pro Ile Met Thr Asp Lys Gly Thr Phe Ile Ile
 115 120 125
 Asn Gly Ala Glu Arg Val Val Val Ser Gln Val His Arg Ser Pro Gly
 130 135 140
 Ile Asn Phe Glu Gln Glu Lys His Ser Lys Gly Asn Val Leu Phe Ser
 145 150 155 160
 Phe Arg Ile Ile Pro Tyr Arg Gly Ser Trp Leu Glu Ala Val Phe Asp
 165 170 175

Ile Asn Asp Leu Ile Tyr Ile His Ile Asp Arg Lys Lys Arg Arg Arg
 180 185 190
 Lys Ile Leu Ala Met Thr Phe Ile Arg Ala Leu Gly Tyr Ser Thr Asp
 195 200 205
 Ala Asp Ile Ile Glu Glu Phe Phe Ser Val Glu Glu Arg Ser Leu Arg
 210 215 220
 Leu Glu Lys Asp Phe Val Ala Leu Val Gly Lys Val Leu Ala Asp Asn
 225 230 235 240
 Val Val Asp Ala Asp Ser Ser Leu Val Tyr Gly Lys Ala Gly Glu Lys
 245 250 255
 Leu Ser Thr Ala Met Leu Lys Arg Ile Leu Asp Ala Gly Val Gln Ser
 260 265 270
 Leu Lys Ile Ala Val Gly Ala Asp Glu Asn His Pro Ile Ile Lys Met
 275 280 285
 Leu Ala Lys Asp Pro Thr Asp Ser Tyr Glu Ala Ala Leu Lys Asp Phe
 290 295 300
 Tyr Arg Arg Leu Arg Pro Gly Glu Pro Ala Thr Leu Val Asn Ala Arg
 305 310 315 320
 Ser Thr Ile Met Arg Leu Phe Phe Asp Ala Lys Arg Tyr Asn Leu Gly
 325 330 335
 Arg Val Gly Arg Tyr Lys Leu Asn Lys Lys Leu Gly Phe Pro Leu Asp
 340 345 350
 Asp Glu Thr Leu Ser Gln Val Thr Leu Arg Lys Glu Asp Val Ile Gly
 355 360 365
 Ala Leu Lys Tyr Leu Ile Arg Leu Arg Met Gly Asp Glu Lys Thr Ser
 370 375 380
 Ile Asp Asp Ile Asp His Leu Ala Asn Arg Arg Val Arg Ser Val Gly
 385 390 395 400
 Glu Leu Ile Gln Asn His Cys Arg Ser Gly Leu Ala Arg Met Glu Lys
 405 410 415
 Ile Val Arg Glu Arg Met Asn Leu Phe Asp Phe Ser Ser Asp Thr Leu
 420 425 430
 Thr Pro Gly Lys Ile Ile Ser Ala Lys Gly Leu Val Ser Val Leu Lys
 435 440 445
 Asp Phe Phe Ser Arg Ser Gln Leu Ser Gln Phe Met Asp Gln Thr Asn
 450 455 460
 Pro Val Ala Glu Leu Thr His Lys Arg Arg Leu Ser Ala Leu Gly Pro
 465 470 475 480
 Gly Gly Leu Asn Arg Glu Arg Ala Gly Phe Glu Val Arg Asp Val His
 485 490 495

Ala Ser His Tyr Gly Arg Ile Cys Pro Ile Glu Thr Pro Glu Gly Pro
 500 505 510
 Asn Ile Gly Leu Ile Thr Ser Leu Ser Ser Phe Ala Lys Ile Asn Glu
 515 520 525
 Phe Gly Phe Ile Glu Thr Pro Tyr Arg Val Val Arg Asp Gly Ile Val
 530 535 540
 Thr Asp Glu Ile Glu Tyr Met Thr Ala Asp Val Glu Glu Glu Cys Val
 545 550 555 560
 Ile Ala Gln Ala Ser Ala Glu Leu Asp Glu Tyr Asp Met Phe Lys Thr
 565 570 575
 Pro Val Cys Trp Ala Arg Tyr Lys Gly Glu Ala Phe Glu Ala Asp Thr
 580 585 590
 Ser Thr Val Thr His Met Asp Val Ser Pro Lys Gln Leu Val Ser Val
 595 600 605
 Val Thr Gly Leu Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala
 610 615 620
 Leu Met Gly Ser Asn Met Gln Arg Gln Ala Val Pro Leu Leu Lys Thr
 625 630 635 640
 Glu Ala Ala Ile Val Gly Thr Gly Leu Glu Gly Arg Ala Ala Lys Asp
 645 650 655
 Ser Gly Ala Ile Ile Val Ala Gln Glu Asp Gly Val Val Glu Tyr Val
 660 665 670
 Asp Ser Tyr Glu Ile Val Val Ala Lys Lys Asn Asn Pro Thr Leu Lys
 675 680 685
 Asp Arg Tyr Gln Leu Lys Lys Phe Leu Arg Ser Asn Ser Gly Thr Cys
 690 695 700
 Ile Asn Gln Thr Pro Leu Cys Ser Val Gly Asp Val Val Thr His Gly
 705 710 715 720
 Asp Val Leu Ala Asp Gly Pro Ala Thr Asp Lys Gly Glu Leu Ala Leu
 725 730 735
 Gly Lys Asn Val Leu Val Ala Phe Met Pro Trp Tyr Gly Tyr Asn Phe
 740 745 750
 Glu Asp Ala Ile Ile Ile Ser Glu Arg Leu Ile Lys Gln Asp Ala Tyr
 755 760 765
 Thr Ser Ile Tyr Ile Glu Glu Phe Glu Leu Thr Ala Arg Asp Thr Lys
 770 775 780
 Leu Gly Lys Glu Glu Ile Thr Arg Asp Ile Pro Asn Val Ser Glu Glu
 785 790 795 800
 Val Leu Ala Asn Leu Gly Glu Asp Gly Val Val Arg Ile Gly Ala Glu
 805 810 815
 Val Lys Pro Gly Asp Ile Leu Val Gly Lys Ile Thr Pro Lys Ser Glu

820					825					830					
Thr	Glu	Leu	Ala	Pro	Glu	Glu	Arg	Leu	Leu	Arg	Ala	Ile	Phe	Gly	Glu
	835						840					845			
Lys	Ala	Ala	Asp	Val	Lys	Asp	Ala	Ser	Leu	Thr	Val	Pro	Pro	Gly	Thr
	850					855					860				
Glu	Gly	Val	Val	Met	Asp	Val	Lys	Val	Phe	Ser	Arg	Lys	Asp	Arg	Leu
	865					870					875				880
Ser	Lys	Ser	Asp	Glu	Leu	Val	Glu	Glu	Ala	Val	His	Leu	Lys	Asp	
			885					890					895		
Leu	Gln	Lys	Glu	Tyr	Lys	Ser	Gln	Leu	Ala	Gln	Leu	Lys	Val	Glu	His
			900					905					910		
Arg	Glu	Lys	Leu	Gly	Ala	Leu	Leu	Asn	Glu	Lys	Ala	Pro	Ala	Ala	
			915				920				925				
Ile	Ile	His	Arg	Arg	Ser	Ala	Asp	Ile	Leu	Val	Gln	Glu	Gly	Ala	Ile
						935					940				
Phe	Asp	Gln	Glu	Thr	Ile	Glu	Leu	Leu	Glu	Arg	Glu	Ser	Leu	Val	Asp
	945					950					955				960
Leu	Leu	Met	Ala	Pro	Cys	Asp	Met	Tyr	Asp	Val	Leu	Lys	Asp	Ile	Leu
			965						970					975	
Ser	Ser	Tyr	Glu	Thr	Ala	Val	Gln	Arg	Leu	Glu	Val	Asn	Tyr	Lys	Thr
			980					985					990		
Glu	Ala	Glu	His	Ile	Lys	Glu	Gly	Asp	Ala	Asp	Leu	Asp	His	Gly	Val
		995					1000						1005		
Ile	Arg	Gln	Val	Lys	Val	Tyr	Val	Ala	Ser	Lys	Arg	Lys	Leu	Gln	Val
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Gly	Asp	Lys	Met	Ala	Gly	Arg	His	Gly	Asn	Lys	Gly	Val	Val	Ser	Lys
	1025			1030					1035					1040	
Ile	Val	Pro	Glu	Ala	Asp	Met	Pro	Phe	Leu	Ala	Asn	Gly	Glu	Thr	Val
			1045					1050					1055		
Gln	Met	Ile	Leu	Asn	Pro	Leu	Gly	Val	Pro	Ser	Arg	Met	Asn	Leu	Gly
		1060					1065						1070		
Gln	Val	Leu	Glu	Thr	His	Leu	Gly	Tyr	Ala	Ala	Lys	Thr	Ala	Gly	Ile
		1075					1080					1085			
Tyr	Val	Lys	Thr	Pro	Val	Phe	Glu	Gly	Phe	Pro	Glu	Ser	Arg	Ile	Trp
	1090					1095						1100			
Asp	Met	Met	Ile	Glu	Gln	Gly	Leu	Pro	Glu	Asp	Gly	Lys	Ser	Tyr	Leu
	1105			1110							1115				1120
Phe	Asp	Gly	Lys	Thr	Gly	Glu	Arg	Phe	Asp	Ser	Lys	Val	Val	Val	Gly
			1125					1130					1135		
Tyr	Ile	Tyr	Met	Leu	Lys	Leu	Ser	His	Leu	Ile	Ala	Asp	Lys	Ile	His
			1140				1145						1150		

Ala Arg Ser Ile Gly Pro Tyr Ser Leu Val Thr Gln Gln Pro Leu Gly
 1155 1160 1165
 Gly Lys Ala Gln Met Gly Gly Gln Arg Phe Gly Glu Met Glu Val Trp
 1170 1175 1180
 Ala Leu Glu Ala Tyr Gly Val Ala His Met Leu Gln Glu Ile Leu Thr
 1185 1190 1195 1200
 Val Lys Ser Asp Asp Val Ser Gly Arg Thr Arg Ile Tyr Glu Ser Ile
 1205 1210 1215
 Val Lys Gly Glu Asn Leu Leu Arg Ser Gly Thr Pro Glu Ser Phe Asn
 1220 1225 1230
 Val Leu Ile Lys Glu Met Gln Gly Leu Gly Leu Asp Val Arg Pro Met
 1235 1240 1245
 Val Val Asp Ala
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 <213> Chlamydia trachomatis serovar D
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 Gly Asp Asp Asn Gly Tyr Gly Trp Gly Ile Ala Lys Met Leu Ala Glu
 20 25 30
 Ala Gly Ala Thr Ile Leu Val Gly Thr Trp Val Pro Ile Tyr Lys Ile
 35 40 45
 Phe Ser Gln Ser Leu Glu Leu Gly Lys Phe Asn Ala Ser Arg Glu Leu
 50 55 60
 Ser Asn Gly Glu Leu Leu Thr Phe Ala Lys Ile Tyr Pro Met Asp Ala
 65 70 75 80
 Ser Phe Asp Thr Pro Glu Asp Ile Pro Gln Glu Ile Leu Glu Asn Lys
 85 90 95
 Arg Tyr Lys Asp Leu Ser Gly Tyr Thr Val Ser Glu Val Val Glu Gln
 100 105 110
 Val Lys Lys His Phe Gly His Ile Asp Ile Leu Val His Ser Leu Ala
 115 120 125
 Asn Ser Pro Glu Ile Ala Lys Pro Leu Leu Asp Thr Ser Arg Lys Gly
 130 135 140
 Tyr Leu Ala Ala Leu Ser Thr Ser Ser Tyr Ser Phe Ile Ser Leu Leu
 145 150 155 160
 Ser His Phe Gly Pro Ile Met Asn Ala Gly Ala Ser Thr Ile Ser Leu
 165 170 175

Thr Tyr Leu Ala Ser Met Arg Ala Val Pro Gly Tyr Gly Gly Gly Met
 180 185 190
 Asn Ala Ala Lys Ala Ala Leu Glu Ser Asp Thr Lys Val Leu Ala Trp
 195 200 205
 Glu Ala Gly Arg Arg Trp Gly Val Arg Val Asn Thr Ile Ser Ala Gly
 210 215 220
 Pro Leu Ala Ser Arg Ala Gly Lys Ala Ile Gly Phe Ile Glu Arg Met
 225 230 235 240
 Val Asp Tyr Tyr Gln Asp Trp Ala Pro Leu Pro Ser Pro Met Glu Ala
 245 250 255
 Glu Gln Val Gly Ala Ala Ala Ala Phe Leu Val Ser Pro Leu Ala Ser
 260 265 270
 Ala Ile Thr Gly Glu Thr Leu Tyr Val Asp His Gly Ala Asn Val Met
 275 280 285
 Gly Ile Gly Pro Glu Met Phe Pro Lys Asp
 290 295

<210> 451
 <211> 298
 <212> PRT
 <213> Chlamydia trachomatis serovar D

<400> 451
 Met Ser Leu Gln Lys Leu Leu Val Thr Asp Ile Asp Gly Thr Ile Thr
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 His Gln Ser His Leu Leu His Asp Arg Val Val Lys Ala Leu His Gln
 20 25 30
 Tyr Tyr Asp Ser Gly Trp Gln Leu Phe Phe Leu Thr Gly Arg Tyr Phe
 35 40 45
 Ser Tyr Ala Tyr Pro Leu Phe Gln Asn Phe Ser Val Pro Phe Leu Leu
 50 55 60
 Gly Ser Gln Asn Gly Ser Val Trp Ser Ser Thr Asp Lys Glu Phe
 65 70 75 80
 Ile Tyr Phe Arg Ser Leu Ser Arg Asp Phe Leu Tyr Val Leu Glu Lys
 85 90 95
 Tyr Phe Glu Asp Leu Asp Leu Ile Ala Cys Ile Glu Ser Gly Ala Ser
 100 105 110
 Asn Arg Asp Val Tyr Phe Arg Lys Gly Leu Gly Lys Thr Ser Gln Glu
 115 120 125
 Leu Lys Ala Ile Leu Asp Ala Val Tyr Phe Pro Thr Pro Glu Ala Ala
 130 135 140
 Arg Leu Leu Val Asp Val Gln Gly His Leu Ser Glu Glu Phe Ser Tyr
 145 150 155 160

Glu	Asp	Phe	Ala	Ile	Ala	Lys	Phe	Phe	Gly	Glu	Arg	Glu	Glu	Val	Lys
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Lys	Ile	Met	Asp	Arg	Phe	Ile	Gln	Ser	Pro	Glu	Val	Ser	Ser	Gln	Val
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Thr	Met	Asn	Tyr	Met	Arg	Trp	Pro	Phe	Asp	Phe	Lys	Tyr	Ala	Val	Leu
		195					200					205			
Leu	Leu	Thr	Leu	Lys	Asp	Val	Ser	Lys	Gly	Phe	Ala	Val	Asp	Gln	Val
		210				215					220				
Val	Gln	Thr	Phe	Tyr	Lys	Glu	Asn	Lys	Pro	Phe	Ile	Met	Ala	Ser	Gly
		225			230					235					240
Asp	Asp	Ala	Asn	Asp	Ile	Asp	Leu	Leu	Ser	Arg	Gly	Asp	Phe	Lys	Ile
			245					250						255	
Val	Ile	Gln	Thr	Ala	Pro	Glu	Glu	Met	His	Gly	Leu	Ala	Asp	Phe	Leu
		260						265					270		
Ala	Pro	Pro	Ala	Lys	Asp	Phe	Gly	Ile	Leu	Ser	Ala	Trp	Glu	Ala	Gly
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Glu	Leu	Arg	Tyr	Lys	Gln	Leu	Val	Asn	Pro						
	290					295									

<210> 452

<211> 153

<212> PRT

<213> Chlamydia trachomatis serovar D

<400> 452

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Ser	Phe	Val	Asp	Val	Pro	Gln	Glu	Leu	Ser	Phe	Val	Asn	Glu	Ala	Phe
			20					25					30		
Ser	Gly	Ser	Met	Arg	Trp	Glu	Val	Gly	Arg	Met	Leu	Gly	Ser	Leu	Leu
		35					40					45			
Leu	Leu	Leu	Gly	Ile	Phe	Gly	Gly	Gly	Cys	Leu	Leu	Phe	Arg	Arg	Phe
	50					55					60				
Leu	Arg	Ser	Arg	Gly	His	Leu	Pro	Ser	Gly	Asn	Ser	Ser	Ile	Lys	Ile
	65				70					75					80
Leu	Asp	Gln	Arg	Val	Leu	Ala	Ser	Lys	Thr	Ser	Ile	Tyr	Val	Ile	Lys
				85					90					95	
Val	Ala	Asn	Lys	Thr	Leu	Val	Val	Ala	Glu	Arg	Gly	Glu	Arg	Val	Thr
			100					105					110		
Leu	Leu	Ser	Glu	Phe	Pro	Asn	Thr	Asp	Leu	Asn	Glu	Leu	Ile	Gln	
		115				120					125				
Lys	Asp	Gln	Lys	Lys	Pro	Ser	Thr	Pro	Arg	Gly	Glu	Met	Leu	Ser	Gly
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Phe Leu Lys Gln Phe Lys Glu Lys Lys
145 150

<210> 453

<211> 569

<212> PRT

<213> Chlamydia trachomatis serovar D

<400> 453

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Thr Ile Ala Cys Leu Pro Glu Asp Val Lys Gln Phe Lys Asp Leu Leu
20 25 30

Tyr Ala Met Tyr Gly Phe Thr Ala Thr Glu Glu Glu Pro Thr Ser Glu
35 40 45

Val His Pro Gly Ala Ile Leu Lys Gly Thr Val Val Asp Ile Ser Lys
50 55 60

Asp Phe Val Val Val Asp Val Gly Leu Lys Ser Glu Gly Val Ile Pro
65 70 75 80

Met Ser Glu Phe Ile Asp Ser Ser Glu Gly Leu Thr Val Gly Ala Glu
85 90 95

Val Glu Val Tyr Leu Asp Gln Thr Glu Asp Asp Glu Gly Lys Val Val
100 105 110

Leu Ser Arg Glu Lys Ala Thr Arg Gln Arg Gln Trp Glu Tyr Ile Leu
115 120 125

Ala His Cys Glu Glu Gly Ser Ile Val Lys Gly Gln Ile Thr Arg Lys
130 135 140

Val Lys Gly Gly Leu Ile Val Asp Ile Gly Met Glu Ala Phe Leu Pro
145 150 155 160

Gly Ser Gln Ile Asp Asn Lys Lys Ile Lys Asn Leu Asp Asp Tyr Val
165 170 175

Gly Lys Val Cys Glu Phe Lys Ile Leu Lys Ile Asn Val Asp Arg Arg
180 185 190

Asn Val Val Val Ser Arg Arg Glu Leu Leu Glu Ala Glu Arg Ile Ser
195 200 205

Lys Lys Ala Glu Leu Ile Glu Gln Ile Thr Ile Gly Glu Arg Arg Lys
210 215 220

Gly Ile Val Lys Asn Ile Thr Asp Phe Gly Val Phe Leu Asp Leu Asp
225 230 235 240

Gly Ile Asp Gly Leu Leu His Ile Thr Asp Met Thr Trp Lys Arg Ile
245 250 255

Arg His Pro Ser Glu Met Val Glu Leu Asn Gln Glu Leu Glu Val Ile
260 265 270

Ile Leu Ser Val Asp Lys Glu Lys Gly Arg Val Ala Leu Gly Leu Lys
 275 280
 Gln Lys Glu His Asn Pro Trp Glu Asp Ile Glu Lys Lys Tyr Pro Pro
 290 295 300
 Gly Lys Arg Val Arg Gly Lys Ile Val Lys Leu Leu Pro Tyr Gly Ala
 305 310 315 320
 Phe Ile Glu Ile Glu Glu Gly Ile Glu Gly Leu Ile His Val Ser Glu
 325 330 335
 Met Ser Trp Val Lys Asn Ile Val Asp Pro Asn Glu Val Val Asn Lys
 340 345 350
 Gly Asp Glu Val Glu Val Val Val Leu Ser Ile Gln Lys Asp Glu Gly
 355 360 365
 Lys Ile Ser Leu Gly Leu Lys Lys Gln Thr Lys His Asn Pro Trp Asp Asn
 370 375 380
 Ile Glu Glu Lys Tyr Pro Ile Gly Leu Arg Val Thr Ala Glu Ile Lys
 385 390 395 400
 Asn Leu Thr Asn Tyr Gly Ala Phe Val Glu Leu Glu Pro Gly Ile Glu
 405 410 415
 Gly Leu Ile His Ile Ser Asp Met Ser Trp Ile Lys Lys Val Ser His
 420 425 430
 Pro Ser Glu Leu Phe Lys Lys Gly Asn Thr Val Glu Ala Val Ile Leu
 435 440 445
 Ser Val Asp Lys Glu Ser Lys Lys Ile Thr Leu Gly Val Lys Gln Leu
 450 455 460
 Thr Pro Asn Pro Trp Asp Glu Ile Glu Val Met Phe Pro Val Gly Ser
 465 470 475 480
 Asp Ile Ser Gly Val Val Thr Lys Ile Thr Ala Phe Gly Ala Phe Val
 485 490 495
 Glu Leu Gln Asn Gly Ile Glu Gly Leu Ile His Val Ser Glu Leu Ser
 500 505 510
 Glu Lys Pro Phe Ala Lys Ile Glu Asp Val Leu Ser Ile Gly Asp Lys
 515 520 525
 Val Ser Ala Lys Val Ile Lys Leu Asp Pro Asp His Lys Lys Val Ser
 530 535 540
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 Ala Glu Glu Glu Ser Ser Asp Arg Asp
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<210> 454

<211> 666

<212> PRT

<213> Chlamydia trachomatis serovar D

<400> 454

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Lys Lys Leu Ser Ala Asp Arg Tyr Arg Phe Ser Leu Phe Ser Ser Gln
      20                      25                      30

Ala Gln Gln Val Thr Leu Val Leu Leu Asp Pro Leu Ser Glu Ile His
      35                      40                      45

Glu Ile Pro Leu Ser Ser Thr Asp His Arg Thr Gly Ala Ile Trp His
      50                      55                      60

Ile Glu Ile Ala Gly Ile Ser Ser Glu Trp Ser Tyr Ala Tyr Lys Leu
      65                      70                      75                      80

Arg Gly Thr Asp Leu Ser Ser Gln Lys Phe Ala Thr Asp Ser Tyr Ile
      85                      90                      95

Ala Asp Pro Tyr Ser Lys Asn Ile Tyr Ser Pro Gln Leu Phe Gly Ser
      100                     105                     110

Pro Lys Gln Glu Lys Asp Tyr Ala Phe Ser Tyr Leu Lys His Glu Asp
      115                     120                     125

Phe Asp Trp Glu Gly Asp Thr Pro Leu His Leu Pro Lys Glu Asn Tyr
      130                     135                     140

Phe Ile Tyr Glu Met His Val Arg Ser Phe Thr Arg Asp Pro Ser Ser
      145                     150                     155                     160

Gln Val Ser His Pro Gly Thr Phe Leu Gly Ile Ile Glu Lys Ile Asp
      165                     170                     175

His Leu Lys Gln Leu Gly Val His Ala Val Glu Leu Leu Pro Ile Phe
      180                     185                     190

Glu Phe Asp Glu Thr Val His Pro Phe Lys Asn Gln Asp Phe Pro His
      195                     200                     205

Leu Cys Asn Tyr Trp Gly Tyr Ser Ser Val Asn Phe Phe Cys Pro Ser
      210                     215                     220

Arg Arg Tyr Thr Tyr Gly Ala Asp Pro Cys Ala Pro Ala Arg Glu Phe
      225                     230                     235                     240

Lys Thr Leu Val Lys Ala Leu His Arg Ala Gly Ile Glu Val Ile Leu
      245                     250                     255

Asp Val Val Phe Asn His Thr Gly Phe Glu Gly Thr Ser Cys Pro Leu
      260                     265                     270

Pro Trp Ile Asp Leu Glu Ser Tyr Tyr Met Val Asn Asp His Gly Asp
      275                     280                     285

Leu Met Asn Phe Ser Gly Cys Gly Asn Thr Val Asn Thr Thr Pro
      290                     295                     300

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Thr Thr Leu Lys Trp Ile Leu Asp Ala Leu Arg Tyr Trp Val Gln Glu
 305 310 315 320
 Met His Val Asp Gly Phe Arg Phe Asp Leu Ala Ser Val Phe Ser Arg
 325 330 335
 Asp Pro Gln Gly Val Pro Leu Pro Leu Thr Pro Ile Leu Gln Ala Ile
 340 345 350
 Ser Ser Asp Ser Ile Leu Ser Glu Thr Lys Leu Ile Ala Glu Pro Trp
 355 360 365
 Asp Ala Gly Gly Leu Tyr Gln Leu Gly His Phe Pro Ser Ile Ser Thr
 370 375 380
 Arg Trp Ser Glu Trp Asn Gly Cys Tyr Arg Asp His Val Lys Ala Phe
 385 390 395 400
 Leu Asn Gly Asp Ala His Gln Val Ser Ser Phe Ala Ser Arg Ile Ser
 405 410 415
 Gly Ser His Asp Ile Tyr Pro Asn Gly Lys Pro Thr Asn Ser Ile Asn
 420 425 430
 Tyr Ile Cys Ser His Asp Gly Phe Thr Leu Tyr Asp Thr Val Ala Tyr
 435 440 445
 Asn Asp Lys His Asn Glu Glu Asn Gly Glu Tyr Asn Arg Asp Gly Thr
 450 455 460
 Ser Ala Asn Tyr Ser Tyr Asn Phe Gly Cys Glu Gly Glu Thr Thr Asp
 465 470 475 480
 Pro Thr Ile Cys Ala Leu Arg Glu Arg Gln Met Lys Asn Phe Phe Leu
 485 490 495
 Ala Leu Phe Leu Ser Gln Gly Ile Pro Met Ile Gln Ser Gly Asp Glu
 500 505 510
 Tyr Gly His Thr Ala Tyr Gly Asn Asn Asn His Trp Cys Leu Asp Thr
 515 520 525
 Lys Ile Asn Tyr Phe Leu Trp Asp Arg Leu Ala Glu Arg Lys Glu Leu
 530 535 540
 Phe Ser Phe Leu Cys Gln Val Ile Ala Leu Arg Lys Ala Tyr Thr Glu
 545 550 555 560
 Leu Phe Asn Thr Ser Phe Leu Ser Glu Asp Thr Ile Thr Trp Leu Asn
 565 570 575
 Thr Lys Gly Ser Pro Arg Glu Trp Gly Ala Asp His Tyr Leu Ala Phe
 580 585 590
 Glu Leu Lys His Leu Asn Tyr Ser Leu Phe Val Ala Phe Tyr Ser Gly
 595 600 605
 Asn Glu Arg Ile Glu Ile Ser Leu Pro Lys Pro Arg Lys Glu His Leu
 610 615 620
 Ala Tyr Glu Lys Ile Val Asp Ser Thr Thr Gly Phe Phe Ser Gln Ile

625	630	635	640
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Ser Arg Arg Lys	Thr Ser Leu Glu Ser Arg		
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<213> Chlamydia pneumoniae

<400> 457

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gtgatatttt	gggagatgat	ctcaccacaa	tttttagaaa	attgcaattt	gtatacagat	1560
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<211> 294

<212> DNA

<213> Chlamydia pneumoniae

<400> 458

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tccctctatg	ttgcgatgta	aacactcgct	ttgttagata	gagaagctag	acagcctgag	180
tttactgaa	agattgtagt	aactgctagc	cctactgtgg	aaagaaagag	atcagaacat	240
acaaattcta	gaaaaaaga	tccctcagca	tataacttga	gtgatgtaaa	gtaa	294

<210> 459

<211> 618

<212> DNA

<213> Chlamydia pneumoniae

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<210> 460
 <211> 1809
 <212> DNA
 <213> Chlamydia pneumoniae

<400> 460
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<210> 461
 <211> 975
 <212> DNA
 <213> Chlamydia pneumoniae

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<210> 462

<211> 1980

<212> DNA

<213> Chlamydia pneumoniae

<400> 462

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<210> 463

<211> 1236

<212> DNA

<213> Chlamydia pneumoniae

<400> 463

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<210> 464

<211> 1215

<212> DNA

<213> *Chlamydia pneumoniae*

<400> 464

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<210> 465

<211> 1632

<212> DNA

<213> *Chlamydia pneumoniae*

<400> 465

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<210> 466

<211> 312

<212> DNA

<213> Chlamydia pneumoniae

<400> 466

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<210> 467

<211> 1089

<212> DNA

<213> Chlamydia pneumoniae

<400> 467

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<210> 468

<211> 1308

<212> DNA

<213> Chlamydia pneumoniae

<400> 468

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<210> 469

<211> 1749

<212> DNA

<213> Chlamydia pneumoniae

<400> 469

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<210> 470

<211> 516

<212> DNA

<213> Chlamydia pneumoniae

<400> 470

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<210> 471
 <211> 1083
 <212> DNA
 <213> Chlamydia pneumoniae

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taa						1083

<210> 472
 <211> 1200
 <212> DNA
 <213> Chlamydia pneumoniae

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tcagcagaca	aagctcagca	attaggagct	atgattgcta	atgctttaga	tgctgtaaat	1140

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<210> 473

<211> 675

<212> DNA

<213> *Chlamydia pneumoniae*

<400> 473

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aaagattact	atttacaat	taaagcattt	ccttggtacc	tttcagcgct	gcactctgc	180
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gagcttgcca	atcatgaatt	cagtcaggct	gtcgaagata	tggttagcac	atttcgcgc	360
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<210> 474

<211> 741

<212> DNA

<213> *Chlamydia pneumoniae*

<400> 474

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<210> 475

<211> 1062

<212> DNA

<213> *Chlamydia pneumoniae*

<400> 475

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<210> 476

<211> 561

<212> DNA

<213> *Chlamydia pneumoniae*

<400> 476

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<210> 477

<211> 3135

<212> DNA

<213> *Chlamydia pneumoniae*

<400> 477

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<210> 478

<211> 1041

<212> DNA

<213> *Chlamydia pneumoniae*

<400> 478

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gagagaattg	ggttgaagcc	tatctatcac	tcacaaatcc	ctttcccttg	gatgagcgaa	960
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<210> 479

<211> 984

<212> DNA

<213> *Chlamydia pneumoniae*

<400> 479

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<210> 480

<211> 444

<212> DNA

<213> *Chlamydia pneumoniae*

<400> 480

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<210> 481

<211> 1581

<212> DNA

<213> *Chlamydia pneumoniae*

<400> 481

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<210> 482

<211> 1908

<212> DNA

<213> Chlamydia pneumoniae

<400> 482

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<210> 483

<211> 945

<212> DNA

<213> Chlamydia pneumoniae

<400> 483

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<210> 484

<211> 3723

<212> DNA

<213> Chlamydia pneumoniae

<400> 484

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<210> 485

<211> 1731

<212> DNA

<213> Chlamydia pneumoniae

<400> 485

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<210> 486

<211> 4224

<212> DNA

<213> Chlamydia pneumoniae

<400> 486

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gactgcttgc	cttctggaag	ttgtgaactg	cgcagctcct	caagaagcta	taatgcacac	4200
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<211> 804
 <212> DNA
 <213> *Chlamydia pneumoniae*

<400> 487
 alggggcaatt caggtttcta tttaacaagat actcaaaaca ctatttttgc agataaacatt 60
 cgtcttggtt aaatgaccac agttctttaa aaagacgagg ttattatagg cacagatata 120
 actccaacag taacaaaatt tagtggcgat aagggaattg taattactac agactcaacc 180
 ataaccacct ctatgcactac tttttctttg gatattggaag ctgtaatacaa agaagtaaca 240
 gataaaatct taactcaaat tgaagatgag ttatgcaaa acattataaa aaacataact 300
 caaagtctaa tagaagaagt aattaagaaa atacacattg atcctctctt ctcatattct 360
 agagcattta aagatgttaa tataactaat aaaattcagt gcaatggctt atttacaana 420
 gaaaataatag ggaatttaga cggagggaaca gaaatagctt cgtcttcagt aacacctgat 480
 aatgctaata gtatgttctt aatttgtgag gatattatag ccacacgcgt ggaaggaaca 540
 gtggccttgg cgttagttaa agaaggagat ttatctcctt gctctattag ttatggatag 600
 tcgcgtggat atcogaatat aatttcaata agagcaacgc tcggaacaaa aacaactgct 660
 ccagttaaat tctctttgag agcaggaggg atggatagtg gtgtgtgtgt ggtaaatgct 720
 atgcacaatt gagaaaaaat tttaggagtt gacgcagttt cgaagattac tatcttagaa 780
 gtaaaaaccac aaacaatgtg ttaa 804

<210> 488
 <211> 306
 <212> DNA
 <213> *Chlamydia pneumoniae*

<400> 488
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 ttccaggaac tagatataca agtaaaaaata gataaagaaa aagttaacttt ttgactttct 120
 ccaacagagc ttatatacaa aagtatactc gtcatataca atttactaaa cagcattgaa 180
 tcatctctag accttttccc agactctcca gtatgtgaag aattagaaaa aaataatctt 240
 aagctcaaaa aagctctgat catgctaatt ctatcaagaa aagacatggt ctcaaaaaa 300
 gaataa 306

<210> 489
 <211> 806
 <212> DNA
 <213> *Chlamydia pneumoniae*

<400> 489
 gtgaaaacaa tagcattttg ctcatthaaa ggagggagtg gtaaaactac cttgtctctc 60
 aatgtttggt gtaatttagc ccaatatagc aacaaaaagg tttgtctgtt ggattttgat 120
 ccacaagcaa accttactac aggtcttggt gtacaactctt gttatgaatc taattttgaac 180
 gacattttta gaagttcagg aaacgttaag gatatacttc aagatacga gatagaaaaac 240
 ttacacatag taactcttag tattctcata gaggagtttc gagaatttaa tagaataatg 300
 tgaatggata caagtcattt cgtttcatct ttacaactta tgaatccaa ttatgatctg 360
 tgtatttttag acactccacc aagctctggg acgtccaccg aagaagcctt tatgtcatca 420
 gatcatttga ttgtttgtct tactctcgaa ccatthttcca tattaggatt acagaaaatc 480
 aaagagtttt gtccagtggt acctaaaaag aaagacttat cagtgttagg aatagttttt 540
 tctttttggg acggaaggaa ttcaacaaat tcaacctact tgaacattat agaattctat 600
 tacgaaggga aagtggttat tagtaaaagta cgaagagaca taacattaag cagatctctt 660
 ttaaaagaaa catccatagc taacgcatac cctaatttcta gagcaagta tgacatctgt 720
 cgtctaacaa aggatagata agataaaacta ttcaataaag aaatgtctgc ccagggaagt 780
 ttgtgagtaa gttagtcaaa gaagca 806

<210> 490
 <211> 293
 <212> PRT
 <213> *Chlamydia pneumoniae*

<400> 490
 Met Ser Lys His Thr Ser Glu Ser Arg Ile Ala Gln Asp Met Leu Glu


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1           5           10           15
Arg Tyr Ser Gly Ser Ser Val Lys Gln Phe Cys Pro Tyr Leu Leu Leu
20 25 30
Thr Asn Phe Ser Tyr Tyr Ile Gln Thr Phe Ala Lys Leu His Gly Val
35 40 45
Pro Val Phe Glu Gly Ser Met Phe Ser Ala Ala His Ala Pro His Leu
50 55 60
Lys Thr Ser Ile Leu Asp Phe Lys Leu Gly Ser Pro Gly Ala Ala Leu
65 70 75 80
Thr Ile Asp Leu Cys Ser Phe Leu Pro Asp Leu Lys Ala Ala Leu Met
85 90 95
Leu Gly Met Cys Gly Gly Leu Arg Ser His Tyr Gln Val Gly Asp Tyr
100 105 110
Phe Val Pro Val Ala Ser Ile Arg Gly Glu Gly Thr Ser Asp Ala Tyr
115 120 125
Phe Pro Pro Glu Val Pro Ala Leu Ala Asn Phe Val Val Gln Lys Ala
130 135 140
Thr Thr Glu Val Leu Glu Asp Lys Lys Ala Asn Tyr His Ile Gly Ile
145 150 155 160
Thr His Thr Thr Asn Ile Arg Phe Trp Glu Phe Asn Lys Lys Phe Arg
165 170 175
Lys Lys Leu Tyr Glu Thr Lys Ala Gln Ser Ala Glu Met Glu Cys Ala
180 185 190
Thr Leu Phe Ala Ala Gly Tyr Arg Arg Asn Leu Pro Ile Gly Ala Leu
195 200 205
Leu Leu Ile Ser Asp Leu Pro Leu Arg Lys Glu Gly Ile Lys Thr Lys
210 215 220
Ser Ser Gly Asn Phe Ile Phe Asn Thr Tyr Thr Glu Asp His Ile Leu
225 230 235 240
Thr Gly Gln Glu Val Ile Glu Asn Leu Glu Lys Val Met Leu Lys Arg
245 250 255
Ala Ala Ser Asp His Lys Lys Asp Gln Gln Tyr Arg Gly Leu Pro His
260 265 270
Met Glu Val Gly Glu Ala Asp Asp Thr Met Ala Ser Gly Ser Glu Thr
275 280 285
Ser Asp Ser Asp Tyr
290

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<210> 491
 <211> 394
 <212> PRT
 <213> Chlamydia pneumoniae

```

<400> 491
Met Ser Lys Glu Thr Phe Gln Arg Asn Lys Pro His Ile Asn Ile Gly
1 5 10 15
Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Ala Ala Ile
20 25 30
Thr Arg Ala Leu Ser Gly Asp Gly Leu Ala Ser Phe Arg Asp Tyr Ser
35 40 45
Ser Ile Asp Asn Thr Pro Glu Glu Lys Ala Arg Gly Ile Thr Ile Asn
50 55 60
Ala Ser His Val Glu Tyr Glu Thr Pro Asn Arg His Tyr Ala His Val
65 70 75 80
Asp Cys Pro Gly His Ala Asp Tyr Val Lys Asn Met Ile Thr Gly Ala
85 90 95
Ala Gln Met Asp Gly Ala Ile Leu Val Val Ser Ala Thr Asp Gly Ala
100 105 110
Met Pro Gln Thr Lys Glu His Ile Leu Leu Ala Arg Gln Val Gly Val
115 120 125
Pro Tyr Ile Val Val Phe Leu Asn Lys Val Asp Met Ile Ser Gln Glu

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130      135      140
Asp Ala Glu Leu Ile Asp Leu Val Glu Met Glu Leu Ser Glu Leu Leu
145      150      155      160
Glu Glu Lys Gly Tyr Lys Gly Cys Pro Ile Ile Arg Gly Ser Ala Leu
      165      170      175
Lys Ala Leu Glu Gly Asp Ala Asn Tyr Ile Glu Lys Val Arg Glu Leu
      180      185      190
Met Gln Ala Val Asp Asp Asn Ile Pro Thr Pro Glu Arg Glu Ile Asp
      195      200      205
Lys Pro Phe Leu Met Pro Ile Glu Asp Val Phe Ser Ile Ser Gly Arg
      210      215      220
Gly Thr Val Val Thr Gly Arg Ile Glu Arg Gly Ile Val Lys Val Ser
225      230      235      240
Asp Lys Val Gln Leu Val Gly Leu Gly Glu Thr Lys Glu Thr Ile Val
      245      250      255
Thr Gly Val Glu Met Phe Arg Lys Glu Leu Pro Glu Gly Arg Ala Gly
      260      265      270
Glu Asn Val Gly Leu Leu Leu Arg Gly Ile Gly Lys Asn Asp Val Glu
      275      280      285
Arg Gly Met Val Val Cys Gln Pro Asn Ser Val Lys Pro His Thr Lys
      290      295      300
Phe Lys Ser Ala Val Tyr Val Leu Gln Lys Glu Glu Gly Gly Arg His
305      310      315      320
Lys Pro Phe Phe Ser Gly Tyr Arg Pro Gln Phe Phe Phe Arg Thr Thr
      325      330      335
Asp Val Thr Gly Val Val Thr Leu Pro Glu Gly Thr Glu Met Val Met
      340      345      350
Pro Gly Asp Asn Val Glu Leu Asp Val Glu Leu Ile Gly Thr Val Ala
      355      360      365
Leu Glu Glu Gly Met Arg Phe Ala Ile Arg Glu Gly Gly Arg Thr Ile
      370      375      380
Gly Ala Gly Thr Ile Ser Lys Ile Asn Ala
385      390

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<210> 492

<211> 560

<212> PRT

<213> Chlamydia pneumoniae

<220>

<221> VARIANT

<222> 553,554,555,556,558,559,560

<223> Xaa = Any Amino Acid

<400> 492

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Met Pro Gln Lys Val Leu Ile Thr Ser Ala Leu Pro Tyr Ala Asn Gly
1      5      10      15
Pro Leu His Phe Gly His Ile Ala Gly Val Tyr Leu Pro Ala Asp Val
      20      25      30
Tyr Ala Arg Phe Arg Arg Leu Leu Gly Asp Asp Val Leu Tyr Ile Cys
      35      40      45
Gly Ser Asp Glu Phe Gly Ile Ala Ile Thr Leu Asn Ala Asp Arg Glu
      50      55      60
Gly Leu Gly Tyr Gln Glu Tyr Val Asp Met Tyr His Lys Leu His Lys
      65      70      75      80
Asp Thr Phe Glu Lys Leu Gly Phe Ala Leu Asp Phe Phe Ser Arg Thr
      85      90      95
Thr Asn Pro Phe His Ala Glu Leu Val Gln Asp Phe Tyr Ser Gln Leu
      100      105      110
Lys Ala Ser Gly Leu Ile Glu Asn Arg Ile Ser Glu Gln Leu Tyr Ser
      115      120      125

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Glu Gln Glu Gln Arg Phe Leu Ala Asp Arg Tyr Val Glu Gly Thr Cys
 130 135 140
 Pro Arg Cys Gly Phe Asp His Ala Arg Gly Asp Glu Cys Gln Ser Cys
 145 150 155
 Gly Ala Asp Tyr Glu Ala Ile Asp Leu Ile Gly Pro Lys Ser Lys Ile
 165 170 175
 Ser Gly Val Glu Leu Val Lys Lys Glu Thr Glu His Ser Tyr Phe Leu
 180 185 190
 Leu Asp Arg Met Lys Asp Ala Leu Leu Ser Phe Ile Gln Gly Cys Tyr
 195 200 205
 Leu Pro Asp His Val Arg Lys Phe Val Val Asp Tyr Ile Glu His Val
 210 215 220
 Arg Ser Arg Ala Ile Thr Arg Asp Leu Ser Trp Gly Ile Pro Val Pro
 225 230 235
 Asp Phe Pro Gly Lys Val Phe Tyr Val Trp Phe Asp Ala Pro Ile Gly
 245 250 255
 Tyr Ile Ser Gly Thr Met Glu Trp Ala Ala Ser Gln Gly Asn Pro Asp
 260 265 270
 Glu Trp Lys Arg Phe Trp Leu Glu Asp Gly Val Glu Tyr Val Gln Phe
 275 280 285
 Ile Gly Lys Asp Asn Leu Pro Phe His Ser Val Val Phe Pro Ala Met
 290 295 300
 Glu Leu Gly Gln Lys Leu Asp Tyr Lys Lys Val Asp Ala Leu Val Val
 305 310 315
 Ser Glu Phe Tyr Leu Leu Glu Gly Arg Gln Phe Ser Lys Ser Glu Gly
 325 330 335
 Asn Tyr Val Asp Met Asp Lys Phe Leu Ser Ser Tyr Ser Leu Asp Lys
 340 345 350
 Leu Arg Tyr Val Leu Ala Ala Thr Ala Pro Glu Thr Ser Asp Ser Glu
 355 360 365
 Phe Thr Phe Leu Asp Phe Lys Thr Arg Cys Asn Ser Glu Leu Val Gly
 370 375 380
 Lys Phe Gly Asn Phe Ile Asn Arg Val Leu Ala Phe Ala Glu Lys Asn
 385 390 395
 His Tyr Asp Lys Leu Ser Tyr His Ser Val Val Leu Glu Asp Ser Asp
 405 410 415
 Arg Ala Phe Leu Glu Glu Ala Arg Gln Leu Val Arg Asp Ala Glu Lys
 420 425 430
 Cys Tyr Arg Glu Tyr Ser Leu Arg Lys Ala Thr Ser Val Ile Met Ser
 435 440 445
 Leu Ala Ala Leu Gly Asn Val Tyr Phe Asn Gln Gln Ala Pro Trp Lys
 450 455 460
 Leu Leu Lys Glu Gly Thr Arg Glu Arg Val Glu Ala Ile Leu Phe Cys
 465 470 475
 Ala Cys Tyr Cys Gln Lys Leu Leu Ala Leu Ile Ser Tyr Pro Ile Ile
 485 490 495
 Pro Glu Ser Ala Val Ala Ile Trp Glu Met Ile Ser Pro Lys Ser Leu
 500 505 510
 Glu Asn Cys Asn Leu Asp Thr Met Tyr Ala Arg Asp Leu Trp Lys Glu
 515 520 525
 Glu Ile Leu Asp Val Ile Asn Glu Glu Phe His Leu Lys Ser Pro Arg
 530 535 540
 Leu Leu Phe Thr Thr Val Glu Thr Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa
 545 550 555 560

<210> 493

<211> 97

<212> PRT

<213> Chlamydia pneumoniae

<400> 493

Met Ile Lys Lys Asp Arg Phe Thr Asn Glu Lys Leu Asn Lys Leu Phe
 1 5 10 15
 Asp Ser Pro Phe Ser Leu Val Asn Tyr Ala Ile Lys Gln Ala Lys Ile
 20 25 30
 Lys Ile Ala Lys Gly Asp Val Arg Ser Ser Asn Val Ala Ile Glu Thr
 35 40 45
 Leu Val Leu Leu Asp Arg Glu Gly Ile Gln Pro Glu Phe Thr Glu Glu
 50 55 60
 Ile Val Val Thr Ala Ser Pro Thr Val Glu Arg Lys Arg Ser Glu His
 65 70 75 80
 Thr Asn Ser Arg Lys Lys Asp Pro Ser Ala Tyr Thr Trp Ser Asp Val
 85 90 95
 Lys

<210> 494

<211> 205

<212> PRT

<213> Chlamydia pneumoniae

<400> 494

Met Asn Lys Ile Leu Val Asp Ser Pro Phe Ser Pro Asp His Gln Lys
 1 5 10 15
 Cys Cys Pro Lys Leu Phe Thr Ile Ser Ala Pro Ala Gly Val Gly Lys
 20 25 30
 Thr Thr Leu Val Arg Met Leu Glu Gln Glu Phe Ser Ser Ala Phe Ala
 35 40 45
 Glu Thr Ile Ser Val Thr Thr Arg Lys Pro Arg Glu Gly Glu Val Pro
 50 55 60
 Gly Lys Asp Tyr His Phe Val Ser His Glu Glu Phe Gln Arg Leu Leu
 65 70 75 80
 Asp Arg Gln Ala Leu Leu Glu Trp Val Phe Leu Phe Gly Glu Cys Tyr
 85 90 95
 Gly Thr Ser Met Leu Glu Ile Glu Arg Ile Trp Ser Leu Gly Lys His
 100 105 110
 Ala Val Ala Val Ile Asp Ile Gln Gly Ala Leu Phe Ile Arg Ser Arg
 115 120 125
 Met Pro Ser Val Ser Ile Phe Ile Ala Pro Pro Ser Gln Glu Glu Leu
 130 135 140
 Glu Arg Arg Leu Ala Ser Arg Gly Ser Glu Glu Gly Ser Gln Arg Lys
 145 150 155 160
 Glu Arg Leu Glu His Ser Leu Ile Glu Leu Ala Ala Asn Gln Phe
 165 170 175
 Asp Tyr Val Ile Ile Asn Asp Asp Leu Asn Gln Ala Tyr Arg Val Leu
 180 185 190
 Lys Ser Ile Phe Ile Ala Glu Glu His Arg Asn Ile Leu
 195 200 205

<210> 495

<211> 602

<212> PRT

<213> Chlamydia pneumoniae

<400> 495

Met Lys Glu Tyr Lys Ile Glu Asn Ile Arg Asn Phe Ser Ile Ile Ala
 1 5 10 15
 His Ile Asp His Gly Lys Ser Thr Ile Ala Asp Arg Leu Leu Glu Ser
 20 25 30
 Thr Ser Thr Val Glu Glu Arg Glu Met Arg Glu Gln Leu Leu Asp Ser
 35 40 45
 Met Asp Leu Glu Arg Glu Arg Gly Ile Thr Ile Lys Ala His Pro Val

[illegible]

Ala Arg Glu Thr Ile Arg Ala Leu Ser Lys Asn Val Thr Ala Lys Cys
 345 550 555
 Tyr Gly Gly Asp Ile Thr Arg Lys Arg Lys Leu Trp Glu Lys Gln Lys
 565 570 575
 Lys Gly Lys Lys Arg Met Lys Glu Phe Gly Lys Val Ser Ile Pro Asn
 580 585 590
 Thr Ala Phe Ile Glu Val Leu Lys Leu Asp
 595 600

<210> 496

<211> 324

<212> PRT

<213> Chlamydia pneumoniae

<400> 496

Met Glu Leu Leu Pro His Glu Lys Gln Val Val Glu Tyr Glu Lys Ala
 1 5 10 15
 Ile Ala Glu Phe Lys Glu Lys Asn Lys Lys Asn Ser Leu Leu Ser Ser
 20 25 30
 Ser Glu Ile Gln Lys Leu Glu Lys Arg Leu Asp Lys Leu Lys Glu Lys
 35 40 45
 Ile Tyr Ser Asp Leu Thr Pro Trp Glu Arg Val Gln Ile Cys Arg His
 50 55 60
 Pro Ser Arg Pro Arg Thr Val Asn Tyr Ile Glu Gly Met Cys Glu Glu
 65 70 75 80
 Phe Val Glu Leu Cys Gly Asp Arg Thr Phe Arg Asp Asp Pro Ala Val
 85 90 95
 Val Gly Gly Phe Val Lys Ile Gln Gly Gln Arg Phe Val Leu Ile Gly
 100 105 110
 Gln Glu Lys Gly Cys Asp Thr Ala Ser Arg Leu His Arg Asn Phe Gly
 115 120 125
 Met Leu Cys Pro Glu Gly Phe Arg Lys Ala Leu Arg Leu Gly Lys Leu
 130 135 140
 Ala Glu Lys Phe Gly Leu Pro Val Val Phe Leu Val Asp Thr Pro Gly
 145 150 155 160
 Ala Tyr Pro Gly Leu Thr Ala Glu Glu Arg Gly Gln Gly Trp Ala Ile
 165 170 175
 Ala Lys Asn Leu Phe Glu Leu Ser Arg Leu Ala Thr Pro Val Ile Ile
 180 185 190
 Val Val Ile Gly Glu Gly Cys Ser Gly Gly Ala Leu Gly Met Ala Val
 195 200 205
 Gly Asp Ser Val Ala Met Leu Glu His Ser Tyr Trp Ser Val Ile Ser
 210 215 220
 Pro Glu Gly Cys Ala Ser Ile Leu Trp Lys Asp Pro Lys Lys Asn Ser
 225 230 235 240
 Glu Ala Ala Ser Met Leu Lys Met His Gly Glu Asn Leu Lys Gln Phe
 245 250 255
 Gly Ile Ile Asp Thr Val Ile Lys Glu Pro Ile Gly Gly Ala His His
 260 265 270
 Asp Pro Ala Leu Val Tyr Ser Asn Val Arg Glu Phe Ile Ile Gln Glu
 275 280 285
 Trp Leu Arg Leu Lys Asp Leu Ala Ile Glu Glu Leu Leu Glu Lys Arg
 290 295 300
 Tyr Glu Lys Phe Arg Ser Ile Gly Leu Tyr Glu Thr Thr Ser Glu Ser
 305 310 315 320
 Gly Pro Glu Ala

<210> 497

<211> 659

<212> PRT

<213> Chlamydia pneumoniae

<400> 497

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Met Lys Leu Leu Leu Lys Ala Val Leu Arg His Lys Asn His Leu Val
1      5      10      15
Ile Leu Gly Cys Ser Leu Leu Ala Ile Leu Gly Leu Thr Phe Ser Ser
20      25      30
Gln Met Glu Ile Phe Ser Leu Gly Met Ile Ala Lys Thr Gly Pro Asp
35      40      45
Ala Phe Leu Leu Phe Gly Arg Lys Glu Ser Gly Lys Leu Val Lys Val
50      55      60
Ser Glu Leu Ser Gln Lys Asp Ile Leu Glu Asn Trp Gln Ala Ile Ser
65      70      75
Lys Asp Ser Glu Thr Leu Thr Val Ser Asp Ala Thr Thr Tyr Ile Ala
85      90      95
Glu His Gly Lys Ser Thr Ala Ser Leu Thr Ser Lys Leu Ser Lys Phe
100     105     110
Val Arg Asn Tyr Ile Asp Val Ser Arg Phe Arg Gly Leu Ala Ile Phe
115     120     125
Leu Ile Cys Val Ala Ile Phe Lys Ala Val Thr Leu Phe Phe Gln Arg
130     135     140
Phe Leu Gly Gln Val Val Ala Ile Arg Val Ser Arg Asp Leu Arg Gln
145     150     155
Asp Tyr Phe Lys Ala Leu Gln Gln Leu Pro Met Thr Phe Phe His Asp
165     170     175
His Asp Ile Gly Asn Leu Ser Asn Arg Val Met Thr Asp Ser Ala Ser
180     185     190
Ile Ala Leu Ala Val Asn Ser Leu Met Ile Asn Tyr Ile Gln Ala Pro
195     200     205
Ile Thr Phe Ile Leu Thr Leu Gly Val Cys Leu Ser Ile Ser Trp Lys
210     215     220
Phe Ser Ile Leu Ile Cys Val Ala Phe Pro Ile Phe Ile Leu Pro Ile
225     230     235
Val Val Ile Ala Arg Lys Ile Lys Asn Leu Ala Lys Arg Ile Gln Lys
245     250     255
Ser Gln Asp Ser Phe Ser Ser Val Leu Tyr Asp Phe Leu Ala Gly Val
260     265     270
Met Thr Val Lys Val Phe Arg Thr Glu Lys Phe Ala Phe Thr Lys Tyr
275     280     285
Cys Glu His Asn Asn Lys Ile Ser Ala Leu Glu Glu Lys Ser Ala Ala
290     295     300
Tyr Gly Leu Leu Pro Arg Pro Leu Leu His Thr Ile Ala Ser Leu Phe
305     310     315
Phe Ala Phe Val Val Val Ile Gly Ile Tyr Lys Phe Ala Ile Pro Pro
320     325     330
Glu Glu Leu Ile Val Phe Cys Gly Leu Leu Tyr Leu Ile Tyr Asp Pro
335     340     345
Ile Lys Lys Phe Gly Asp Glu Asn Thr Ser Ile Met Arg Gly Cys Ala
350     355     360
Ala Ala Glu Arg Phe Tyr Glu Val Leu Asn His Pro Asp Leu His Ser
365     370     375
Gln Lys Glu Arg Glu Ile Glu Phe Leu Gly Leu Ser Asn Thr Ile Thr
380     385     390
Phe Glu Asn Val Ser Phe Gly Tyr Gln Glu Asp Lys His Ile Leu Lys
395     400     405
Asn Leu Ser Phe Thr Leu His Lys Gly Glu Ala Leu Gly Ile Val Gly
410     415     420
Pro Thr Gly Ser Gly Lys Thr Thr Leu Val Lys Leu Leu Pro Arg Leu
425     430     435
Tyr Glu Val Ser Gln Gly Lys Ile Leu Ile Asp Ser Leu Pro Ile Thr
440     445     450
455     460

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Glu Tyr Asn Lys Gly Ser Leu Arg Asn His Ile Ala Cys Val Leu Gln
 465 470 475 480
 Asn Pro Phe Leu Phe Tyr Asp Thr Val Trp Asn Asn Leu Thr Cys Gly
 485 490 495
 Lys Asp Met Glu Glu Glu Ala Val Leu Glu Ala Leu Lys Arg Ala Tyr
 500 505 510
 Ala Asp Glu Phe Ile Leu Lys Leu Pro Lys Gly Val His Ser Val Leu
 515 520 525
 Glu Glu Ser Gly Lys Asn Leu Ser Gly Gly Gln Gln Gln Arg Leu Ala
 530 535 540
 Ile Ala Arg Ala Leu Leu Lys Asn Ala Ser Ile Leu Ile Leu Asp Glu
 545 550 555
 Ala Thr Ser Ala Leu Asp Ala Ile Ser Glu Asn Tyr Ile Lys Asn Ile
 565 570 575
 Ile Gly Glu Leu Lys Gly Gln Cys Thr Gln Ile Ile Ala His Lys
 580 585 590
 Leu Thr Thr Leu Glu His Val Asp Arg Val Leu Tyr Ile Glu Asn Gly
 595 600 605
 Gln Lys Ile Ala Glu Gly Thr Lys Glu Glu Leu Leu Gln Thr Cys Pro
 610 615 620
 Glu Phe Leu Lys Met Trp Glu Leu Ser Gly Thr Lys Glu Tyr Asn Arg
 625 630 635
 Val Phe Val Pro Asp His Lys Leu Val Ala Asn Pro Thr Asp Met Ala
 645 650 655
 Ile Thr Thr

<210> 498

<211> 411

<212> PRT

<213> Chlamydia pneumoniae

<400> 498

Met Ile Pro Thr Met Leu Met Phe Phe Ile Ile Cys Phe Thr Leu Cys
 1 5 10 15
 Ser Gly Phe Ile Ser Leu Ser Gln Ile Ala Leu Phe Ser Leu Pro Thr
 20 25 30
 Ser Leu Ile Ser His Tyr Lys Arg Ser Lys Ser Lys Lys Gln Gln Arg
 35 40 45
 Val Ala Thr Leu Leu Leu His Pro His His Leu Leu Ile Thr Leu Ile
 50 55 60
 Phe Cys Asp Ile Gly Leu Asn Ile Ala Ile Gln Asn Cys Phe Ala Ile
 65 70 75 80
 Leu Phe Gly Asp Ala Ala Ser Trp Trp Phe Thr Val Gly Leu Pro Leu
 85 90 95
 Ala Ile Thr Leu Ile Leu Gly Glu Ile Leu Pro Lys Ala Val Ala Leu
 100 105 110
 Pro Phe Asn Thr Gln Ile Ala Ser Ser Val Ala Pro Leu Ile Leu Cys
 115 120 125
 Val Thr Lys Ile Phe Lys Pro Leu Leu His Trp Gly Ile Val Gly Ile
 130 135 140
 Asn Tyr Val Val Gln Trp Ile Leu Ser Lys Gln Gln Ile Asp Ile Ile
 145 150 155 160
 Gln Pro Gln Glu Leu Lys Glu Val Leu Gln Ser Cys Lys Asp Phe Gly
 165 170 175
 Val Val Asn Gln Glu Glu Ser Arg Leu Leu Tyr Gly Tyr Leu Ser Leu
 180 185 190
 Ser Asp Cys Ser Val Lys Glu Arg Met Gln Pro Arg Gln Asp Ile Leu
 195 200 205
 Phe Tyr Asp Ile Gln Thr Pro Leu Glu Asn Leu Tyr Leu Leu Phe Ser
 210 215 220

Lys Gln His Cys Ser Arg Val Pro Ile Cys Asn Asp Asn Leu Gln Asn
 225 230 235 240
 Leu Leu Gly Ile Cys Thr Ala Arg Ser Leu Leu Leu His Asp Lys Pro
 245 250 255
 Leu Gln Ser Ser Asp Asp Leu Leu Pro Leu Leu Lys Lys Pro Tyr Tyr
 260 265 270
 Met Pro Glu Thr Ile Ser Ala Lys Met Ala Leu Cys Gln Met Ala Ala
 275 280 285
 Glu Asp Glu Thr Leu Gly Met Ile Ile Asp Glu Tyr Gly Ser Ile Glu
 290 295 300
 Gly Leu Ile Thr Gln Glu Asp Leu Phe Glu Ile Val Ala Gly Glu Ile
 305 310 315
 Val Asp Gln Arg Asp Asn Lys Ile Leu Tyr Thr Thr Ser Gly Ala Asp
 325 330 335
 Val Ile Ile Ala Ser Gly Thr Leu Glu Leu Arg Glu Phe Ser Glu Ile
 340 345 350
 Phe Asp Ile Asn Leu Pro Thr Asn Asn Asn Ile Ala Thr Ile Gly Gly
 355 360 365
 Trp Leu Ile Glu Gln Ile Gly Thr Ile Pro Thr Thr Thr Met Lys Leu
 370 375 380
 Ser Trp Asn Asn Leu Leu Phe Gln Val Leu Asp Ala Pro Asn Arg
 385 390 395 400
 Ile Arg Arg Val Tyr Ile Arg Lys Leu Tyr Asp
 405 410

<210> 499

<211> 404

<212> PRT

<213> Chlamydia pneumoniae

<400> 499

Met Thr Asn Ser Ala Leu Phe Trp Ile Gly Val Asn Ile Ile Cys Ile
 1 5 10 15
 Val Leu Gln Gly Phe Tyr Ser Met Met Glu Met Ala Cys Val Ser Phe
 20 25 30
 Asn Arg Val Arg Leu Gln Tyr Tyr Leu Thr Lys Asp His Lys Lys Ala
 35 40 45
 Arg Tyr Ile Asn Phe Leu Ile Arg Arg Pro Tyr Arg Leu Phe Gly Thr
 50 55 60
 Val Met Leu Gly Val Asn Ile Ala Leu Gln Val Gly Ser Glu Ser Ser
 65 70 75 80
 Arg Asn Cys Tyr Arg Ala Leu Gly Ile Thr Pro Asp Tyr Ala Pro Phe
 85 90 95
 Thr Gln Ile Phe Ile Val Val Ile Phe Ala Glu Leu Leu Pro Leu Thr
 100 105 110
 Ile Ser Arg Lys Ile Pro Glu Lys Leu Ala Leu Trp Gly Ala Pro Ile
 115 120 125
 Leu Tyr Tyr Ser His Tyr Ile Phe Tyr Pro Leu Ile Gln Leu Ile Gly
 130 135 140
 Ser Leu Thr Glu Gly Leu Tyr Tyr Leu Leu Asn Ile Arg Lys Glu Lys
 145 150 155 160
 Leu Asn Ser Thr Leu Ser Arg Asp Glu Phe Gln Lys Ala Leu Glu Thr
 165 170 175
 His His Glu Glu Gln Asp Phe Asn Thr Ile Ala Thr Asn Ile Phe Ser
 180 185 190
 Leu Ser Ala Thr Cys Ala Asp Gln Val Cys Gln Pro Leu Glu Gln Val
 195 200 205
 Thr Met Leu Pro Ser Ser Ala Asn Val Lys Asp Phe Cys Arg Thr Ile
 210 215 220
 Lys Asn Thr Asp Ile Asn Phe Ile Pro Val Tyr His Lys Ala Arg Lys
 225 230 235 240

Asn Val Ile Gly Ile Ala His Pro Lys Asp Phe Val Asn Lys Ala Leu
 245 255
 Asp Glu Pro Leu Ile Asn Asn Leu His Ser Pro Trp Phe Ile Thr Ala
 260 270
 Lys Ser Lys Leu Ile Arg Ile Leu Lys Glu Phe Arg Asp Asn Arg Ser
 275 285
 Ser Val Ala Val Val Leu Asn Ala Ser Gly Glu Pro Ile Gly Ile Leu
 290 300
 Ser Leu Asn Ala Ile Phe Lys Ile Leu Phe Asn Thr Thr Asn Ile Ala
 305 310 315 320
 His Leu Lys Pro Lys Thr Ile Ser Val Ile Glu Arg Thr Phe Pro Gly
 325 335
 Asn Ser Arg Ile Lys Asp Leu Gln Lys Glu Leu Asp Ile Gln Phe Pro
 340 345 350
 Gln Tyr Pro Val Glu Thr Leu Ala Gln Leu Val Leu Gln Leu Asp
 355 365
 Ser Pro Ala Glu Val Gly Thr Ser Val Ile Ile Asn Asn Leu Leu Leu
 370 375 380
 Glu Val Lys Glu Met Ser Leu Ser Gly Ile Lys Thr Val Ser Ile Lys
 385 390 395 400
 Asn Leu Leu Ser

<210> 500

<211> 543

<212> FRT

<213> Chlamydia pneumoniae

<400> 500

Met Phe Gly Ser Glu Ser Leu Arg Tyr Gln Leu Leu Ile Gln Asp Phe
 1 5 10 15
 Ala Lys Val Ser Glu Glu Gly Ile Gly Leu Leu Glu Ser Lys Glu Tyr
 20 25 30
 Ser Leu Leu Gln Ala Lys Leu Val Leu Arg Ala Leu Ala Gln Asn Ser
 35 40 45
 Ser Phe Asp Asp Trp Phe Arg Ser Phe Lys Lys Cys Gln Ile Ser Tyr
 50 55 60
 Pro Glu Leu Ala His Asp Arg Asp Val Leu Glu Glu Phe Gly Ile Gln
 65 70 75 80
 Val Leu Arg Glu Gly Ile Glu Asn Pro Ser Val Thr Val Arg Ala Val
 85 90 95
 Ser Val Leu Ala Ile Gly Leu Ala Arg Asp Phe Arg Leu Val Pro Leu
 100 105 110
 Leu Leu Gln Ser Cys Asn Asp Asp Ser Ala Ile Val Arg Ser Leu Ala
 115 120 125
 Leu Gln Val Ala Val Asn Tyr Gly Ser Glu Ser Leu Lys Lys Ala Ile
 130 135 140
 Val Glu Leu Ala Arg Asn Asp Asp Ser Ile His Val Arg Ile Thr Ala
 145 150 155 160
 Tyr Gln Val Val Ala Leu Leu Gln Ile Glu Glu Leu Leu Pro Phe Leu
 165 170 175
 Arg Glu Arg Ala Glu Asn Lys Leu Val Asp Ser Val Glu Arg Arg Glu
 180 185 190
 Ala Trp Lys Ala Cys Leu Glu Leu Ser Ser Gln Phe Leu Glu Thr Gly
 195 200 205
 Val Ala Lys Asp Asp Ile Asp Gln Ala Leu Phe Thr Cys Glu Val Leu
 210 215 220
 Arg Asn Gly Met Leu Pro Glu Thr Thr Glu Ile Phe Thr Glu Leu Leu
 225 230 235 240
 Ser Val Glu His Pro Glu Val Gln Glu Ser Leu Leu Ser Ala Leu
 245 250 255

Ala Trp Ser His Gln Leu Gln Asn His Lys Glu Phe Leu Ser Lys Val
 260 265 270
 Arg His Val Met Cys Thr Ser Pro Phe Ala Lys Val Arg Phe Gln Ala
 275 280 285
 Ala Ala Leu Leu His Leu His Gly Asp Pro Leu Gly Arg Asp Ser Leu
 290 295 300
 Val Glu Gly Leu Arg Ser Pro Gln Pro Leu Val Cys Glu Ala Ala Ser
 305 310 315
 Ala Ala Leu Cys Ser Leu Gly Ile His Gly Val Pro Leu Ala Lys Glu
 325 330 335
 His Leu Glu Ser Leu Ser Ser Arg Lys Ala Ala Asn Leu Ser Ile
 340 345 350
 Leu Leu Leu Val Ser Arg Glu Asp Ile Glu Arg Ala Gly Asp Val Ile
 355 360 365
 Ala Arg Tyr Leu Ser Asn Pro Glu Met Cys Trp Ala Ile Glu Tyr Phe
 370 375 380
 Leu Trp Asp Ala Gln Trp Asn Leu Arg Gly Asp Thr Phe Pro Leu Tyr
 385 390 395
 Ser Asp Met Ile Lys Arg Glu Ile Gly Arg Lys Leu Ile Arg Leu Leu
 405 410 415
 Ala Val Ala Arg Tyr Ser Gln Ala Lys Ala Val Thr Ala Thr Phe Leu
 420 425 430
 Ser Gly Gln Gln Ala Gln Gly Trp Ser Phe Phe Ser Gly Met Phe Trp
 435 440 445
 Glu Glu Gly Asp Val Lys Thr Ser Glu Asp Leu Val Thr Asp Ala Cys
 450 455 460
 Phe Ala Ala Lys Leu Glu Gly Ala Leu Ala Ser Leu Cys Gln Lys Lys
 465 470 475
 Asp Gln Ala Ser Leu Gln Arg Val Ser Gln Leu Tyr Asn Asp Ser Arg
 485 490 495
 Trp Gln Asp Lys Leu Ala Ile Leu Glu Ser Val Ala Phe Ser Glu Asn
 500 505 510
 Leu Asp Ala Val Pro Phe Leu Leu Asp Cys Cys His His Glu Ala Pro
 515 520 525
 Ser Leu Arg Ser Ala Ala Ala Gly Ala Leu Phe Ser Ile Phe Lys
 530 535 540

<210> 501

<211> 103

<212> PRT

<213> Chlamydia pneumoniae

<400> 501

Met Ser Phe Lys Arg Phe Leu Gln Gln Ile Pro Val Arg Ile Cys Leu
 1 5 10 15
 Leu Ile Ile Tyr Leu Tyr Gln Trp Leu Ile Ser Pro Leu Leu Gly Ser
 20 25 30
 Cys Cys Arg Phe Phe Pro Ser Cys Ser His Tyr Ala Glu Gln Ala Leu
 35 40 45
 Lys Ser His Gly Phe Leu Met Gly Cys Trp Leu Ser Ile Lys Arg Ile
 50 55 60
 Gly Lys Cys Gly Pro Trp His Pro Gly Gly Ile Asp Met Val Pro Lys
 65 70 75 80
 Thr Ala Leu Gln Glu Val Leu Glu Pro Tyr Gln Glu Ile Asp Gly Gly
 85 90 95
 Asp Ser Ser His Phe Ser Glu
 100

<210> 502

<211> 362

<212> PRT

<213> Chlamydia pneumoniae

<400> 502

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Met Ala Phe Lys Arg Lys Thr Arg Trp Leu Trp Gln Val Leu Ile Leu
 1      5      10      15
Ser Val Gly Leu Asn Met Leu Phe Leu Leu Phe Tyr Ser Ala Ile
      20      25      30
Phe Arg Lys Asp Ile Tyr Lys Leu His Leu Phe Ser Gly Pro Leu Ile
      35      40      45
Ala Lys Ser Ser Arg Lys Val Tyr Leu Ser Glu Asp Phe Leu Asn Glu
      50      55      60
Ile Ser Gln Ala Ser Leu Asp Asp Leu Ile Ser Leu Phe Lys Asp Glu
      65      70      75
Arg Tyr Met Tyr Gly Arg Pro Ile Lys Leu Trp Ala Leu Ser Val Ala
      85      90      95
Ile Ala Ser His His Ile Asp Ile Thr Pro Val Leu Ser Lys Pro Leu
      100      105      110
Thr Tyr Thr Glu Leu Lys Gly Ser Ser Val Arg Trp Leu Pro Asn
      115      120      125
Ile Asp Leu Lys Asp Phe Pro Val Ile Leu Asp Tyr Leu Arg Cys His
      130      135      140
Lys Tyr Pro Tyr Thr Ser Lys Gly Leu Phe Leu Leu Ile Glu Lys Met
      145      150      155
Val Gln Glu Gly Trp Val Asp Glu Asp Cys Leu Tyr His Phe Cys Ser
      165      170      175
Thr Pro Glu Phe Leu Tyr Leu Arg Thr Leu Leu Val Gly Ala Asp Val
      180      185      190
Gln Ala Ser Ser Val Ala Ser Leu Ala Arg Met Val Ile Arg Cys Gly
      195      200      205
Ser Glu Arg Phe Phe His Phe Cys Asn Glu Glu Ser Arg Thr Ser Met
      210      215      220
Ile Ser Ala Thr Gln Arg Gln Lys Val Leu Lys Ser Tyr Leu Asp Cys
      225      230      235
Glu Glu Ser Leu Ala Ala Leu Leu Leu Val His Asp Ser Asp Val
      245      250      255
Val Leu His Glu Phe Cys Asp Glu Asp Leu Glu Lys Val Ile Arg Leu
      260      265      270
Met Pro Gln Glu Ser Pro Tyr Ser Gln Asn Phe Phe Ser Arg Leu Gln
      275      280      285
His Ser Pro Arg Arg Glu Leu Ala Cys Met Ser Thr Gln Arg Val Glu
      290      295      300
Ala Pro Arg Val Gln Glu Asp Gln Asp Glu Glu Tyr Val Val Gln Asp
      305      310      315
Gly Asp Ser Leu Trp Leu Ile Ala Lys Arg Phe Gly Ile Pro Met Asp
      325      330      335
Lys Ile Ile Gln Lys Asn Gly Leu Asn His His Arg Leu Phe Pro Gly
      340      345      350
Lys Val Leu Lys Leu Pro Ala Lys Gln Ser
      355      360

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<210> 503

<211> 582

<212> PRT

<213> Chlamydia pneumoniae

<400> 503

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Met Ser Gly Lys Lys Asp Gly Val Arg Gly Met Ile Phe Val Pro Leu
 1      5      10      15
Ser Ile Leu Val Leu Ile Phe Leu Pro Leu Pro Gln Ile Leu Leu Asp
      20      25      30
Phe Gly Leu Cys Ile Ser Phe Ala Leu Ser Leu Leu Thr Val Cys Trp

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Val	Phe	Thr	Leu	Asn	Ser	Ser	Asn	Ser	Ala	Lys	Leu	Phe	Pro	Pro	Phe
50						55					60				
Phe	Leu	Tyr	Leu	Cys	Leu	Leu	Arg	Leu	Gly	Leu	Asn	Leu	Ala	Ser	Thr
65						70				75					80
Arg	Trp	Ile	Val	Ser	Ser	Gly	Thr	Ala	Ser	Ser	Leu	Ile	Val	Ser	Leu
				85					90					95	
Gly	Ser	Phe	Phe	Ser	Leu	Gly	Ser	Leu	Trp	Ala	Ala	Thr	Phe	Ala	Cys
			100					105					110		
Leu	Leu	Leu	Phe	Phe	Val	Asn	Phe	Leu	Met	Val	Ser	Lys	Gly	Ser	Glu
			115				120					125			
Arg	Ile	Ala	Glu	Val	Arg	Ser	Arg	Phe	Phe	Leu	Glu	Ala	Leu	Pro	Ala
	130					135						140			
Lys	Gln	Met	Ala	Leu	Asp	Ser	Asp	Leu	Val	Ser	Gly	Arg	Ala	Ser	Tyr
145					150					155					160
Lys	Ala	Val	Lys	Lys	Gln	Lys	Asn	Ala	Leu	Ile	Glu	Glu	Gly	Asp	Phe
				165					170					175	
Phe	Ser	Ala	Met	Glu	Gly	Val	Phe	Arg	Phe	Val	Lys	Gly	Asp	Ala	Ile
			180					185					190		
Ile	Ser	Cys	Ile	Leu	Leu	Leu	Val	Asn	Val	Val	Ser	Val	Thr	Cys	Leu
		195					200					205			
Tyr	Tyr	Thr	Ser	Gly	Tyr	Ala	Leu	Glu	Gln	Met	Trp	Phe	Thr	Val	Leu
	210					215						220			
Gly	Asp	Ala	Leu	Val	Ser	Gln	Val	Pro	Ala	Leu	Leu	Thr	Ser	Cys	Ala
225					230					235					240
Ala	Ala	Thr	Leu	Ile	Ser	Lys	Ile	Asp	Lys	Glu	Glu	Ser	Leu	Leu	Asn
				245					250					255	
Tyr	Leu	Phe	Glu	Tyr	Tyr	Lys	Gln	Leu	Arg	Gln	His	Phe	Arg	Val	Val
			260					265					270		
Ser	Leu	Leu	Ile	Phe	Ser	Leu	Cys	Cys	Ile	Pro	Ser	Ser	Pro	Lys	Phe
			275				280					285			
Pro	Ile	Val	Leu	Leu	Ala	Ser	Leu	Leu	Trp	Leu	Ala	Tyr	Arg	Lys	Glu
	290					295					300				
Glu	Pro	Ala	Ser	Glu	Asp	Ser	Cys	Ile	Glu	Arg	Ala	Phe	Ser	Tyr	Val
305					310					315					320
Glu	Gly	Ala	Cys	Pro	Lys	Glu	Gln	Glu	Ser	Gln	Phe	Tyr	Gln	Val	Tyr
				325					330					335	
Arg	Ala	Ala	Ser	Glu	Glu	Val	Phe	Glu	Asp	Leu	Gly	Val	Arg	Leu	Pro
				340				345					350		
Val	Leu	Thr	Ser	Leu	Arg	Ile	Glu	Glu	Arg	Pro	Trp	Leu	Arg	Val	Phe
			355				360					365			
Gly	Gln	Asn	Val	Tyr	Leu	Asp	Glu	Met	Thr	Pro	Glu	Ala	Val	Leu	Pro
	370					375					380				
Phe	Leu	Arg	Asn	Ile	Ala	His	Glu	Ala	Leu	Asn	Ala	Glu	Val	Val	Gln
385					390					395					400
Lys	Tyr														

Lys Asp Phe Arg Ala Ile Val Thr Ser Cys Glu Thr Arg Phe Glu Met
 530 535 540
 Lys Lys Met Leu Asp Pro His Phe Pro Asp Leu Leu Val Leu Ser His
 545 550 555 560
 Asp Glu Leu Pro Lys Glu Ile Pro Ile Ser Phe Leu Gly Ile Val Ser
 565 570 575
 Asp Glu Val Leu Val Pro
 580

<210> 504

<211> 435

<212> PRT

<213> Chlamydia pneumoniae

<400> 504

Met Phe Ser Arg Trp Ile Thr Leu Phe Leu Leu Phe Ile Ser Leu Thr
 1 5 10 15
 Gly Cys Ser Ser Tyr Ser Ser Lys His Lys Gln Ser Leu Ile Ile Pro
 20 25 30
 Ile His Asp Asp Pro Val Ala Phe Ser Pro Glu Gln Ala Lys Arg Ala
 35 40 45
 Met Asp Leu Ser Ile Ala Gln Leu Leu Phe Asp Gly Leu Thr Arg Glu
 50 55 60
 Thr His Arg Glu Ser Asn Asp Leu Glu Leu Ala Ile Ala Ser Arg Tyr
 65 70 75 80
 Thr Val Ser Glu Asp Phe Cys Ser Tyr Thr Phe Phe Ile Lys Asp Ser
 85 90 95
 Ala Leu Trp Ser Asp Gly Thr Pro Ile Thr Ser Glu Asp Ile Arg Asn
 100 105 110
 Ala Trp Glu Tyr Ala Gln Glu Asn Ser Pro His Ile Gln Ile Phe Gln
 115 120 125
 Gly Leu Asn Phe Ser Thr Pro Ser Ser Asn Ala Ile Thr Ile His Leu
 130 135 140
 Asp Ser Pro Asn Pro Asp Phe Pro Lys Leu Leu Ala Phe Pro Ala Phe
 145 150 155 160
 Ala Ile Phe Lys Pro Glu Asn Pro Lys Leu Phe Ser Gly Pro Tyr Thr
 165 170 175
 Leu Val Glu Tyr Phe Pro Gly His Asn Ile His Leu Lys Lys Asn Pro
 180 185 190
 Asn Tyr Tyr Asp Tyr His Cys Val Ser Ile Asn Ser Ile Lys Leu Leu
 195 200 205
 Ile Ile Pro Asp Ile Tyr Thr Ala Ile His Leu Leu Asn Arg Gly Lys
 210 215 220
 Val Asp Trp Val Gly Gln Pro Trp His Gln Gly Ile Pro Trp Glu Leu
 225 230 235 240
 His Lys Gln Ser Gln Tyr His Tyr Tyr Thr Tyr Pro Val Glu Gly Ala
 245 250 255
 Phe Trp Leu Cys Leu Asn Thr Lys Ser Pro His Leu Asn Asp Leu Gln
 260 265 270
 Asn Arg His Arg Leu Ala Thr Cys Ile Asp Lys Arg Ser Ile Ile Glu
 275 280 285
 Glu Ala Leu Gln Gly Thr Gln Gln Pro Ala Glu Thr Leu Ser Arg Gly
 290 295 300
 Ala Pro Gln Pro Asn Gln Tyr Lys Lys Gln Lys Pro Leu Thr Pro Gln
 305 310 315 320
 Glu Lys Leu Val Leu Thr Tyr Pro Ser Asp Ile Leu Arg Cys Gln Arg
 325 330 335
 Ile Ala Glu Ile Leu Lys Glu Gln Trp Lys Ala Ala Gly Ile Asp Leu
 340 345 350
 Ile Leu Glu Gly Leu Glu Tyr His Leu Phe Val Asn Lys Arg Lys Val
 355 360 365

Gln Asp Tyr Ala Ile Ala Thr Gln Thr Gly Val Ala Tyr Tyr Pro Gly
 370 375 380
 Ala Asn Leu Ile Ser Glu Glu Asp Lys Leu Leu Gln Asn Phe Glu Ile
 385 390 395 400
 Ile Pro Ile Tyr Tyr Leu Ser Tyr Asp Tyr Leu Thr Gln Asp Phe Ile
 405 410 415
 Glu Gly Val Ile Tyr Asn Ala Ser Gly Ala Val Asp Leu Lys Tyr Thr
 420 425 430
 Tyr Phe Pro
 435

<210> 505

<211> 171

<212> PRT

<213> Chlamydia pneumoniae

<400> 505

Met Lys Lys Leu Leu Phe Ser Thr Phe Leu Leu Val Leu Gly Ser Thr
 1 5 10 15
 Ser Ala Ala His Ala Asn Leu Gly Tyr Val Asn Leu Lys Arg Cys Leu
 20 25 30
 Glu Glu Ser Asp Leu Gly Lys Lys Glu Thr Glu Glu Leu Glu Ala Met
 35 40 45
 Lys Gln Gln Phe Val Lys Asn Ala Glu Lys Ile Glu Glu Leu Thr
 50 55 60
 Ser Ile Tyr Asn Lys Leu Gln Asp Glu Asp Tyr Met Glu Ser Leu Ser
 65 70 75 80
 Asp Ser Ala Ser Glu Glu Leu Arg Lys Lys Phe Glu Asp Leu Ser Gly
 85 90 95
 Glu Tyr Asn Ala Tyr Gln Ser Gln Tyr Tyr Gln Ser Ile Asn Gln Ser
 100 105 110
 Asn Val Lys Arg Ile Gln Lys Leu Ile Gln Glu Val Lys Ile Ala Ala
 115 120 125
 Glu Ser Val Arg Ser Lys Glu Lys Leu Glu Ala Ile Leu Asn Glu Glu
 130 135 140
 Ala Val Leu Ala Ile Ala Pro Gly Thr Asp Lys Thr Thr Glu Ile Ile
 145 150 155 160
 Ala Ile Leu Asn Glu Ser Phe Lys Lys Gln Asn
 165 170

<210> 506

<211> 360

<212> FRT

<213> Chlamydia pneumoniae

<400> 506

Met Ser Glu Ala Pro Val Tyr Thr Leu Lys Gln Leu Ala Glu Leu Leu
 1 5 10 15
 Gln Val Glu Val Gln Gly Asn Ile Glu Thr Pro Ile Ser Gly Val Glu
 20 25 30
 Asp Ile Ser Gln Ala Gln Pro His His Ile Ala Phe Leu Asp Asn Glu
 35 40 45
 Lys Tyr Ser Ser Phe Leu Lys Asn Thr Lys Ala Gly Ala Ile Ile Leu
 50 55 60
 Ser Arg Ser Gln Ala Met Gln His Ala His Leu Lys Lys Asn Phe Leu
 65 70 75 80
 Ile Thr Asn Glu Ser Pro Ser Leu Thr Phe Gln Lys Cys Ile Glu Leu
 85 90 95
 Phe Ile Glu Pro Val Thr Ser Gly Phe Pro Gly Ile His Pro Thr Ala
 100 105 110
 Val Ile His Pro Thr Ala Arg Ile Glu Lys Asn Val Thr Ile Glu Pro

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115          120          125
Tyr Val Val Ile Ser Gln His Ala His Ile Gly Ser Asp Thr Tyr Ile
130          135          140
Gly Ala Gly Ser Val Ile Gly Ala His Ser Val Leu Gly Ala Asn Cys
145          150          155
Leu Ile His Pro Lys Val Val Ile Arg Glu Arg Val Leu Met Gly Asn
165          170          175
Arg Val Val Val Gln Pro Gly Ala Val Leu Gly Ser Cys Gly Phe Gly
180          185          190
Tyr Ile Thr Asn Ala Phe Gly His His Lys Pro Leu Lys His Leu Gly
195          200          205
Tyr Val Ile Val Gly Asp Asp Val Glu Ile Gly Ala Asn Thr Thr Ile
210          215          220
Asp Arg Gly Arg Phe Lys Asn Thr Val Ile His Glu Gly Thr Lys Ile
225          230          235
Asp Asn Gln Val Gln Val Ala His His Val Glu Ile Gly Lys His Ser
245          250          255
Ile Ile Val Ala Gln Ala Gly Ile Ala Gly Ser Thr Lys Ile Gly Glu
260          265          270
His Val Ile Ile Gly Gly Gln Thr Gly Ile Thr Gly His Ile Ser Ile
275          280          285
Ala Asp His Val Ile Met Ile Ala Gln Thr Gly Val Thr Lys Ser Ile
290          295          300
Thr Ser Pro Gly Ile Tyr Gly Gly Ala Pro Ala Arg Pro Tyr Gln Glu
305          310          315
Thr His Arg Leu Ile Ala Lys Ile Arg Asn Leu Pro Lys Thr Glu Glu
325          330          335
Arg Leu Ser Lys Leu Glu Lys Gln Val Arg Asp Leu Ser Thr Pro Ser
340          345          350
Leu Ala Glu Ile Pro Ser Glu Ile
355          360

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<210> 507

<211> 399

<212> PRT

<213> Chlamydia pneumoniae

<400> 507

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Met Ala Ala Ser Gly Gly Thr Gly Gly Leu Gly Gly Thr Gln Gly Val
1          5          10
Asn Leu Ala Ala Val Glu Ala Ala Ala Lys Ala Asp Ala Ala Glu
20          25          30
Val Val Ala Ser Gln Glu Gly Ser Glu Met Asn Met Ile Gln Gln Ser
35          40          45
Gln Asp Leu Thr Asn Pro Ala Ala Thr Arg Thr Lys Lys Lys Glu
50          55          60
Glu Lys Phe Gln Thr Leu Glu Ser Arg Lys Lys Gly Glu Ala Gly Lys
65          70          75
Ala Glu Lys Lys Ser Glu Ser Thr Glu Glu Lys Pro Asp Thr Asp Leu
85          90          95
Ala Asp Lys Tyr Ala Ser Gly Asn Ser Glu Ile Ser Gly Gln Glu Leu
100          105          110
Arg Gly Leu Arg Asp Ala Ile Gly Asp Asp Ala Ser Pro Glu Asp Ile
115          120          125
Leu Ala Leu Val Gln Glu Lys Ile Lys Asp Pro Ala Leu Gln Ser Thr
130          135          140
Ala Leu Asp Tyr Leu Val Gln Thr Thr Pro Pro Ser Gln Gly Lys Leu
145          150          155
Lys Glu Ala Leu Ile Gln Ala Arg Asn Thr His Thr Glu Gln Phe Gly
165          170          175
Arg Thr Ala Ile Gly Ala Lys Asn Ile Leu Phe Ala Ser Gln Glu Tyr

```


[illegible]

```
<210> 508
<211> 224
<212> PRT
<213> Chlamydia pneumoniae
```

Met	Thr	Ser	Trp	Ile	Glu	Leu	Leu	Asp	Lys	Gln	Ile	Glu	Asp	Gln	His
1				5				10					15		
Met	Leu	Lys	His	Glu	Phe	Tyr	Gln	Arg	Trp	Ser	Glu	Gly	Lys	Leu	Glu
			20					25					30		
Lys	Gln	Gln	Leu	Gln	Ala	Tyr	Ala	Lys	Asp	Tyr	Tyr	Leu	His	Ile	Lys
			35				40					45			
Ala	Phe	Pro	Cys	Tyr	Leu	Ser	Ala	Leu	His	Ala	Arg	Cys	Asp	Asp	Leu
			50			55					60				
Gln	Ile	Arg	Arg	Gln	Ile	Leu	Glu	Asn	Leu	Met	Asp	Glu	Glu	Ala	Gln
			65			70				75					80
Asn	Pro	Asn	His	Ile	Asp	Leu	Trp	Arg	Gln	Phe	Ala	Leu	Ser	Leu	Gly
			85					90					95		
Val	Ser	Glu	Glu	Glu	Leu	Ala	Asn	His	Glu	Phe	Ser	Gln	Ala	Ala	Gln
			100					105					110		
Asp	Met	Val	Ala	Thr	Phe	Arg	Arg	Leu	Cys	Asp	Met	Pro	Gln	Leu	Ala
			115				120					125			
Val	Gly	Leu	Gly	Ala	Leu	Tyr	Thr	Tyr	Glu	Ile	Gln	Ile	Pro	Gln	Val
			130			135					140				
Cys	Val	Glu	Lys	Ile	Arg	Gly	Leu	Lys	Glu	Tyr	Phe	Gly	Val	Ser	Ala
			145			150				155					160
Arg	Gly	Tyr	Ala	Tyr	Phe	Thr	Val	His	Gln	Glu	Ala	Asp	Ile	Lys	His
			165						170				175		
Ala	Ser	Glu	Glu	Lys	Glu	Met	Leu	Gln	Thr	Leu	Val	Gly	Arg	Glu	Asn
			180					185					190		
Pro	Asp	Ala	Val	Leu	Gln	Gly	Ser	Gln	Glu	Val	Leu	Asp	Thr	Leu	Trp
			195				200					205			
Asn	Phe	Leu	Ser	Ser	Phe	Ile	Asn	Ser	Thr	Glu	Pro	Cys	Ser	Cys	Lys

210 215 220

<210> 509
 <211> 246
 <212> PRT
 <213> Chlamydia pneumoniae

<400> 509
 Met Lys Ile Thr Thr Val Lys Thr Pro Lys Ile Tyr Pro Tyr Asp Asp
 1 5 10 15
 Leu Tyr Ser Ile Leu Glu Ser Ser Leu Pro Lys Leu Asn Glu Arg Ser
 20 25 30
 Ile Val Val Ile Thr Ser Lys Ile Val Ser Leu Cys Glu Gly Ala Val
 35 40 45
 Val Glu Leu Glu Lys Val Ser Lys Asp Glu Leu Ile Lys Gln Glu Ala
 50 55 60
 Asp Ala Tyr Val Phe Val Glu Lys Tyr Gly Ile Tyr Leu Thr Lys Lys
 65 70 75 80
 Trp Gly Ile Leu Ile Pro Ser Ala Gly Ile Asp Glu Ser Asn Val Glu
 85 90 95
 Gly Tyr Phe Val Leu Tyr Pro Arg Asp Phe Leu Leu Ser Val Asn Thr
 100 105 110
 Leu Gly Asp Trp Leu Arg Asn Phe Tyr His Leu Glu His Cys Gly Ile
 115 120 125
 Ile Ile Ser Asp Ser His Thr Thr Pro Leu Arg Arg Gly Thr Met Gly
 130 135 140
 Leu Gly Leu Cys Trp Asn Gly Phe Phe Pro Leu Tyr Asn Tyr Val Gly
 145 150 155 160
 Lys Pro Asp Cys Phe Gly Arg Ala Leu Lys Met Thr Tyr Ser Asn Leu
 165 170 175
 Leu Asp Gly Leu Ser Ala Ala Val Leu Cys Met Gly Glu Gly Asp
 180 185 190
 Glu Gln Thr Pro Ile Ala Ile Ile Glu Glu Ala Pro Lys Ile Thr Phe
 195 200 205
 His Ser Ser Pro Thr Thr Leu Gln Asp Met Ser Thr Leu Ala Ile Ala
 210 215 220
 Glu Asp Glu Asp Leu Tyr Gly Pro Leu Leu Gln Ser Met Ala Trp Glu
 225 230 235 240
 Thr Pro Ala Pro Thr Ser
 245

<210> 510
 <211> 353
 <212> PRT
 <213> Chlamydia pneumoniae

<400> 510
 Met Asn Lys Lys Arg Gln Lys Asp Lys Leu Lys Ile Cys Val Ile Ile Ser
 1 5 10 15
 Thr Leu Ile Leu Val Gly Ile Phe Ala Arg Ala Pro Arg Gly Asp Thr
 20 25 30
 Phe Lys Thr Phe Leu Lys Ser Glu Glu Ala Ile Ile Tyr Ser Asn Gln
 35 40 45
 Cys Asn Glu Asp Met Arg Lys Ile Leu Cys Asp Ala Ile Glu His Ala
 50 55 60
 Asp Glu Glu Ile Phe Leu Arg Ile Tyr Asn Leu Ser Glu Pro Lys Ile
 65 70 75 80
 Gln Gln Ser Leu Thr Arg Gln Ala Gln Ala Lys Asn Lys Val Thr Ile
 85 90 95
 Tyr Tyr Gln Lys Phe Lys Ile Pro Gln Ile Leu Lys Gln Ala Ser Asn
 100 105 110

Val Thr Leu Val Glu Gln Pro Pro Ala Gly Arg Lys Leu Met His Gln
 115 120
 Lys Ala Leu Ser Ile Asp Lys Lys Asp Ala Trp Leu Gly Ser Ala Asn
 130 135 140
 Tyr Thr Asn Leu Ser Leu Arg Leu Asp Asn Asn Ile Leu Gly Met
 145 150 155
 His Ser Ser Glu Leu Cys Asp Leu Ile Ile Thr Asn Thr Ser Gly Asp
 165 170 175
 Phe Ser Ile Lys Asp Gln Thr Gly Lys Tyr Phe Val Leu Pro Gln Asp
 180 185 190
 Arg Lys Ile Ala Ile Gln Ala Val Leu Glu Lys Ile Gln Thr Ala Gln
 195 200 205
 Lys Thr Ile Gln Val Ala Met Phe Ala Leu Thr His Ser Glu Ile Ile
 210 215 220
 Gln Ala Leu His Gln Ala Lys Gln Arg Gly Ile His Val Asp Ile Ile
 225 230 235
 Ile Asp Arg Ser His Ser Lys Leu Thr Phe Lys Gln Leu Arg Gln Leu
 245 250 255
 Asn Ile Asn Lys Asp Phe Val Ser Ile Asn Thr Ala Pro Cys Thr Leu
 260 265 270
 His His Lys Phe Ala Val Ile Asp Asn Lys Thr Leu Leu Ala Gly Ser
 275 280 285
 Ile Asn Trp Ser Lys Gly Arg Phe Ser Leu Asn Asp Glu Ser Leu Ile
 290 295 300
 Ile Leu Glu Asn Leu Thr Lys Gln Gln Asn Gln Lys Leu Arg Met Ile
 305 310 315
 Trp Lys Asp Leu Ala Lys His Ser Glu His Pro Thr Val Asp Asp Glu
 325 330 335
 Glu Lys Glu Ile Ile Glu Lys Ser Leu Pro Val Glu Glu Gln Glu Ala
 340 345 350
 Ala

<210> 511

<211> 186

<212> PRT

<213> Chlamydia pneumoniae

<400> 511

Met Ala Leu Asn Phe Lys Ile Asn Arg Gln Ile Arg Ala Pro Lys Val
 1 5 10 15
 Arg Leu Ile Gly Ser Ala Gly Glu Gln Leu Gly Ile Leu Ala Ile Lys
 20 25 30
 Asp Ala Leu Asp Leu Ala Arg Glu Ala Gly Leu Asp Leu Val Glu Val
 35 40 45
 Ala Ser Asn Ser Glu Pro Pro Val Cys Lys Ile Met Asp Tyr Gly Lys
 50 55 60
 Tyr Arg Tyr Gly Leu Thr Lys Lys Glu Lys Asp Ser Lys Lys Ala Gln
 65 70 75 80
 His Gln Val Arg Ile Lys Glu Val Lys Leu Lys Pro Asn Ile Asp Glu
 85 90 95
 Asn Asp Phe Ser Thr Lys Leu Lys Gln Ala Arg Thr Phe Val Glu Lys
 100 105 110
 Gly Asn Lys Val Lys Ile Thr Cys Met Phe Arg Gly Arg Glu Leu Ala
 115 120 125
 Tyr Pro Glu His Gly Phe Lys Val Val Gln Lys Met Ser Gln Gly Leu
 130 135 140
 Glu Asp Ile Gly Phe Val Glu Ala Glu Pro Lys Leu Ala Gly Arg Ser
 145 150 155 160
 Leu Ile Cys Val Val Ala Pro Gly Thr Val Lys Thr Lys Lys Lys Gln
 165 170 175

Glu Lys Ser His Ala Gln Asp Glu Asn Gln
180 185

<210> 512

<211> 276

<212> PRT

<213> Chlamydia pneumoniae

<220>

<221> VARIANT

<222> 269,270,271,272,274,275,276

<223> Xaa = Any Amino Acid

<400> 512

```
Met Gly Asn Ser Gly Phe Tyr Leu Gln Asp Thr Gln Asn Thr Ile Phe
 1          5          10          15
Ala Asp Asn Ile Arg Leu Gly Gln Met Thr Thr Val Leu Lys Lys Asp
 20          25          30
Glu Val Ile Ile Gly Thr Asp Thr Thr Pro Thr Val Thr Phe Ser
 35          40          45
Gly Asp Lys Gly Ile Val Ile Thr Thr Asp Ser Thr Ile Thr Pro Ser
 50          55          60
Ser Thr Thr Phe Ser Leu Asp Met Glu Ala Val Ile Lys Glu Val Thr
 65          70          75
Asp Lys Ile Leu Thr Gln Ile Glu Asp Glu Leu Val Lys Asp Ile Ile
 85          90          95
Lys Asn Ile Thr Gln Ser Leu Ile Glu Glu Val Ile Lys Lys Ile His
100          105          110
Ile Asp Pro Ser Phe Ser Tyr Ser Arg Ala Phe Lys Asp Val Asn Ile
115          120          125
Thr Asn Lys Ile Gln Cys Asn Gly Leu Phe Thr Lys Glu Asn Ile Gly
130          135          140
Asn Leu Asp Gly Gly Thr Glu Ile Ala Ser Ser Val Thr Pro Asp
145          150          155
Asn Ala Asn Ser Met Phe Leu Ile Cys Ala Asp Ile Ile Ala Thr Arg
165          170          175
Met Glu Gly Thr Val Ala Leu Ala Leu Val Lys Glu Gly Asp Leu Ser
180          185          190
Pro Cys Ser Ile Ser Tyr Gly Tyr Ser Ala Gly Tyr Pro Asn Ile Ile
195          200          205
Ser Leu Arg Ala Thr Val Gly Asn Lys Thr Thr Ala Pro Val Lys Phe
210          215          220
Ser Leu Arg Ala Gly Gly Met Asp Ser Gly Val Val Trp Val Asn Ala
225          230          235
Met Pro Asn Gly Glu Lys Ile Leu Gly Val Asp Ala Val Ser Lys Ile
245          250          255
Thr Ile Leu Glu Val Lys Pro Gln Thr Asn Gly Thr Xaa Xaa Xaa Xaa
260          265          270
Phe Xaa Xaa Xaa
275
```

<210> 513

<211> 1044

<212> PRT

<213> Chlamydia pneumoniae

<400> 513

```
Met Val Glu Val Glu Glu Lys His Tyr Thr Ile Val Lys Arg Asn Gly
 1          5          10          15
Met Phe Val Pro Phe Asn Gln Asp Arg Ile Phe Gln Ala Leu Glu Ala
 20          25          30
```

Ala Phe Arg Asp Thr Arg Ser Leu Glu Thr Ser Ser Pro Leu Pro Lys
 35 40 45
 Asp Leu Glu Glu Ser Ile Ala Gln Ile Thr His Lys Val Val Lys Glu
 50 55 60
 Val Leu Ala Lys Ile Ser Glu Gly Gln Val Val Thr Val Val Glu Arg Ile
 65 70 75
 Gln Asp Leu Val Glu Ser Gln Leu Tyr Ile Ser Gly Leu Gln Asp Val
 85 90 95
 Ala Arg Asp Tyr Ile Val Tyr Arg Asp Gln Arg Lys Ala Glu Arg Gly
 100 105 110
 Asn Ser Ser Ser Ile Ile Ala Ile Ile Arg Arg Asp Gly Gly Ser Ala
 115 120 125
 Lys Phe Asn Pro Met Lys Ile Ser Ala Ala Leu Glu Lys Ala Phe Arg
 130 135 140
 Ala Thr Leu Gln Ile Asn Gly Met Thr Pro Ala Thr Leu Ser Glu
 145 150 155
 Ile Asn Asp Leu Thr Leu Arg Ile Val Glu Asp Val Leu Ser Leu His
 165 170 175
 Gly Glu Glu Ala Ile Asn Leu Glu Glu Ile Gln Asp Ile Val Glu Lys
 180 185 190
 Gln Leu Met Val Ala Gly Tyr Tyr Asp Val Ala Lys Asn Tyr Ile Leu
 195 200 205
 Tyr Arg Glu Ala Arg Ala Arg Ala Asn Lys Asp Gln Asp Gly
 210 215 220
 Gln Glu Glu Phe Val Pro Gln Glu Glu Thr Tyr Val Val Gln Lys Glu
 225 230 235
 Asp Gly Thr Thr Tyr Leu Leu Arg Lys Thr Asp Leu Glu Lys Arg Phe
 245 250 255
 Ser Trp Ala Cys Lys Arg Phe Pro Lys Thr Thr Asp Ser Gln Leu Leu
 260 265 270
 Ala Asp Met Ala Phe Met Asn Leu Tyr Ser Gly Ile Lys Glu Asp Glu
 275 280 285
 Val Thr Thr Ala Cys Ile Met Ala Ala Arg Ala Asn Ile Glu Arg Glu
 290 295 300
 Pro Asp Tyr Ala Phe Ile Ala Ala Glu Leu Leu Thr Ser Ser Leu Tyr
 305 310 315
 Gln Glu Thr Leu Gly Cys Ser Ser Gln Asp Pro Asn Leu Ser Glu Ile
 325 330 335
 His Lys Lys His Phe Lys Glu Tyr Ile Leu Asn Gly Glu Glu Tyr Arg
 340 345 350
 Leu Asn Pro Gln Leu Lys Asp Tyr Asp Leu Asp Ala Leu Ser Glu Val
 355 360 365
 Leu Asp Leu Ser Arg Asp Gln Gln Phe Ser Tyr Met Gly Val Gln Asn
 370 375 380
 Leu Tyr Asp Arg Tyr Phe Asn Leu His Glu Gly Arg Arg Leu Glu Thr
 385 390 395
 Ala Gln Ile Phe Trp Met Arg Val Ser Met Gly Leu Ala Leu Asn Glu
 405 410 415
 Gly Glu Gln Lys Asn Phe Trp Ala Ile Thr Phe Tyr Asn Leu Leu Ser
 420 425 430
 Thr Phe Arg Tyr Thr Pro Ala Thr Pro Thr Leu Phe Asn Ser Gly Met
 435 440 445
 Arg His Ser Gln Leu Ser Ser Cys Tyr Leu Ser Thr Val Lys Asp Asp
 450 455 460
 Leu Ser His Ile Tyr Lys Val Ile Ser Asp Asn Ala Leu Leu Ser Lys
 465 470 475
 Trp Ala Gly Gly Ile Gly Asn Asp Trp Thr Asp Val Arg Ala Thr Gly
 485 490 495
 Ala Val Ile Lys Gly Thr Asn Gly Lys Ser Gln Gly Val Ile Pro Phe
 500 505 510
 Ile Lys Val Ala Asn Asp Thr Ala Ile Ala Val Asn Gln Gly Gly Lys

Arg	Lys	515	Gly	Ala	Met	Cys	Val	Tyr	Leu	Glu	Asn	Trp	His	Leu	Asp	Tyr
Glu	530	Phe	Leu	Glu	Asn	Arg	Lys	Asn	Thr	Gly	Asp	Glu	Arg	Arg	Arg	560
545	Thr	His	Asp	Ile	Asn	Thr	Ala	Ser	Trp	Ile	Pro	Asp	Leu	Phe	Phe	Lys
Arg	Leu	Glu	Lys	Lys	Gly	Met	Trp	Trp	Leu	Phe	Ser	Pro	Asp	Asp	Val	
Pro	Gly	Leu	His	Glu	Ala	Tyr	Gly	Leu	Glu	Phe	Glu	Lys	Leu	Tyr	Glu	
Glu	Tyr	Glu	Arg	Lys	Val	Glu	Ser	Gly	Glu	Ile	Arg	Leu	Tyr	Lys	Lys	
625	Val	Glu	Ala	Glu	Val	Leu	Trp	Arg	Lys	Met	Leu	Ser	Met	Leu	Tyr	Glu
Thr	Gly	His	Pro	Trp	Ile	Thr	Phe	Lys	Asp	Pro	Ser	Asn	Ile	Arg	Ser	
Asn	Gln	Asp	His	Val	Gly	Val	Val	Arg	Cys	Ser	Asn	Leu	Cys	Thr	Glu	
Ile	Leu	Leu	Asn	Cys	Ser	Glu	Ser	Glu	Thr	Ala	Val	Cys	Asn	Leu	Gly	
Ser	Ile	Asn	Leu	Val	Glu	His	Ile	Arg	Asn	Asp	Lys	Leu	Asp	Glu	Glu	
Lys	Leu	Lys	Glu	Thr	Ile	Ser	Ile	Ala	Ile	Arg	Ile	Leu	Asp	Asn	Val	
705	Ile	Asp	Leu	Asn	Phe	Tyr	Pro	Thr	Pro	Glu	Ala	Lys	Gln	Ala	Asn	Leu
Thr	His	Arg	Ala	Val	Gly	Leu	Gly	Val	Met	Gly	Phe	Gln	Asp	Val	Leu	
Tyr	Glu	Leu	Asn	Ile	Ser	Tyr	Ala	Ser	Gln	Glu	Ala	Val	Glu	Phe	Ser	
Asp	Glu	Cys	Ser	Glu	Ile	Ile	Ala	Tyr	Tyr	Ala	Ile	Leu	Ala	Ser	Ser	
Leu	Leu	Ala	Lys	Glu	Arg	Gly	Thr	Tyr	Ala	Ser	Tyr	Ser	Gly	Ser	Lys	
785	Trp	Asp	Arg	Gly	Tyr	Leu	Pro	Leu	Asp	Thr	Ile	Glu	Leu	Leu	Lys	Glu
Thr	Arg	Gly	Glu	His	Asn	Val	Leu	Val	Asp	Thr	Ser	Ser	Ser	Lys	Lys	Asp
Trp	Thr	Pro	Val	Arg	Asp	Thr	Ile	Gln	Lys	Tyr	Gly	Met	Arg	Asn	Ser	
Gln	Val	Met	Ala	Ile	Ala	Pro	Thr	Ala	Thr	Ile	Ser	Asn	Ile	Ile	Gly	
850	Val	Thr	Gln	Ser	Ile	Glu	Pro	Met	Tyr	Lys	His	Leu	Phe	Val	Lys	Ser
865	Asn	Leu	Ser	Gly	Glu	Phe	Thr	Ile	Pro	Asn	Thr	Tyr	Leu	Ile	Lys	Lys
Leu	Lys	Glu	Leu	Gly	Leu	Trp	Asp	Ala	Glu	Met	Leu	Asp	Asp	Leu	Lys	
Tyr	Phe	Asp	Gly	Ser	Leu	Leu	Glu	Ile	Glu	Arg	Ile	Pro	Asn	His	Leu	
Lys	Lys	Leu	Phe	Leu	Thr	Ala	Phe	Glu	Ile	Glu	Pro	Glu	Trp	Ile	Ile	
945	Glu	Cys	Thr	Ser	Arg	Arg	Gln	Lys	Trp	Ile	Asp	Met	Gly	Val	Ser	Leu
Asn	Leu	Tyr	Leu	Ala	Glu	Pro	Asp	Gly	Lys	Lys	Leu	Ser	Asn	Met	Tyr	
Leu	Thr	Ala	Trp	Lys	Lys	Gly	Leu	Lys	Thr	Thr	Tyr	Tyr	Leu	Arg	Ser	
Gln	Ala	Ala	Thr	Ser	Val	Glu	Lys	Ser	Phe	Ile	Asp	Ile	Asn	Lys	Arg	

Gly Ile Gln Pro Arg Trp Met Lys Asn Lys Ser Ala Ser Thr Ser Ile
 1010 1015 1020
 Val Val Glu Arg Lys Thr Thr Pro Val Cys Ser Met Glu Glu Gly Cys
 1025 1030 1035 1040
 Glu Ser Cys Gln

<210> 514

<211> 346

<212> PRT

<213> Chlamydia pneumoniae

<400> 514

Met Glu Ala Asp Ile Leu Asp Gly Lys Leu Lys Arg Val Glu Val Ser
 1 5 10 15
 Lys Lys Gly Leu Val Asn Cys Asn Gln Val Asp Val Asn Gln Leu Val
 20 25 30
 Pro Ile Lys Tyr Lys Trp Ala Trp Glu His Tyr Leu Asn Gly Cys Ala
 35 40 45
 Asn Asn Trp Leu Pro Thr Glu Val Pro Met Ala Arg Asp Ile Glu Leu
 50 55 60
 Trp Lys Ser Asp Glu Leu Ser Glu Asp Glu Arg Arg Val Ile Leu Leu
 65 70 75 80
 Asn Leu Gly Phe Phe Ser Thr Ala Glu Ser Leu Val Gly Asn Asn Ile
 85 90 95
 Val Leu Ala Ile Phe Lys His Ile Thr Asn Pro Glu Ala Arg Gln Tyr
 100 105 110
 Leu Leu Arg Gln Ala Phe Glu Glu Ala Val His Thr His Thr Phe Leu
 115 120 125
 Tyr Ile Cys Glu Ser Leu Gly Leu Asp Glu Gly Glu Val Phe Asn Ala
 130 135 140
 Tyr Asn Glu Arg Ala Ser Ile Arg Ala Lys Asp Asp Phe Gln Met Thr
 145 150 155 160
 Leu Thr Val Asp Val Leu Asp Pro Asn Phe Ser Val Gln Ser Ser Glu
 165 170 175
 Gly Leu Gly Gln Phe Ile Lys Asn Leu Val Gly Tyr Tyr Ile Ile Met
 180 185 190
 Glu Gly Ile Phe Phe Tyr Ser Gly Phe Val Met Ile Leu Ser Phe His
 195 200 205
 Arg Gln Asn Lys Met Thr Gly Ile Gly Glu Gln Tyr Gln Tyr Ile Leu
 210 215 220
 Arg Asp Glu Thr Ile His Leu Asn Phe Gly Ile Asp Leu Ile Asn Gly
 225 230 235 240
 Ile Lys Glu Glu Asn Pro Glu Val Trp Thr Thr Glu Leu Gln Glu Glu
 245 250 255
 Ile Val Ala Leu Ile Glu Lys Ala Val Glu Leu Glu Ile Glu Tyr Ala
 260 265 270
 Lys Asp Cys Leu Pro Arg Gly Ile Leu Gly Leu Arg Ser Ser Met Phe
 275 280 285
 Ile Asp Tyr Val Arg His Ile Ala Asp Arg Arg Leu Glu Arg Ile Gly
 290 295 300
 Leu Lys Pro Ile Tyr His Ser Arg Asn Pro Phe Pro Trp Met Ser Glu
 305 310 315 320
 Thr Met Asp Leu Asn Lys Glu Lys Asn Phe Phe Glu Thr Arg Val Thr
 325 330 335
 Glu Tyr Gln Thr Ala Gly Asn Leu Ser Trp
 340 345

<210> 515

<211> 327

<212> PRT

<213> Chlamydia pneumoniae

<400> 515

```

Met Asp Ala Lys Met Gly Tyr Ile Phe Lys Val Met Arg Trp Ile Phe
 1          5          10          15
Cys Phe Val Ala Cys Gly Ile Thr Phe Gly Cys Thr Asn Ser Gly Phe
          20          25          30
Gln Asn Ala Asn Ser Arg Pro Cys Ile Leu Ser Met Asn Arg Met Ile
          35          40          45
His Asp Cys Val Glu Arg Val Val Gly Asn Arg Leu Ala Thr Ala Val
 50          55          60
Leu Ile Lys Gly Ser Leu Asp Pro His Ala Tyr Glu Met Val Lys Gly
 65          70          75          80
Asp Lys Asp Lys Ile Ala Gly Ser Ala Val Ile Phe Cys Asn Gly Leu
          85          90          95
Gly Leu Glu His Thr Leu Ser Leu Arg Lys His Leu Glu Asn Asn Pro
          100          105          110
Asn Ser Val Lys Leu Gly Glu Arg Leu Ile Ala Arg Gly Ala Phe Val
          115          120          125
Pro Leu Glu Glu Asp Gly Ile Cys Asp Pro His Ile Trp Met Asp Leu
          130          135          140
Ser Ile Trp Lys Glu Ala Val Ile Glu Ile Thr Glu Val Leu Ile Glu
          145          150          155          160
Lys Phe Pro Glu Trp Ser Ala Glu Phe Lys Ala Asn Ser Glu Glu Leu
          165          170          175
Val Cys Glu Met Ser Ile Leu Asp Ser Trp Ala Lys Gln Cys Leu Ser
          180          185          190
Thr Ile Pro Glu Asn Leu Arg Tyr Leu Val Ser Gly His Asn Ala Phe
          195          200          205
Ser Tyr Phe Thr Arg Arg Tyr Leu Ala Thr Pro Glu Val Ala Ser
          210          215          220
Gly Ala Trp Arg Ser Cys Ile Ser Pro Glu Gly Leu Ser Pro Glu
          225          230          235          240
Ala Gln Ile Ser Val Arg Asp Ile Met Ala Val Val Asp Tyr Ile Asn
          245          250          255
Glu His Asp Val Ser Val Val Phe Pro Glu Asp Thr Leu Asn Gln Asp
          260          265          270
Ala Leu Lys Lys Ile Val Ser Ser Leu Lys Lys Ser His Leu Val Arg
          275          280          285
Leu Ala Gln Lys Pro Leu Tyr Ser Asp Asn Val Asp Asp Asn Tyr Phe
          290          295          300
Ser Thr Phe Lys His Asn Val Cys Leu Ile Thr Glu Leu Gly Gly
          305          310          315          320
Val Ala Leu Glu Cys Gln Arg
          325

```

<210> 516

<211> 101

<212> PRT

<213> Chlamydia pneumoniae

<400> 516

```

Met Asn Asn Arg Gln Asn Thr Asn Asp Phe Ile Arg Ile Val Lys Asp
 1          5          10          15
Val Glu Lys Ala Phe Pro Glu Leu Asp Ile Lys Val Lys Ile Asp Lys
          20          25          30
Glu Lys Val Thr Phe Leu Thr Ser Pro Thr Glu Leu Tyr His Lys Ser
          35          40          45
Ile Ser Val Ile Leu Asn Leu Leu Asn Ser Ile Glu Ser Ser Leu Asp
          50          55          60
Leu Phe Pro Asp Ser Pro Val Val Glu Glu Leu Glu Lys Asn Asn Leu

```


65 70 75 80
Lys Leu Lys Lys Ala Leu Ile Met Leu Ile Leu Ser Arg Lys Asp Met
 85
Phe Ser Lys Thr Glu
 90 95

```
<210> 517
<211> 261
<212> PRT
<213> Chlamydia pneumoniae
```

[illegible]

```
<210> 518
<211> 526
<212> PRT
<213> Chlamydia pneumoniae
```

Met	Asn	Val	Leu	Lys	Tyr	Thr	Lys	His	Ser	Pro	Ser	Ala	His	Ala	Trp
1				5					10					15	
Lys	Leu	Ile	Gly	Thr	Ser	Pro	Lys	His	Gly	Ile	Tyr	Leu	Pro	Leu	Phe
			20					25					30		
Ser	Ile	His	Thr	Thr	Asn	Ser	Cys	Gly	Ile	Gly	Glu	Phe	Leu	Asp	Leu
		35					40					45			
Ile	Pro	Leu	Ile	Ser	Trp	Cys	Gln	Lys	Gln	Gly	Phe	Ser	Val	Ile	Gln
	50					55					60				

Leu Leu Pro Leu Asn Asp Thr Gly Glu Asp Thr Ser Pro Tyr Asn Ser
 65 70 75 80
 Ile Ser Ser Val Ala Leu Asn Pro Leu Phe Leu Ser Ser Ser Leu
 85 90 95
 Pro Asn Ile Asp Thr Ile Pro Glu Val Ala Lys Lys Leu Gln Asp Met
 100 105 110
 His Glu Leu Cys Ser Thr Pro Ser Val Ser Tyr Thr Gln Val Lys Glu
 115 120 125
 Lys Lys Trp Ala Phe Leu Arg Glu Tyr Tyr Gln Lys Cys Lys Ser Ser
 130 135 140
 Ser Leu Glu Gly Asn Ser Asn Phe Ser Glu Phe Leu Glu Ser Glu Arg
 145 150 155 160
 Tyr Trp Leu Tyr Pro Tyr Gly Thr Phe Arg Ala Ile Lys His His Met
 165 170 175
 His Gly Glu Pro Ile Asn Asn Trp Pro Lys Ser Leu Thr Asp Gln Glu
 180 185 190
 Asn Phe Pro Asp Leu Thr Lys Lys Phe His Asp Glu Val Leu Phe Phe
 195 200 205
 Ser Tyr Leu Gln Phe Leu Cys Tyr Gln Gln Leu Cys Glu Val Lys Ala
 210 215 220
 Tyr Ala Asp Gln His His Val Leu Leu Lys Gly Asp Leu Pro Ile Leu
 225 230 235 240
 Ile Ser Lys Asp Ser Cys Asp Val Trp Tyr Phe Arg Asp Tyr Phe Ser
 245 250 255
 Ser Ser Arg Ser Val Gly Ala Pro Pro Asp Leu Tyr Asn Ser Glu Gly
 260 265 270
 Gln Asn Trp His Leu Pro Ile Tyr Asn Phe Ser Gln Leu Ala Lys Asp
 275 280 285
 Asp Tyr Ile Trp Trp Lys Glu Arg Leu Arg Tyr Ala Gln Asn Phe Tyr
 290 295 300
 Ser Val Tyr Arg Leu Asp His Ile Ile Gly Phe Arg Leu Trp Ile
 305 310 315 320
 Trp Asp Ser Ser Gly Arg Gly Arg Phe Ile Pro Asp Asn Pro Lys Asp
 325 330 335
 Tyr Ile Lys Gln Gly Thr Glu Ile Leu Ser Thr Met Leu Gly Ala Ser
 340 345 350
 Ser Met Leu Pro Ile Gly Glu Asp Leu Gly Ile Ile Pro Gln Asp Val
 355 360 365
 Lys Thr Thr Leu Thr His Leu Gly Ile Cys Gly Thr Arg Ile Pro Arg
 370 375 380
 Trp Glu Arg Asn Trp Glu Ser Asp Ser Ala Phe Ile Pro Leu Lys Asp
 385 390 395 400
 Tyr Asn Pro Leu Ser Val Thr Thr Leu Ser Thr His Asp Ser Asp Thr
 405 410 415
 Phe Ala Gln Trp Trp Leu Asn Ser Pro Lys Glu Ala Lys Gln Phe Ala
 420 425 430
 Lys Phe Leu His Leu Pro Phe Gln Lys Thr Leu Thr Thr Gln
 435 440 445
 Ile Asp Ile Leu Lys Leu Ser His Glu Ser Ala Ser Ile Phe His Ile
 450 455 460
 Asn Leu Phe Asn Asp Tyr Leu Ala Leu Cys Pro Asp Leu Val Ser Lys
 465 470 475 480
 Asn Leu Gln Arg Glu Arg Ile Asn Thr Pro Gly Thr Ile Ser Lys Lys
 485 490 495
 Asn Trp Ser Tyr Arg Val Arg Pro Ser Leu Glu Glu Leu Ala Ile His
 500 505 510
 Lys Lys Phe Asn Gly Tyr Ile Glu Lys Ile Leu Thr Gly Leu
 515 520 525

<210> 519

<211> 147

<212> PRT

<213> Chlamydia pneumoniae

<400> 519

```

Met Gln Asn Gln Tyr Glu Gln Leu Leu Glu Ser Leu Ala Pro Leu Leu
 1      5'      10      15
Asn Thr Thr Leu Ala Pro Asp Lys Asn Asn Ser Cys Leu Ile Arg Phe
 20      25      30
Ser Asp Thr His Val Pro Val Gln Ile Glu Glu Asp Gly Asn Ser Gly
 35      40      45
Asp Leu Ala Val Ser Thr Leu Leu Gly Thr Leu Pro Glu Asn Val Phe
 50      55      60
Arg Glu Arg Ile Phe Lys Ala Ala Leu Ser Val Asn Gly Ser Phe Gln
 65      70      75      80
Ser Ser Ile Lys Gly Ile Leu Gly Tyr Gly Glu Val Thr Gln Gln Leu
 85      90      95
Tyr Leu Ser Asp Ile Leu Ser Met Asn Tyr Leu Asn Gly Glu Lys Leu
100      105      110
Phe Glu Tyr Leu Lys Leu Phe Ser Leu His Ala Lys Ile Trp Met Glu
115      120      125
Ser Leu Arg Thr Gly Asn Leu Pro Asp Leu His Val Leu Gly Ile Tyr
130      135      140
Tyr Val Ala
145

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<210> 520

<211> 635

<212> PRT

<213> Chlamydia pneumoniae

<400> 520

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Met Ile Pro Phe Thr Lys Thr Ile Gly Phe Arg Leu Trp Leu Ala Cys
 1      5      10      15
Ala Val Ala Ile Ile Ala Pro Leu Gly Ile Asn Ile Val Trp Leu Asn
 20      25      30
Leu Asp Gln Tyr Arg Thr Ile Val Ser Ala Ile Ser Thr Ala Leu Lys
 35      40      45
Glu Asn Ala Ala Phe Lys Ala Asn Thr Leu Thr Gln Ile Val Pro Leu
 50      55      60
Asn Val Asp Val Leu Ser Leu Phe Ser Asp Val Leu Asp Leu Asp Ala
 65      70      75      80
Gly Ile Pro Glu Thr Pro Asn Val Leu Leu Ser Asn Glu Met Gln Lys
 85      90      95
Val Phe Gln Gly Ile Tyr Asn Glu Ile Ser Leu Ile Lys Val Phe Pro
100      105      110
Asn Gly Asp Lys Ile Val Val Ala Ser Ser Ile Pro Glu His Leu Gly
115      120      125
Glu Asn Tyr Asn His Lys Ile Asp Ile Pro Lys Asn Thr Pro Phe Leu
130      135      140
Ala Ala Leu Lys Gln Ser Pro Lys Asn Gln Glu Val Phe Ser Val Met
145      150      155      160
Gln Ala Asn Val Phe Asp Ala Lys Thr Gln Glu Leu Gln Gly Ile Leu
165      170      175
Tyr Thr Thr Phe Ser Ala Glu Ser Leu Leu Lys Asp Leu Leu Ile Asn
180      185      190
Lys Gln Ser Tyr Leu Thr Val Lys Thr Ala Ile Leu Ser Lys Tyr Gly
195      200      205
Val Ile Leu Lys Ala Ser Asp Pro Ala Leu His Leu His Thr Val Tyr
210      215      220
Pro Asp Met Thr Lys Glu Lys Phe Cys Gln Val Phe Leu Asn Asp Asp
225      230      235      240

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Pro Cys Pro Ile Asp Ser Glu Leu Gly Pro Leu Thr Leu Ser Pro Leu
 245 250 255
 Asp Ile Gly Glu Asn Phe Tyr Ser Phe Lys Ile Lys Asp Thr Glu Ile
 260 265 270
 Trp Gly Cys Ile Glu Asn Val Pro Ser Ile Asp Ile Ala Val Leu Ser
 275 280 285
 Tyr Ala Lys Lys Glu Glu Ser Phe Ala Pro Leu Trp Arg Arg Ala Arg
 290 300 305
 Met Tyr Thr Ala Tyr Phe Phe Cys Ile Leu Leu Gly Ser Leu Ile Ala
 310 315 320
 Phe Ile Val Ala Arg Arg Leu Ser Leu Pro Ile Arg Lys Leu Ala Thr
 325 330 335
 Ala Met Ile Glu Ser Arg Lys Asn Lys Asn Cys Leu Tyr Thr Asp Asp
 340 345 350
 Ser Leu Gly Phe Glu Ile Asn Arg Gly His Ile Phe Asn Ala Met
 355 360 365
 Val Glu Asn Leu His Lys Gln Gln His Leu Ala Lys Thr Asn Phe Glu
 370 375 380
 Met Lys Glu Asn Ala Gln Asn Ala Leu His Leu Gly Glu Gln Ala Gln
 385 390 395 400
 Gln Arg Leu Leu Pro Asn Thr Leu Pro Ser Tyr Pro His Ile Glu Leu
 405 410 415
 Ala Lys Ala Tyr Ile Pro Ala Ile Thr Val Gly Gly Asp Phe Phe Asp
 420 425 430
 Val Phe Val Val Gly Glu Gly Ser Lys Ala Arg Leu Phe Leu Ile Val
 435 440 445
 Ala Asp Ala Ser Gly Lys Gly Val Asn Ala Cys Gly Tyr Ser Leu Phe
 450 455 460
 Leu Lys Asn Met Leu Arg Thr Phe Leu Ser Arg Ser Ser Leu Gln
 465 470 475 480
 Gln Ala Ile Gln Glu Thr Ser Arg Leu Phe Tyr Asn Asn Thr Lys Asn
 485 490 495
 Ser Gly Met Phe Val Thr Leu Cys Val Tyr Cys Tyr His Gln Thr Ser
 500 505 510
 Asn Thr Met Glu Tyr Tyr Ser Cys Gly His Pro Pro Ala Cys Tyr Leu
 515 520 525
 Asp Pro Asp Gly Glu Thr Ser Trp Leu Phe His Pro Gly Met Ala Leu
 530 535 540
 Gly Phe Leu Pro Glu Val Ala Asn Ile Thr Ser Lys Leu Phe His Pro
 545 550 555 560
 Lys Pro Gly Ser Leu Phe Val Leu Tyr Ser Asp Gly Ile Thr Glu Ala
 565 570 575
 His Asn Asn Asn Asn Asp Met Phe Gly Glu Glu Arg Leu Gln Ala Ala
 580 585 590
 Ile Gln Gly Leu Thr Gly Lys Ser Ala Ala Asp Ala Val His Arg Leu
 595 600 605
 Met Leu Ser Val Lys Thr Phe Val Gly Asn Ser His Gln His Asp Asp
 610 615 620
 Ile Thr Leu Leu Ile Leu Lys Val Leu Glu Ser
 625 630 635

<210> 521

<211> 314

<212> PRT

<213> Chlamydia pneumoniae

<400> 521

Met Phe Ser Tyr Ile Lys Asn Arg Ile Leu Phe Asn Leu Leu Ser Leu
 1 5 10 15
 Trp Ile Val Leu Thr Leu Thr Phe Leu Val Met Lys Thr Ile Pro Glu
 20 25 30

Asp Pro Phe Asn Asp Glu Gly Cys Asn Val Leu Ser Glu Glu Val Leu
 35 40
 Gln Thr Leu Lys Ser Arg Tyr Gly Leu Asp Lys Pro Leu Tyr Gln Gln
 50 55
 Tyr Thr Gln Tyr Leu His Ser Ile Ala Lys Leu Asp Phe Gly Asn Ser
 65 70 75 80
 Leu Val Tyr Lys Asp Arg Lys Val Thr Asn Ile Ile Ser Thr Ala Phe
 85 90 95
 Pro Ile Ser Ala Ile Leu Gly Leu Gln Ser Leu Phe Leu Ser Ile Gly
 100 105 110
 Gly Gly Ile Ala Leu Gly Thr Ile Ala Ala Leu Lys Lys Lys Gln
 115 120 125
 Arg Arg Tyr Ile Leu Gly Ala Ser Ile Leu Gln Ile Ser Ile Pro Ala
 130 135 140
 Phe Ile Phe Ala Thr Leu Leu Gln Tyr Val Phe Ala Val Lys Ile Pro
 145 150 155 160
 Leu Leu Pro Ile Ala Cys Trp Gly Ser Phe Thr His Thr Ile Leu Pro
 165 170 175
 Thr Leu Ala Leu Ala Val Thr Pro Met Ala Phe Ile Ile Gln Leu Thr
 180 185 190
 Tyr Ser Ser Val Ser Ala Ala Leu Asn Lys Asp Tyr Val Leu Leu Ala
 195 200 205
 Tyr Ala Lys Gly Leu Ser Pro Leu Lys Val Val Ile Lys His Ile Leu
 210 215 220
 Pro Tyr Ala Ile Phe Pro Thr Ile Ser Tyr Ser Ala Phe Leu Thr Thr
 225 230 235 240
 Thr Val Ile Thr Gly Thr Phe Ala Ile Glu Asn Ile Phe Cys Ile Pro
 245 250 255
 Gly Leu Gly Lys Trp Phe Ile Cys Ser Ile Lys Gln Arg Asp Tyr Pro
 260 265 270
 Val Ala Leu Gly Leu Ser Val Phe Tyr Gly Thr Leu Phe Met Leu Ser
 275 280 285
 Ser Leu Leu Ser Asp Leu Ile Gln Ser Ile Ile Asp Pro Gln Ile Arg
 290 295 300
 Tyr Ala His Gly Lys Glu Lys Lys Arg Lys
 305 310

<210> 522

<211> 1240

<212> FRT

<213> Chlamydia pneumoniae

<400> 522

Met Thr Trp Ile Pro Leu His Cys His Ser Gln Tyr Ser Val Leu Asp
 1 5 10 15
 Ala Met Ser Ser Ile Lys Asp Phe Val Ala Lys Gly Gln Glu Phe Gly
 20 25 30
 Ile Pro Ala Leu Ala Leu Thr Asp His Gly Asn Leu Tyr Gly Ala Val
 35 40 45
 Asp Phe Tyr Lys Glu Cys Thr Gln Lys Gly Ile Gln Pro Ile Ile Gly
 50 55 60
 Cys Glu Cys Tyr Ile Ala Pro Gly Ser Arg Phe Asp Lys Lys Lys Glu
 65 70 75 80
 Lys Arg Ser Arg Ala Ala His His Leu Ile Leu Leu Cys Lys Asn Glu
 85 90 95
 Gln Gly Tyr Arg Asn Leu Cys Ile Leu Thr Ser Leu Ala Phe Thr Glu
 100 105 110
 Gly Phe Tyr Tyr Phe Pro Arg Ile Asp Lys Asp Leu Leu Arg Gln Tyr
 115 120 125
 Ser Glu Gly Leu Ile Cys Leu Ser Gly Cys Leu Ser Ser Val Ser
 130 135 140

Asp Ala Ala Leu Lys Ser Pro Glu Ala Leu Leu Leu Glu Leu Gln Trp
 145 150 155 160
 Phe Gln Asp Leu Phe Lys Asp Asp Tyr Phe Thr Glu Val Gln Leu His
 165 170 175
 Lys Met Ser Glu Glu Ser Ile Ala Gly Phe Lys Glu Glu Trp Leu Lys
 180 185 190
 Gln Glu Tyr Tyr Ser Leu Ile Glu Lys Gln Ile Lys Val Asn Thr Ala
 195 200 205
 Val Leu Glu Ala Ser Lys Arg Leu Gly Ile Pro Thr Val Ala Thr Asn
 210 215 220
 Asp Ile His Tyr Ile Asn Ala Asn Asp Trp Gln Ala His Glu Ile Leu
 225 230 235 240
 Leu Asn Val Gln Ser Gly Glu Thr Val Arg Ile Ala Lys Gln Asn Thr
 245 250 255
 His Ile Pro Asn Pro Lys Arg Lys Val Tyr Arg Ser Arg Glu Tyr Tyr
 260 265 270
 Phe Lys Ser Pro Ala Gln Met Ala Glu Leu Phe Lys Asp Ile Pro Glu
 275 280 285
 Val Ile Ser Asn Thr Leu Glu Val Ala Lys Arg Cys Asp Phe Thr Phe
 290 295 300
 Asp Phe Ser Lys Lys His Tyr Pro Ile Tyr Val Pro Glu Ser Leu Lys
 305 310 315 320
 Thr Leu Asn Ser Tyr Thr Glu Glu Asp Arg Tyr Gln Ala Ser Ala Val
 325 330 335
 Phe Leu Lys Gln Leu Ala Glu Glu Ala Leu Pro Lys Lys Tyr Ser Ser
 340 345 350
 Glu Val Leu Ala His Ile Ala Lys Lys Phe Pro His Arg Asp Pro Ile
 355 360 365
 Asp Ile Val Lys Glu Arg Met Asp Met Glu Met Ala Ile Ile Ile Pro
 370 375 380
 Lys Gly Met Cys Asp Tyr Leu Leu Ile Val Trp Asp Ile Ile His Trp
 385 390 395 400
 Ala Lys Ala Asn Gly Ile Pro Val Gly Pro Gly Arg Gly Ser Gly Ala
 405 410 415
 Gly Ser Val Leu Leu Phe Leu Leu Gly Ile Thr Glu Ile Glu Pro Ile
 420 425 430
 Arg Phe Asp Leu Phe Phe Glu Arg Phe Ile Asn Pro Glu Arg Leu Ser
 435 440 445
 Tyr Pro Asp Ile Asp Ile Asp Ile Cys Met Ala Gly Arg Glu Arg Val
 450 455 460
 Ile Asn Tyr Ala Ile Glu Arg His Gly Lys Asp Asn Val Ala Gln Ile
 465 470 475 480
 Ile Thr Phe Gly Thr Met Lys Ala Lys Met Ala Val Lys Asp Val Gly
 485 490 495
 Arg Thr Leu Asp Met Ala Leu Ser Lys Val Asn His Ile Ala Lys His
 500 505 510
 Ile Pro Asp Leu Asn Thr Thr Leu Ser Lys Ala Leu Glu Thr Asp Pro
 515 520 525
 Asp Leu His Gln Leu Tyr Ile Asn Asp Ala Glu Ser Ala Gln Val Ile
 530 535 540
 Asp Met Ala Leu Cys Leu Glu Gly Ser Ile Arg Asn Thr Gly Val His
 545 550 555 560
 Ala Ala Gly Val Ile Ile Cys Gly Asp Gln Leu Thr Asn His Ile Pro
 565 570 575
 Ile Cys Ile Ser Lys Asp Ser Thr Met Ile Thr Thr Gln Tyr Ser Met
 580 585 590
 Lys Pro Val Glu Ser Val Gly Met Leu Lys Val Asp Leu Leu Gly Leu
 595 600 605
 Lys Thr Leu Thr Ser Ile Asn Ile Ala Met Ser Ala Ile Glu Lys Lys
 610 615 620
 Thr Gly Gln Ser Leu Ala Met Ala Thr Leu Pro Leu Asp Asp Ala Thr

625						630										635								640
Thr	Phe	Ser	Leu	Leu	His	Gln	Gly	Lys	Thr	Met	Gly	Ile	Phe	Gln	Met	650								645
Glu	Ser	Lys	Gly	Met	Gln	Glu	Leu	Ala	Lys	Asn	Leu	Arg	Pro	Asp	Leu	655								650
Phe	Glu	Glu	Ile	Ile	Ala	Met	Gly	Ala	Leu	Tyr	Arg	Pro	Gly	Pro	Met	660								655
Asp	Met	Ile	Pro	Ser	Phe	Ile	Asn	Arg	Lys	His	Gly	Lys	Glu	Ile	Ile	665								660
Glu	Tyr	Asp	His	Pro	Leu	Met	Glu	Ser	Ile	Leu	Lys	Glu	Thr	Tyr	Gly	700								665
705																715								670
Ile	Met	Val	Tyr	Gln	Glu	Gln	Val	Met	Gln	Ile	Ala	Gly	Ala	Leu	Ala	730								675
Ser	Tyr	Ser	Leu	Gly	Glu	Gly	Asp	Val	Leu	Arg	Arg	Ala	Met	Gly	Lys	745								680
Lys	Asp	Phe	Gln	Gln	Met	Glu	Gln	Glu	Arg	Glu	Lys	Phe	Cys	Lys	Arg	755								685
Ala	Cys	Asn	Asn	Gly	Ile	Asp	Pro	Glu	Leu	Ala	Thr	Val	Ile	Phe	Asp	760								690
Lys	Met	Glu	Lys	Phe	Ala	Ala	Tyr	Gly	Phe	Asn	Lys	Ser	His	Ala	Ala	775								695
785																790								700
Ala	Tyr	Gly	Leu	Ile	Thr	Tyr	Thr	Thr	Ala	Tyr	Leu	Lys	Ala	Asn	Tyr	805								705
Pro	Lys	Glu	Trp	Leu	Ala	Ala	Leu	Leu	Thr	Cys	Asp	Ser	Asp	Asp	Ile	810								710
Glu	Lys	Ile	Gly	Lys	Leu	Ile	Arg	Glu	Ala	Gln	Ser	Met	Gly	Ile	Pro	825								715
Ile	Leu	Pro	Pro	His	Ile	Asn	Val	Ser	Ser	Asn	His	Phe	Val	Ala	Thr	840								720
Asp	Glu	Gly	Ile	Arg	Phe	Ala	Met	Gly	Ala	Ile	Lys	Gly	Ile	Gly	Arg	855								725
Gly	Leu	Ile	Glu	Ser	Ile	Val	Glu	Glu	Arg	Asp	His	His	Gly	Pro	Tyr	860								730
Glu	Ser	Ile	Arg	Asp	Phe	Ile	Gln	Arg	Ser	Asp	Leu	Lys	Lys	Val	Ser	875								735
Lys	Lys	Ser	Ile	Glu	Ser	Leu	Ile	Asp	Ala	Gly	Cys	Phe	Asp	Cys	Phe	885								740
Asp	Ser	Asn	Arg	Asp	Leu	Leu	Leu	Ala	Ser	Val	Glu	Pro	Leu	Tyr	Glu	890								745
Ala	Ile	Ala	Lys	Asp	Lys	Lys	Glu	Ala	Ala	Ser	Gly	Val	Met	Thr	Phe	905								750
945																910								755
Phe	Thr	Leu	Gly	Ala	Met	Asp	Arg	Lys	Asn	Glu	Val	Pro	Ile	Cys	Leu	920								760
Pro	Lys	Asp	Ile	Pro	Thr	Arg	Ser	Lys	Lys	Glu	Leu	Lys	Lys	Lys	Glu	935								765
Lys	Glu	Leu	Leu	Gly	Ile	Tyr	Leu	Thr	Glu	His	Pro	Met	Asp	Thr	Val	940								770
Arg	Asp	His	Leu	Ser	Arg	Leu	Ser	Val	Val	Leu	Ala	Gly	Phe	Glu	Glu	955								775
Asn	Leu	Pro	His	Gly	Ser	Val	Val	Arg	Thr	Val														

Cys Asp Gln Ala Phe Asp Arg Ile Lys Asn Gln Val Gln Lys Met Ser
 1125 1130 1135
 Phe Thr Met Ser Thr Ser Gly Lys Glu Thr Lys Ala Lys Gly Asn Lys
 1140 1145 1150
 Pro Asn Glu Asn Gly His Thr Gln Ala Leu Ala Pro Val Thr Leu Ser
 1155 1160 1165
 Leu Asp Leu Asn Glu Leu Arg His Ser His Leu Cys Ile Leu Lys Lys
 1170 1175 1180
 Ile Val Gln Lys His Pro Gly Ser Arg Thr Leu Val Leu Val Phe Thr
 1185 1190 1195 1200
 Gln Asp Asn Glu Arg Val Ala Ser Met Ser Pro Asp Asp Ala Tyr Phe
 1205 1210 1215
 Val Cys Glu Asp Ile Glu Glu Leu Arg Gln Glu Leu Val Thr Ala Asp
 1220 1225 1230
 Leu Pro Val Arg Val Ile Thr Val
 1235 1240

<210> 523

<211> 576

<212> PRT

<213> Chlamydia pneumoniae

<400> 523

Met Thr Asp Phe Pro Thr His Phe Lys Gly Pro Lys Leu Asn Pro Ile
 1 5 10 15
 Lys Val Asn Pro Asn Phe Phe Glu Arg Asn Pro Lys Val Ala Arg Val
 20 25 30
 Leu Gln Ile Thr Ala Val Val Leu Gly Ile Ile Ala Leu Leu Ser Gly
 35 40 45
 Ile Val Leu Ile Ile Gly Thr Pro Leu Gly Ala Pro Ile Ser Met Ile
 50 55 60
 Leu Gly Gly Cys Leu Leu Ala Ser Gly Gly Ala Leu Phe Val Gly Gly
 65 70 75 80
 Thr Ile Ala Thr Ile Leu Gln Ala Arg Asn Ser Tyr Lys Lys Ala Val
 85 90 95
 Asn Gln Lys Lys Leu Ser Glu Pro Leu Met Glu Arg Pro Glu Leu Lys
 100 105 110
 Ala Leu Asp Tyr Ser Leu Asp Leu Lys Glu Val Trp Asp Leu His His
 115 120 125
 Ser Val Val Lys His Leu Lys Lys Leu Asp Leu Asn Leu Ser Lys Thr
 130 135 140
 Gln Arg Glu Val Leu Asn Gln Ile Lys Ile Asp Asp Glu Gly Pro Ser
 145 150 155 160
 Leu Gly Glu Cys Ala Ala Met Ile Ser Glu Asn Tyr Asp Ala Cys Leu
 165 170 175
 Lys Met Leu Ala Tyr Arg Glu Glu Leu Leu Lys Glu Gln Thr Gln Tyr
 180 185 190
 Gln Glu Thr Arg Phe Asn Gln Asn Leu Thr His Arg Asn Lys Val Leu
 195 200 205
 Leu Ser Ile Leu Ser Arg Ile Thr Asp Asn Ile Ser Lys Ala Gly Gly
 210 215 220
 Val Phe Ser Leu Lys Phe Ser Thr Leu Ser Ser Arg Met Ser Arg Ile
 225 230 235 240
 His Thr Thr Thr Thr Val Ile Leu Ala Leu Ser Ala Val Val Ser Val
 245 250 255
 Met Val Val Ala Ala Leu Ile Pro Gly Gly Ile Leu Ala Leu Pro Ile
 260 265 270
 Leu Leu Ala Val Ala Ile Ser Ala Gly Val Ile Val Thr Gly Leu Ser
 275 280 285
 Tyr Leu Val Arg Gln Ile Leu Ser Asn Thr Lys Arg Asn Arg Gln Asp
 290 295 300

Phe Tyr Lys Asp Phe Val Lys Asn Val Asp Ile Glu Leu Leu Asn Gln
 305 310 315 320
 Thr Val Thr Leu Gln Arg Phe Leu Phe Glu Met Leu Lys Gly Val Leu
 325 330 335
 Lys Glu Glu Glu Glu Val Ser Leu Glu Gly Gln Asp Trp Tyr Thr Gln
 340 345 350
 Tyr Ile Thr Asn Ala Pro Ile Glu Lys Arg Leu Ile Glu Glu Ile Arg
 355 360 365
 Val Thr Tyr Lys Glu Ile Asp Ala Gln Thr Lys Lys Met Lys Thr Asp
 370 375 380
 Leu Glu Phe Leu Glu Asn Glu Val Arg Ser Gly Arg Leu Ser Val Ala
 385 390 395 400
 Ser Pro Ser Glu Asp Pro Ser Glu Thr Pro Ile Phe Thr Gln Gly Lys
 405 410 415
 Glu Phe Ala Lys Leu Arg Arg Gln Thr Ser Gln Asn Ile Ser Thr Ile
 420 425 430
 Tyr Gly Pro Asp Asn Glu Asn Ile Asp Pro Glu Phe Ser Thr Pro Trp
 435 440 445
 Met Pro Lys Lys Glu Glu Glu Ile Asp His Ser Leu Glu Pro Val Thr
 450 455 460
 Lys Leu Glu Pro Gly Ser Arg Glu Glu Leu Leu Leu Val Glu Gly Val
 465 470 475 480
 Asn Pro Thr Leu Arg Glu Leu Asn Met Arg Ile Ala Leu Leu Gln Gln
 485 490 495
 Gln Leu Ser Ser Val Arg Lys Trp Arg His Pro Arg Gly Glu His Tyr
 500 505 510
 Gly Asn Val Ile Tyr Ser Asp Thr Glu Leu Asp Arg Ile Gln Met Leu
 515 520 525
 Glu Gly Ala Phe Tyr Asn His Leu Arg Glu Ala Gln Glu Ile Thr
 530 535 540
 Gln Ser Leu Gly Asp Leu Val Asp Ile Gln Asn Arg Ile Leu Gly Ile
 545 550 555 560
 Ile Val Glu Gly Asp Ser Asp Ser Arg Thr Glu Glu Glu Pro Gln Glu
 565 570 575

<210> 524

<211> 439

<212> PRT

<213> Chlamydia pneumoniae

<220>

<221> VARIANT

<222> 428, 429, 430, 431, 432, 433, 434, 435, 437, 438, 439

<223> Xaa = Any Amino Acid

<400> 524

Ile Thr Ile Ala Val Asn Ser Thr Ser Gly Leu Lys Ile Ser Gly
 1 5 10 15
 Asp Leu Lys Phe His Asn Asn Glu Gly Ser Phe Tyr Asp Asn Pro Gly
 20 25 30
 Leu Lys Ala Asn Leu Asn Leu Pro Phe Leu Asp Leu Ser Ser Thr Ser
 35 40 45
 Gly Thr Val Asn Leu Asp Asp Phe Asn Pro Ile Pro Ser Ser Met Ala
 50 55 60
 Ala Pro Asp Tyr Gly Tyr Gln Gly Ser Trp Thr Leu Val Pro Lys Val
 65 70 75 80
 Gly Ala Gly Gly Lys Val Thr Leu Val Ala Glu Trp Gln Ala Leu Gly
 85 90 95
 Tyr Thr Pro Lys Pro Glu Leu Arg Ala Thr Leu Val Pro Asn Ser Leu
 100 105 110
 Trp Asn Ala Tyr Val Asn Ile His Ser Ile Gln Gln Glu Ile Ala Thr

115	120	125
Ala Met Ser Asp Ala Pro Ser His Pro Gly Ile Trp Ile Gly Gly Ile		
130	135	140
Gly Asn Ala Phe His Gln Asp Lys Gln Lys Glu Asn Ala Gly Phe Arg		
145	150	155
Leu Ile Ser Arg Gly Tyr Ile Val Gly Gly Ser Met Thr Thr Pro Gln		
160	165	170
Glu Tyr Thr Phe Ala Val Ala Phe Ser Gln Leu Phe Gly Lys Ser Lys		
175	180	185
Asp Tyr Val Val Ser Asp Ile Lys Ser Gln Val Tyr Ala Gly Ser Leu		
190	195	200
Cys Ala Gln Ser Ser Tyr Val Ile Pro Leu His Ser Ser Leu Arg Arg		
205	210	215
His Val Leu Ser Lys Val Leu Pro Glu Leu Pro Gly Glu Thr Pro Leu		
220	225	230
Val Leu His Gly Gln Val Ser Tyr Gly Arg Asn His His Asn Met Thr		
235	240	245
Thr Lys Leu Ala Asn Asn Thr Gln Gly Lys Ser Asp Trp Asp Ser His		
250	255	260
Ser Phe Ala Val Glu Val Gly Gly Ser Leu Pro Val Asp Leu Asn Tyr		
265	270	275
Arg Tyr Leu Thr Ser Tyr Ser Pro Tyr Val Lys Leu Gln Val Val Ser		
280	285	290
Val Asn Gln Lys Gly Phe Gln Glu Val Ala Ala Asp Pro Arg Ile Phe		
295	300	305
Asp Ala Ser His Leu Val Asn Val Ser Ile Pro Met Gly Leu Thr Phe		
310	315	320
Lys His Glu Ser Ala Lys Pro Pro Ser Ala Leu Leu Leu Thr Leu Gly		
325	330	335
Tyr Ala Val Asp Ala Tyr Arg Asp His Pro His Cys Leu Thr Ser Leu		
340	345	350
Thr Asn Gly Thr Ser Trp Ser Thr Phe Ala Thr Asn Leu Ser Arg Gln		
355	360	365
Ala Phe Phe Ala Glu Ala Ser Gly His Leu Lys Leu Leu His Gly Leu		
370	375	380
385	390	395
Asp Cys Phe Ala Ser Gly Ser Cys Glu Leu Arg Ser Ser Ser Arg Ser		
400	405	410
Tyr Asn Ala Asn Cys Gly Thr Arg Tyr Ser Phe Xaa Xaa Xaa Xaa Xaa		
415	420	425
Xaa Xaa Xaa Phe Xaa Xaa Xaa		
430	435	

<210> 525

<211> 867

<212> DNA

<213> C. Trachomatis D serovar

<400> 525

atgacccatc	agcataaaaa	aatcagcgaa	gaaacaatcg	cctgtgacat	gctagagcgc	60
tataccggct	ctaccgttca	agagttccag	cctatctccc	ttcttactaa	ttttgcgat	120
tacgtggagt	tttttcgctga	aatctatcag	gtccctgttt	ctcagaggatc	catgttttgc	180
gcagcgcgatg	cgctcacaat	tcacacctca	atcatcgatt	ttaaaattagg	ctctccaggga	240
cgagctctta	ccgtagatct	gtgtttcttc	cttcccaatg	ctacagcagc	gatcatgttg	300
ggcagtgtgtg	gaggcttaag	atcccactac	caaataggag	attattttgt	ccctgtttgc	360
agcatcccgaa	aagatggaac	atcagatgca	tacttccccc	cagaggtccc	tgcattagct	420
aatttttgtcg	tacaaaaaat	gatcaccaat	attctcgag	ccaaaaacct	cccttaccat	480
ataggcatca	cccacacgac	taacattcgg	ttttgggagt	ttaataaaga	gttcctgtga	540
aaactatatg	aaaataaagc	tcaaacgtgc	gagatggagt	gtgccacctt	atttgtcga	600
ggataccgaa	ggaattcttc	tttaggagca	cttttgtctga	tatcgatctc	acctttgcga	660
aaagatggaa	ttaaaaactaa	ggaagcagtc	tcggcagtc	taaaactctca	caccaaaagag	720
catatactaa	caggcgctga	ggtgtttgcc	tctctacaag	agaaatcagg	cccaggaatc	780

aagaaaacaa aaggtttgcc gcacatggag tttgggcaag ccgatgatgc tctttctgaa 840
 caaactgaag tttctggcgg ggatttc 867

<210> 526

<211> 1182

<212> DNA

<213> C. Trachomatis D serovar

<400> 526

atgtcaaaag	aaacttttca	acgttaataag	cctcatatca	acatagggac	caittggccac	60
gttgacaaag	gtaagactac	gttgacagct	gctattacgc	gtgcgtttgc	tggagatggg	120
ttggctgatt	ttcgtgatta	tagctctatt	gaaacaacgc	ctgaagaaaa	agctcgcggt	180
attacaatta	acgcttcoca	cgttgagtag	gaacaagcta	atcgctacta	cgctcacgtg	240
gaactgccgt	gtcacgcgtg	ctatgttaaa	aaacatgatc	ccggtgcagc	tcaaaaggac	300
ggggctattc	tagtagtttc	tgcaacagac	ggagotatgc	ctcaaaactaa	agagcatatt	360
cttttggcaa	gacaagtgtg	ggttccttac	atcgtgtgtt	ttctcaataa	aattgacatg	420
atttccgaag	aagaacgctg	attggtcgac	ttagttgaga	tggagttggt	tgagcttctt	480
gaagagaag	gatacaaaag	gtgtccaatc	atcagaggtt	ctgctctgaa	agcttggaaa	540
ggggatgctg	catacataga	gaaggttcga	gagctaatgc	aagcogtoga	tgataaacatc	600
ctcactccag	aaagagaaat	tgacaagcct	ttcttaatgc	ctattgagga	cgatttctct	660
atctccggac	gaggaactct	agtaactgga	cgtattgagc	gtggaattgt	taagtttcc	720
gataaagtct	agttgtgcgg	ctctagagat	actaaagaaa	cgattgttac	tggggttgaa	780
atgttcagaa	aaagaactccc	agaaggtcgt	gcaggagaga	acgttggatt	gctcctcaga	840
ggatattgta	agaacgatgt	ggaaagagga	atggtgtgtt	gcttgccaaa	cagtggtaaa	900
ccctacacac	agttccattg	tgctgtttac	gttttgcmaa	aagaagaagg	tggacgacat	960
aagcctttct	tcacaggata	tagacctcaa	ttcttcttcc	gtacaacaga	cgtaacaggt	1020
gtgttaactc	tgccctgaggg	aattgagatg	gtcatgcctg	gggataacgt	tgcatttgaa	1080
gtgcaattga	ttagccctgt	ggctttagaa	gaaggtatga	gatttgcgat	tctgtaagggt	1140
gtgctgtaaa	toggtgctgg	aactatttct	aagatcattg	ca	1182	

<210> 527

<211> 1650

<212> DNA

<213> C. Trachomatis D serovar

<400> 527

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<210> 528

<211> 300

<212> DNA

<213> C. Trachomatis D serovar

<400> 528

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taogctgaaa	gagatgatcg	agagagacat	ttgtctgcta	caggagagag	acgaagagaa	240
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<210> 529

<211> 615

<212> DNA

<213> C. Trachomatis D serovar

<400> 529

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<210> 530

<211> 1806

<212> DNA

<213> C. Trachomatis D serovar

<400> 530

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<210> 531

<211> 972

<212> DNA

<213> C. Trachomatis D serovar

<400> 531

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<210> 532

<211> 1938

<212> DNA

<213> C. Trachomatis D serovar

<400> 532

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<210> 533

<211> 1242

<212> DNA

<213> C. Trachomatis D serovar

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<210> 534

<211> 1212

<212> DNA

<213> C. Trachomatis D serovar

<400> 534

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<210> 535

<211> 1617

<212> DNA

<213> C. Trachomatis D serovar

<400> 535

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<210> 536

<211> 312

<212> DNA

<213> C. Trachomatis D serovar

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<210> 537

<211> 1008

<212> DNA

<213> C. Trachomatis D serovar

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<210> 538

<211> 1278

<212> DNA

<213> C. Trachomatis D serovar

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<210> 539

<211> 1815

<212> DNA

<213> C. Trachomatis D serovar

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<210> 540

<211> 519

<212> DNA

<213> C. Trachomatis D serovar

<400> 540

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<210> 541

<211> 1062

<212> DNA

<213> C. Trachomatis D serovar

<400> 541

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<210> 542

<211> 1263

<212> DNA

<213> C. Trachomatis D serovar

<400> 542

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<210> 543

<211> 693

<212> DNA

<213> C. Trachomatis D serovar

<400> 543

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<210> 544

<211> 729

<212> DNA

<213> C. Trachomatis D serovar

<400> 544

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<210> 545

<211> 1149

<212> DNA

<213> C. Trachomatis D serovar

<400> 545

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<210> 546

<211> 579

<212> DNA

<213> C. Trachomatis D serovar

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<210> 547

<211> 3159

<212> DNA

<213> C. Trachomatis D serovar

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 <211> 1038
 <212> DNA
 <213> C. Trachomatis D serovar

<400> 548

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<210> 549

<211> 978

<212> DNA

<213> C. Trachomatis D serovar

<400> 549

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<210> 550

<211> 438

<212> DNA

<213> C. Trachomatis D serovar

<400> 550

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<211> 1581

<212> DNA

<213> C. Trachomatis D serovar

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<211> 1950

<212> DNA

<213> C. Trachomatis D serovar

<400> 552

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 <212> DNA
 <213> C. Trachomatis D serovar

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 <213> C. Trachomatis D serovar

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<210> 555

<211> 1689

<212> DNA

<213> C. Trachomatis D serovar

<400> 555

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<210> 556

<211> 5253

<212> DNA

<213> C. Trachomatis D serovar

<400> 556

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<211> 792

<212> DNA

<213> C. Trachomatis D serovar

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<210> 558

<211> 306

<212> DNA

<213> C. Trachomatis D serovar

<400> 558

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<210> 559

<211> 729

<212> DNA

<213> C. Trachomatis D serovar

<400> 559

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<210> 560

<211> 289

<212> PRT

<213> C. Trachomatis D serovar

<400> 560

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Leu	Leu	Leu	Thr	Asn	Phe	Ala	Tyr	Tyr	Val	Asp	Val	Phe	Ala	Glu	Ile
			35				40					45			
Tyr	Gln	Val	Pro	Val	Ser	Arg	Gly	Ser	Met	Phe	Ser	Ala	Ala	His	Ala
			50			55				60					
Pro	Gln	Ile	His	Thr	Ser	Ile	Ile	Asp	Phe	Lys	Leu	Gly	Ser	Pro	Gly
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 85 90 95
 Ala Ile Met Leu Gly Met Cys Gly Gly Leu Arg Ser His Tyr Gln Ile
 100 105 110
 Gly Asp Tyr Phe Val Pro Val Ala Ser Ile Arg Lys Asp Gly Thr Ser
 115 120 125
 Asp Ala Tyr Phe Pro Pro Glu Val Pro Ala Leu Ala Asn Phe Val Val
 130 135 140
 Gln Lys Met Ile Thr Asn Ile Leu Glu Ala Lys Asn Leu Pro Tyr His
 145 150 155 160
 Ile Gly Ile Thr His Thr Thr Asn Ile Arg Phe Trp Glu Phe Asn Lys
 165 170 175
 Glu Phe Arg Arg Lys Leu Tyr Glu Asn Lys Ala Gln Thr Val Glu Met
 180 185 190
 Glu Cys Ala Thr Leu Phe Ala Ala Gly Tyr Arg Arg Asn Leu Pro Leu
 195 200 205
 Gly Ala Leu Leu Leu Ile Ser Asp Leu Pro Leu Arg Lys Asp Gly Ile
 210 215 220
 Lys Thr Lys Glu Ser Ser Ser Ala Val Leu Asn Ser His Thr Lys Glu
 225 230 235 240
 His Ile Leu Thr Gly Val Glu Val Phe Ala Ser Leu Gln Glu Lys Ser
 245 250 255
 Gly Pro Gly Ile Lys Lys Thr Lys Gly Leu Pro His Met Glu Phe Gly
 260 265 270
 Gln Ala Asp Asp Ser Leu Ser Glu Gln Thr Glu Val Ser Gly Gly Asp
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<210> 561

<211> 394

<212> PRT

<213> C. Trachomatis D serovar

<400> 561

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 20 25 30
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 35 40 45
 Ser Ile Asp Asn Thr Pro Glu Glu Lys Ala Arg Gly Ile Thr Ile Asn
 50 55 60
 Ala Ser His Val Glu Tyr Glu Thr Ala Asn Arg His Tyr Ala His Val
 65 70 75 80
 Asp Cys Pro Gly His Ala Asp Tyr Val Lys Asn Met Ile Thr Gly Ala
 85 90 95
 Ala Gln Met Asp Gly Ala Ile Leu Val Val Ser Ala Thr Asp Gly Ala
 100 105 110
 Met Pro Gln Thr Lys Glu His Ile Leu Leu Ala Arg Gln Val Gly Val
 115 120 125
 Pro Tyr Ile Val Val Phe Leu Asn Lys Ile Asp Met Ile Ser Glu Glu
 130 135 140
 Asp Ala Glu Leu Val Asp Leu Val Glu Met Glu Leu Val Glu Leu Leu
 145 150 155 160
 Glu Glu Lys Gly Tyr Lys Gly Cys Pro Ile Ile Arg Gly Ser Ala Leu
 165 170 175
 Lys Ala Leu Glu Gly Asp Ala Ala Tyr Ile Glu Lys Val Arg Glu Leu
 180 185 190
 Met Gln Ala Val Asp Asp Asn Ile Pro Thr Pro Glu Arg Glu Ile Asp
 195 200 205

Lys Pro Phe Leu Met Pro Ile Glu Asp Val Phe Ser Ile Ser Gly Arg
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 Gly Thr Val Val Thr Gly Arg Ile Glu Arg Gly Ile Val Lys Val Ser 240
 225 230 235
 Asp Lys Val Gln Leu Val Gly Leu Arg Asp Thr Lys Glu Thr Ile Val 255
 245 250 255
 Thr Gly Val Glu Met Phe Arg Lys Glu Leu Pro Glu Gly Arg Ala Gly 270
 260 265 270
 Glu Asn Val Gly Leu Leu Leu Arg Gly Ile Gly Lys Asn Asp Val Glu 285
 275 280 285
 Arg Gly Met Val Val Cys Leu Pro Asn Ser Val Lys Pro His Thr Gln 300
 290 295 300
 Phe Lys Cys Ala Val Tyr Val Leu Gln Lys Glu Glu Gly Gly Arg His 320
 305 310 315
 Lys Pro Phe Phe Thr Gly Tyr Arg Pro Gln Phe Phe Arg Thr Thr 335
 325 330 335
 Asp Val Thr Gly Val Val Thr Leu Pro Glu Gly Ile Glu Met Val Met 350
 340 345 350
 Pro Gly Asp Asn Val Glu Phe Glu Val Gln Leu Ile Ser Pro Val Ala 365
 355 360 365
 Leu Glu Glu Gly Met Arg Phe Ala Ile Arg Glu Gly Arg Thr Ile 380
 370 375 380
 Gly Ala Gly Thr Ile Ser Lys Ile Ile Ala
 385 390

<210> 562

<211> 550

<212> PRT

<213> C. Trachomatis D serovar

<400> 562

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 Cys Gly Ser Asp Glu Tyr Gly Ile Ala Ile Thr Leu Asn Ala Glu Leu
 50 55 60
 Ala Gly Met Gly Tyr Gln Glu Tyr Val Asp Met Tyr His Lys Leu His
 65 70 75 80
 Lys Asp Thr Phe Lys Lys Leu Gly Ile Ser Val Asp Phe Phe Ser Arg
 85 90 95
 Thr Thr Asn Thr Tyr His Pro Ala Ile Val Gln Asp Phe Tyr Arg Asn
 100 105 110
 Leu Gln Glu Arg Gly Leu Val Glu Asn Gln Val Thr Glu Gln Leu Tyr
 115 120 125
 Ser Glu Glu Glu Gly Lys Phe Leu Ala Asp Arg Tyr Val Val Gly Thr
 130 135 140
 Cys Pro Lys Cys Gly Phe Asp Arg Ala Arg Gly Asp Glu Cys Gln Gln
 145 150 155 160
 Cys Gly Ala Asp Tyr Glu Ala Arg Asp Leu Lys Glu Pro Arg Ser Lys
 165 170 175
 Leu Thr Gly Ala Ala Leu Ser Leu Arg Asp Thr Glu His Ala Tyr Leu
 180 185 190
 His Leu Glu Arg Met Lys Glu Asp Leu Leu Ala Phe Val Gln Gly Ile
 195 200 205
 Tyr Leu Arg Pro His Met Arg Asn Phe Val Thr Asp Tyr Ile Glu His
 210 215 220
 Leu Arg Pro Arg Ala Val Thr Arg Asp Leu Ser Trp Gly Ile Pro Val
 225 230 235 240

Pro Asp Leu Glu Asn Lys Val Phe Tyr Val Trp Phe Asp Ala Pro Ile
 245 255
 Gly Tyr Ile Ser Gly Thr Met Asp Trp Ala Ala Ser Ile Gly Asp Pro
 260 265 270
 Glu Ala Trp Lys Lys Phe Trp Leu Asp Asp Thr Val Thr Tyr Ala Gln
 275 280 285
 Phe Ile Gly Lys Asp Asn Thr Ser Phe His Ala Ala Ile Phe Pro Ala
 290 295 300
 Met Glu Ile Gly Gln Ser Leu Pro Tyr Lys Lys Val Asp Ala Leu Val
 305 310 315 320
 Thr Ser Glu Phe Leu Leu Leu Glu Gly Phe Gln Phe Ser Lys Ser Asp
 325 330 335
 Gly Asn Phe Ile Asp Met Asp Ala Phe Leu Glu Thr Tyr Ser Leu Asp
 340 345 350
 Lys Leu Arg Tyr Val Leu Ala Ala Ile Ala Pro Glu Thr Ser Asp Ser
 355 360 365
 Glu Phe Ser Phe Gln Glu Phe Lys Thr Arg Cys Asn Ser Glu Leu Val
 370 375 380
 Gly Lys Tyr Gly Asn Phe Val Asn Arg Val Leu Ala Phe Ala Val Lys
 385 390 395 400
 Asn Gly Cys Thr Glu Leu Ser Ser Pro Gln Leu Glu Gln Lys Asp Leu
 405 410 415
 Asp Phe Ile Ser Lys Ser Gln Lys Leu Ala Lys Asp Ala Ala Glu His
 420 425 430
 Tyr Ala Gln Tyr Ser Leu Arg Lys Ala Cys Ser Thr Ile Met Glu Leu
 435 440 445
 Ala Ala Leu Gly Asn Gly Tyr Phe Asn Asp Glu Ala Pro Trp Lys Leu
 450 455 460
 Ala Lys Glu Gly Asn Trp Asn Arg Val Arg Ala Ile Leu Phe Cys Ala
 465 470 475 480
 Cys Tyr Cys Gln Lys Leu Leu Ala Leu Ile Ser Tyr Pro Ile Met Pro
 485 490 495
 Glu Thr Ala Leu Lys Ile Leu Glu Met Ile Ala Pro His Ser Leu Asp
 500 505 510
 Leu Gly Ser Gln Asp Pro Asp Arg Leu Gln Ser Leu Trp Thr Asp Ser
 515 520 525
 Phe Phe Asp Tyr Ser Glu Glu Lys Phe Ser Leu Lys Glu Pro Glu Leu
 530 535 540
 Leu Phe Thr Met Val Glu
 545 550

<210> 563

<211> 100

<212> PRT

<213> C. Trachomatis D serovar

<400> 563

Met Ala Arg Lys Asp Arg Leu Thr Asn Glu Arg Leu Asn Lys Leu Phe
 1 5 10 15
 Asp Ser Pro Phe Ser Leu Val Asn Tyr Val Ile Lys Gln Ala Lys Asn
 20 25 30
 Lys Ile Ala Arg Gly Asp Val Arg Ser Ser Asn Val Ala Ile Glu Ala
 35 40 45
 Leu Asn Phe Leu Asp Leu Tyr Gly Ile Gln Ser Glu Tyr Ala Glu Arg
 50 55 60
 Asp Asp Arg Glu Arg His Leu Ser Ala Thr Gly Glu Arg Arg Arg Glu
 65 70 75 80
 Gln Gly Phe Gly Thr Ser Arg Arg Lys Asp Pro Ser Leu Tyr Asn Trp
 85 90 95
 Ser Asp Val Lys
 100

<210> 564
 <211> 205
 <212> PRT
 <213> C. Trachomatis D serovar

<400> 564
 Met Ser Val Lys Val Ile Ser Pro Phe Ser Gln Asp Gly Val Gln Cys
 1 5 10 15
 Phe Pro Lys Leu Phe Ile Ile Ser Ala Pro Ala Gly Ala Gly Lys Thr
 20 25 30
 Thr Leu Thr His Met Leu Gln Arg Glu Phe Pro Asp Ala Phe Glu Lys
 35 40 45
 Thr Val Ser Ser Thr Thr Arg Ser Ala Arg Pro Gly Glu Val His Gly
 50 55 60
 Val Asp Tyr Leu Phe Val Ser Glu Asp Asp Phe Lys Gln Ser Leu Asp
 65 70 75
 Arg Glu Asp Phe Leu Glu Trp Val Phe Leu Phe Gly Thr Tyr Tyr Gly
 85 90 95
 Thr Ser Lys Ala Glu Ile Ser Arg Val Leu Gln Lys Gly Lys His Cys
 100 105 110
 Ile Ala Val Ile Asp Val Gln Gly Ala Leu Ala Leu Lys Lys Gln Met
 115 120 125
 Pro Ala Val Thr Ile Phe Ile Gln Ala Pro Ser Gln Glu Glu Leu Glu
 130 135 140
 Arg Arg Leu Asn Ala Arg Asp Ser Glu Lys Asp Phe Gln Lys Lys Glu
 145 150 155
 Arg Leu Glu His Ser Ala Val Glu Ile Ala Ala Ala Ser Glu Phe Asp
 165 170 175
 Tyr Val Val Val Asn Asp Asp Leu Ile Thr Ala Tyr Gln Val Leu Arg
 180 185 190
 Ser Ile Phe Ile Ala Glu Glu His Arg Met Ser His Gly
 195 200 205

<210> 565
 <211> 602
 <212> PRT
 <213> C. Trachomatis D serovar

<400> 565
 Met Lys Pro Tyr Lys Ile Glu Asn Ile Arg Asn Phe Ser Ile Ile Ala
 1 5 10 15
 His Ile Asp His Gly Lys Ser Thr Ile Ala Asp Arg Leu Leu Glu Ser
 20 25 30
 Thr Ser Thr Ile Glu Gln Arg Glu Met Arg Glu Gln Leu Leu Asp Ser
 35 40 45
 Met Asp Leu Glu Arg Glu Arg Gly Ile Thr Ile Lys Ala His Pro Val
 50 55 60
 Thr Met Thr Tyr Glu Tyr Glu Gly Glu Thr Tyr Glu Leu Asn Leu Ile
 65 70 75
 Asp Thr Pro Gly His Val Asp Phe Ser Tyr Glu Val Ser Arg Ser Leu
 85 90 95
 Ala Ala Cys Glu Gly Ala Leu Leu Ile Val Asp Ala Ala Gln Gly Val
 100 105 110
 Gln Ala Gln Ser Leu Ala Asn Val Tyr Leu Ala Leu Glu Arg Asp Leu
 115 120 125
 Glu Ile Ile Pro Val Leu Asn Lys Ile Asp Leu Pro Ala Ala Gln Pro
 130 135 140
 Glu Ala Ile Lys Lys Gln Ile Glu Glu Phe Ile Gly Leu Asp Thr Ser
 145 150 155
 Asn Thr Ile Ala Cys Ser Ala Lys Thr Gly Gln Gly Ile Pro Glu Ile
 160

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165      170      175
Leu Glu Ser Ile Ile Arg Leu Val Pro Pro Lys Pro Pro Gln Glu
180      185      190
Thr Glu Leu Lys Ala Leu Ile Phe Asp Ser His Tyr Asp Pro Tyr Val
195      200      205
Gly Ile Met Val Tyr Val Arg Val Ile Ser Gly Glu Ile Lys Lys Gly
210      215      220
Asp Arg Ile Thr Phe Met Ala Thr Lys Gly Ser Ser Phe Glu Val Leu
225      230      235
Gly Ile Gly Ala Phe Leu Pro Glu Ala Thr Leu Met Glu Gly Ser Leu
240      245      250
Arg Ala Gly Gln Val Gly Tyr Phe Ile Ala Asn Leu Lys Lys Val Lys
255      260      270
Asp Val Lys Ile Gly Asp Thr Val Thr Thr Val Lys His Pro Ala Lys
275      280      285
Glu Pro Leu Glu Gly Phe Lys Glu Ile Lys Pro Val Val Phe Ala Gly
290      295      300
Ile Tyr Pro Ile Asp Ser Ser Asp Phe Asp Thr Leu Lys Asp Ala Leu
305      310      315
Gly Arg Leu Gln Leu Asn Asp Ser Ala Leu Thr Ile Glu Gln Glu Asn
320      325      330
Ser His Ser Leu Gly Phe Gly Phe Arg Cys Gly Phe Leu Gly Leu Leu
335      340      345
His Leu Glu Ile Ile Phe Glu Arg Ile Ser Arg Glu Phe Asp Leu Asp
350      355      360
Ile Ile Ala Thr Ala Pro Ser Val Ile Tyr Lys Val Val Leu Lys Asn
365      370      375
Gly Lys Thr Leu Phe Ile Asp Asn Pro Thr Ala Tyr Pro Asp Pro Ala
380      385      390
Leu Ile Glu His Met Glu Glu Pro Trp Val His Val Asn Ile Ile Thr
395      400      405
Pro Gln Glu Tyr Leu Ser Asn Ile Met Ser Leu Cys Met Asp Lys Arg
410      415      420
Gly Ile Cys Leu Lys Thr Asp Met Leu Asp Gln His Arg Leu Val Leu
425      430      435
Ser Tyr Glu Leu Pro Leu Asn Glu Ile Val Ser Asp Phe Asn Asp Lys
440      445      450
Leu Lys Ser Val Thr Lys Gly Tyr Gly Ser Phe Asp Tyr Arg Leu Gly
455      460      465
Asp Tyr Lys Lys Gly Ala Ile Ile Lys Leu Glu Ile Leu Ile Asn Asp
470      475      480
Glu Ala Val Asp Ala Phe Ser Cys Leu Val His Arg Asp Lys Ala Glu
485      490      495
Ser Lys Gly Arg Ser Ile Cys Glu Lys Leu Val Asp Val Ile Pro Pro
500      505      510
Gln Leu Phe Lys Ile Pro Ile Gln Ala Ala Ile Asn Lys Lys Ile Ile
515      520      525
Ala Arg Glu Thr Ile Arg Ala Leu Ala Lys Asn Val Thr Ala Lys Cys
530      535      540
Tyr Gly Gly Asp Ile Thr Arg Lys Arg Lys Leu Trp Asp Lys Gln Lys
545      550      555
Lys Gly Lys Lys Arg Met Lys Glu Phe Gly Lys Val Ser Ile Pro Asn
560      565      570
Thr Ala Phe Val Glu Val Leu Lys Met Glu
575      580      585
590      595      600

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<210> 566

<211> 324

<212> PRT

<213> C. Trachomatis D serovar

<400> 566

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Met Glu Leu Leu Pro His Glu Lys Gln Val Val Glu Tyr Glu Lys Thr
 1      5      10      15
Ile Ala Glu Phe Lys Glu Lys Asn Lys Glu Asn Ser Leu Leu Ser Ser
 20      25      30
Ser Glu Ile Gln Lys Leu Asp Lys Arg Leu Asp Arg Leu Lys Glu Lys
 35      40      45
Ile Tyr Ser Asp Leu Thr Pro Trp Glu Arg Val Gln Ile Cys Arg His
 50      55      60
Pro Ser Arg Pro Arg Thr Val Asn Tyr Ile Glu Gly Met Cys Glu Glu
 65      70      75
Phe Val Glu Leu Cys Gly Asp Arg Thr Phe Arg Asp Asp Pro Ala Val
 85      90      95
Val Gly Gly Phe Ala Lys Ile Gln Gly Gln Arg Phe Met Leu Ile Gly
100      105      110
Gln Glu Lys Gly Cys Asp Thr Lys Ser Arg Met His Arg Asn Phe Gly
115      120
Met Leu Cys Pro Glu Gly Phe Arg Lys Ala Leu Arg Leu Ala Lys Met
130      135      140
Ala Glu Lys Phe Gly Leu Pro Ile Ile Phe Leu Val Asp Thr Pro Gly
145      150      155
Ala Phe Pro Gly Leu Thr Ala Glu Glu Arg Gly Gln Gly Trp Ala Ile
165      170      175
Ala Thr Asn Leu Phe Glu Leu Ala Arg Leu Ala Thr Pro Ile Ile Val
180      185      190
Ile Val Ile Gly Glu Gly Cys Ser Gly Gly Ala Leu Gly Met Ala Ile
195      200      205
Gly Asp Val Val Ala Met Leu Glu His Ser Tyr Tyr Ser Val Ile Ser
210      215      220
Pro Glu Gly Cys Ala Ser Ile Leu Trp Lys Asp Pro Lys Lys Asn Ser
225      230      235
Asp Ala Ala Ala Met Leu Lys Met His Gly Glu Asp Leu Lys Gly Phe
245      250      255
Ala Ile Val Asp Ala Val Ile Lys Glu Pro Ile Gly Gly Ala His His
260      265      270
Asn Pro Ala Ala Thr Tyr Arg Ser Val Gln Glu Tyr Val Leu Gln Glu
275      280      285
Trp Leu Lys Leu Lys Asp Leu Pro Val Glu Glu Leu Leu Glu Lys Arg
290      295      300
Tyr Gln Lys Phe Arg Thr Ile Gly Leu Tyr Glu Thr Ser Ser Glu Ser
305      310      315      320
Asp Ser Glu Ala

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<210> 567

<211> 646

<212> PRT

<213> C. Trachomatis D serovar

<400> 567

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Met Lys Leu Leu Leu Lys Ala Ile Leu Arg His Lys Lys His Leu Val
 1      5      10      15
Leu Phe Gly Phe Ser Leu Leu Ser Ile Leu Gly Leu Thr Ile Thr Ser
 20      25      30
Gln Ala Glu Ile Phe Ser Leu Gly Leu Ile Ala Lys Thr Gly Pro Asp
 35      40      45
Thr Phe Leu Leu Phe Gly Lys Gln Glu Gly Ala Ser Leu Val Lys Arg
 50      55      60
Lys Glu Leu Ser Lys Asp Gln Leu Leu Glu Gln Trp Asp Asn Ile Val
 65      70      75      80
Gly Glu Gly Asp Thr Leu Ser Leu Pro Gln Ala Asn Ala Tyr Ile Ala

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Ile Val Gly Gln Leu Lys Gly Arg Cys Thr Gln Ile Ile Ile Ala His
 580 585 590
 Lys Leu Ser Thr Leu Glu Tyr Val Asp Arg Ile Val Tyr Leu Glu Gln
 595 600 605
 Gly Lys Lys Ile Ala Glu Gly Thr Lys Glu Glu Leu Leu Asp Ser Cys
 610 615 620
 Pro Ala Phe Gln Arg Met Trp Val Leu Ser Gly Ala Lys Asp Trp Glu
 625 630 635 640
 Leu Asn Ala Val Val Lys
 645

<210> 568

<211> 414

<212> PRT

<213> C. Trachomatis D serovar

<400> 568

Met Phe Ser Ser Ala Ile Val Ile Leu Thr Ala Ile Phe Val Leu Cys
 1 5 10 15
 Ser Gly Phe Val Ser Leu Ser His Ile Ala Leu Phe Ser Leu Pro Ser
 20 25 30
 Ser Leu Ile Ala His Tyr Ser His Ser Lys Asn Arg Gln Leu Arg Gln
 35 40 45
 Ile Ala Asn Leu Met Ala Tyr Pro Asn His Leu Leu Met Thr Leu Val
 50 55 60
 Phe Phe Asp Ile Gly Ile Asn Ile Gly Val Gln Asn Cys Ile Ala Thr
 65 70 75 80
 Leu Val Gly Asp Ser Ala Ser Leu Leu Leu Thr Val Gly Val Pro Leu
 85 90 95
 Ala Leu Thr Leu Val Leu Gly Glu Ile Val Pro Lys Val Ile Ala Ile
 100 105 110
 Pro Tyr Asn Ala Arg Ile Ala Lys Ile Val Thr Pro Ile Ile Phe Ala
 115 120 125
 Ser Thr Lys Ser Phe Arg Pro Ile Phe Asp Trp Ala Ile Ser Gly Ile
 130 135 140
 Asn Phe Ile Val Gln Lys Met Leu Ala Arg Gln Glu Ser Asp Phe Ile
 145 150 155 160
 Gln Pro Gln Glu Leu Lys Glu Val Leu Arg Ser Cys Lys Asp Phe Gly
 165 170 175
 Val Val Asn His Glu Glu Ser Arg Leu Leu Phe Gly Tyr Leu Ser Met
 180 185 190
 Glu Glu Gly Ser Ile Lys Glu Arg Met Thr Pro Lys Gln Glu Ile Ile
 195 200 205
 Phe Tyr Asp Val Leu Thr Pro Ile Glu Asn Leu Tyr Lys Leu Phe Ser
 210 215 220
 Gly Pro Lys Gln Ser Tyr Ser Lys Val Leu Val Cys Lys Gly Gly Leu
 225 230 235 240
 Gln Asn Leu Leu Gly Val Cys Ser Ala Lys Leu Leu Leu Tyr Lys
 245 250 255
 Glu Lys Leu Gln Ser Ala Glu Glu Leu Leu Pro Leu Leu Arg Lys Pro
 260 265 270
 His Tyr Ile Pro Glu Thr Val Ser Ala Lys Thr Ala Leu Tyr His Leu
 275 280 285
 Ala Gly Glu Asp Cys Gly Leu Gly Ile Ile Ile Asp Gly Tyr Gly Ser
 290 295 300
 Ile Glu Gly Leu Ile Thr Gln Asn Asp Leu Phe Lys Ile Val Ser Asp
 305 310 315 320
 Gly Val Ala His Asn Arg Pro Ser Phe Lys Gln Phe Ala His Ser Asp
 325 330 335
 Lys Asn Val Val Ile Ala Ala Gly Thr Tyr Glu Leu Ser Asp Phe Tyr
 340 345 350

Asp Leu Phe Gly Val Asp Leu Pro Thr Thr Ala Asn Cys Val Thr Ile
 355 360
 Gly Gly Trp Leu Thr Glu Gln Leu Gly Glu Ile Pro Glu Thr Gly Thr
 370 375 380
 Lys Phe Ala Trp Gly Gln Phe Val Phe Gln Ile Leu Asp Ala Ala Pro
 385 390 395 400
 Asn Cys Val Lys Arg Val Tyr Ile Arg Lys Thr His Gly Asn
 405 410

<210> 569

<211> 404

<212> PRT

<213> C. Trachomatis D serovar

<400> 569

Met Glu Thr Asn Ser Pro Phe Phe Trp Leu Gly Val Asn Leu Leu Cys
 1 5 10 15
 Ile Phe Val Gln Gly Phe Phe Ser Met Met Glu Met Ala Cys Ile Ser
 20 25 30
 Phe Asn Arg Val Arg Leu Gln Tyr Tyr Leu Thr Lys Ser Asn Lys Lys
 35 40 45
 Ala Ser Tyr Ile Asn Phe Leu Val Arg Arg Pro Tyr Arg Leu Phe Gly
 50 55 60
 Thr Val Met Leu Gly Val Asn Ile Ala Leu Gln Ile Gly Ser Glu Ser
 65 70 75 80
 Ser Arg Thr Cys Tyr Lys Leu Leu Gly Ile Ser Pro Glu Tyr Ala Pro
 85 90 95
 Ala Thr Gln Ile Ile Leu Val Val Ile Phe Ala Glu Leu Ile Pro Leu
 100 105 110
 Ala Ile Ser Arg Lys Ile Pro Glu Lys Ile Ala Leu Lys Gly Ala Pro
 115 120 125
 Ile Leu Tyr Phe Ala His Tyr Leu Phe Tyr Pro Leu Ile Gln Cys Val
 130 135 140
 Gly Gly Ile Thr Asn Met Ile Tyr Phe Ile Leu Asn Ile Lys Glu Glu
 145 150 155 160
 Thr Leu His Ser Thr Leu Ser Arg Asp Glu Leu Gln Lys Thr Leu Glu
 165 170 175
 Thr His His Glu Glu His Asp Phe Asn Val Ile Ala Thr Asn Ile Phe
 180 185 190
 Ser Leu Ser Ala Thr Ser Val Glu Gln Val Cys Gln Tyr Leu Asn Gln
 195 200 205
 Ile Pro Ile Leu Ser Ala Thr Ala Ser Val Arg Asp Val Cys Gln Leu
 210 215 220
 Val Arg Arg His Arg Leu Asp Phe Val Pro Val Tyr His Lys Val Lys
 225 230 235 240
 Lys Asn Val Val Gly Ile Ala Phe Pro Lys Asn Leu Ile Asn Arg Asn
 245 250 255
 Pro Ser Asp Pro Val Val Pro Tyr Leu Ser Ser Pro Trp Phe Ile Thr
 260 265 270
 Ala Lys Ser Lys Leu Ile His Ala Ile Gln Glu Phe Arg Lys Asn Ser
 275 280 285
 Ser Asn Val Ala Ile Val Leu Asn Asn Asn Gly Glu Pro Met Gly Val
 290 295 300
 Leu Gly Leu His Thr Val Phe Lys Thr Leu Phe Asn Thr Arg Asn Ile
 305 310 315 320
 Ala Gln Leu Lys Pro Lys Pro Thr Ser Leu Ile Glu Arg Thr Phe Ser
 325 330 335
 Gly Asn Thr Pro Leu Ser Glu Ile Glu Asn Glu Leu Asp Ile Ile Phe
 340 345 350
 Met Asp Asn Asp Cys Thr Thr Ile Glu Gln Leu Met Leu Lys Leu Leu
 355 360 365

Asp Thr Pro Pro Glu Val Gly Ala Ser Ile Ile Ile Asn Asp Leu Leu
 370 375 380
 Leu Glu Val Lys Glu Ile Ser Leu Tyr Gly Ile Lys Thr Val Ala Ile
 385 390 395 400
 Lys Asp Thr Leu

<210> 570
 <211> 539
 <212> PRT
 <213> C. Trachomatis D serovar

<400> 570
 Met Cys Cys Val Asp Gly Ser Asn Ser Ile Gln Gln Arg Met Arg Phe
 1 5 10 15
 Cys Glu Tyr Arg Thr Ala Ala Gln Glu Ala Lys Thr Ser Leu Ser Ser
 20 25 30
 Asp Cys Ser Leu Leu Glu Ala Arg Leu Ala Leu Arg Ala Leu Lys
 35 40 45
 His His Glu Tyr Ser Ala Trp Arg Glu Ala Phe Leu Arg Ser Gln Glu
 50 55 60
 Arg Phe Pro Ser Leu Glu Ala Asp Arg Asp Ile His Glu Asp Leu Ala
 65 70 75 80
 Ala Ser Leu Leu Gln Lys Asn Ile Arg His Ser Ser Leu Thr Val Arg
 85 90 95
 Val Ile Thr Ile Leu Ala Val Gly Met Ala Arg Asp Tyr Arg Leu Val
 100 105 110
 Pro Ile Val Leu Gln Ala Leu Ser Asp Asp Ser Asp Thr Val Arg Glu
 115 120 125
 Ile Ala Val Gln Val Ala Val Met Tyr Gly Ser Ser Cys Leu Leu Arg
 130 135 140
 Ala Val Gly Asp Leu Ala Lys Asn Asp Ser Ser Ile Gln Val Arg Ile
 145 150 155 160
 Thr Ala Tyr Arg Ala Ala Val Leu Glu Ile Gln Asp Leu Val Pro
 165 170 175
 His Leu Arg Val Val Val Gln Asn Thr Gln Leu Asp Gly Thr Glu Arg
 180 185 190
 Arg Glu Ala Trp Arg Ser Leu Cys Val Leu Thr Arg Pro His Ser Gly
 195 200 205
 Val Leu Thr Gly Ile Asp Gln Ala Leu Met Thr Cys Glu Met Leu Lys
 210 215 220
 Glu Tyr Pro Glu Lys Cys Thr Glu Glu Gln Ile Arg Thr Leu Leu Ala
 225 230 235 240
 Ala Asp His Pro Glu Val Gln Val Ala Thr Leu Gln Ile Ile Leu Arg
 245 250 255
 Gly Gly Arg Val Phe Arg Ser Ser Ser Ile Met Glu Ser Val Gln Lys
 260 265 270
 Leu Ala Cys Asn Ser Leu Ser Ala Arg Val Gln Met Gln Ala Ala Ala
 275 280 285
 Ile Leu Tyr Leu Glu Gly Asp Pro Phe Gly Glu Asp Lys Leu Thr Glu
 290 295 300
 Gly Leu Ser Ala Thr Ser Ser Ile Leu Cys Glu Ala Ala Ser Glu Ala
 305 310 315 320
 Val Cys Ser Leu Gly Ile His Gly Val His Leu Ala Gly Arg Phe Leu
 325 330 335
 Ser Lys Val Gln Gly Met Arg Ser Arg Val Asn Leu Ala Phe Ala Leu
 340 345 350
 Leu Val Ser Arg Glu Lys Val Glu Glu Ala Gly Asp Val Val Ala Ser
 355 360 365
 Phe Ile His Arg Ile Glu Pro Cys Arg Ala Ile Glu Gln Phe Leu Cys
 370 375 380

Glu Asp Gln Lys Ile Phe Val Ala Ser Ser Pro Leu Gln Val Glu Ile
 385 390 395
 Met Lys Arg Asp Leu Ala Lys Lys Ile Ile Arg Leu Leu Val Ala Ala
 405 410 415
 Gln Tyr Ser Lys Ala Lys Met Val Val Ala Gln Tyr Leu Ala Gly Gln
 420 425 430
 Gln Val Gly Trp Ser Phe Cys Ser Glu Val Phe Trp Glu Gly Asp
 435 440 445
 Ser Glu Asp Phe Val Glu Pro Leu Gln Glu Glu Ser Phe Ala Phe Ala
 450 455 460
 Leu Glu Lys Ala Leu Ser Phe Leu Gln Arg Glu Gly Gly Glu Ala Gly
 465 470 475 480
 Leu His Ala Val Ile Ser Leu Tyr Pro His Ser Arg Trp Gln Asp Lys
 485 490 495
 Leu Thr Ile Leu Glu Ala Ile Ala Tyr Ser Glu Asn Arg Ile Ala Thr
 500 505 510
 Cys Phe Leu Arg Glu Arg Cys Leu Gln Glu Ala Ala Ser Leu Gln Ser
 515 520 525
 Ala Ala Ala Gly Ala Val Phe Ala Leu Phe Lys
 530 535

<210> 571

<211> 104

<212> PRT

<213> C. Trachomatis D serovar

<400> 571

Met Gln Thr Ser Arg Ile Ser Ser Phe Phe Arg Gly Leu Val His Leu
 1 5 10 15
 Tyr Arg Trp Ala Ile Ser Pro Phe Leu Gly Ala Pro Cys Arg Phe Phe
 20 25 30
 Pro Thr Cys Ser Glu Tyr Ala Leu Val Ala Leu Lys Lys His Pro Leu
 35 40 45
 Arg Lys Ser Leu Phe Leu Ile Ala Lys Arg Leu Leu Lys Cys Gly Pro
 50 55 60
 Trp Cys Ile Gly Gly Ile Asp Leu Val Pro Arg Thr Ser Val Glu Glu
 65 70 75 80
 Tyr Leu Ser Ser Pro Thr Pro Leu Ala Glu Ser Pro Asp Asp Arg Thr
 85 90 95
 Val Pro His Thr Gln Glu Thr Ser
 100

<210> 572

<211> 336

<212> PRT

<213> C. Trachomatis D serovar

<400> 572

Met Gln Leu Phe Phe Gly Arg Phe Tyr Glu Val Ala Cys Ile Val Ala
 1 5 10 15
 Ser Ile Leu Arg Glu Arg Asp Val Gly Val Phe Met Gly Ile Glu Gly
 20 25 30
 Arg Gly Ser Gly Ala Met Gln Ser Lys Lys Thr Ile Lys Trp Leu Lys
 35 40 45
 Gln Ala Leu Val Leu Ser Ser Ile Val Asn Ile Leu Leu Leu Leu
 50 55 60
 Ile Tyr Ser Thr Val Phe Arg Lys Asp Ile Tyr Lys Leu Arg Val Phe
 65 70 75 80
 Pro Gly Asn Leu Ile Ala Lys Ser Ser Arg Ile Gly Lys Ile Pro Glu
 85 90 95
 Asp Ile Leu Glu Arg Leu Glu Asn Ala Ser Phe Ala Asp Leu Leu Ala

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      100      105      110
Leu Leu Gln Glu Arg Met Val Phe Gly His Pro Leu Lys Ser Trp
      115      120
Ala Leu Gly Val Ser Ile Gln Lys Tyr Phe Val Asp Ile Ala Pro Met
      130      135      140
Leu Thr His Pro Leu Thr Phe Ile Arg Leu Lys Ser Pro Glu Arg Thr
      145      150      155
Trp Leu Leu Pro Asp Ile Asn Asp Gln Glu Phe Thr Arg Ile Cys Gln
      160      165      170      175
Tyr Leu Leu Thr Glu Arg Phe Pro Phe Ser Ser Arg Gly Phe Phe Arg
      180      185
Ile Met Val Arg Asp Cys Glu Ala Gly Met Val Asp Glu Asp Val Leu
      190      200      205
Tyr Arg Phe Cys His Leu Pro Glu Phe Leu Tyr Val Arg Ser Leu Leu
      210      215      220
Phe Gly Ala Glu Ile Glu Ala Ala Ser Val Ala Ser Leu Ala Arg Met
      225      230      235
Ile Ile Gln Gly Gly Glu Asp Leu Phe Phe Ser Leu Cys Cys Leu Glu
      240      245      250      255
Asn Arg Gln Thr Ala Ile Ser Asp His Gln Arg Arg Cys Phe Leu Lys
      260      265      270
Ala Tyr Val Asp Arg Gln Glu Pro Leu Ala Ala Leu Leu Leu Val
      275      280      285
His Asp Ala Asp Trp Val Leu His Glu Phe Ser Asp Ser Asp Leu Gln
      290      295      300
Ser Phe Ile Gln Leu Leu Pro Arg Glu Ala His Tyr Thr Lys Lys Phe
      305      310      315      320
Leu Gly Cys Val Ala Gln Ser Cys Arg Leu Gly Ile Leu Leu Glu Gly
      325      330      335

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<210> 573

<211> 426

<212> PRT

<213> C. Trachomatis D serovar

<400> 573

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Met Tyr Val Arg Ser Ile Phe Phe Ser Ile Ile Ala Phe Leu Thr Val
      5      10      15
Gly Cys Ser Phe Ser Pro Pro Glu Ser Gly Leu Ile Ile Ala Ile His
      20      25      30
Asp Asp Pro Arg Ser Leu Ser Pro Glu Lys Gly Glu Asn Ala Phe His
      35      40      45
Phe Ser Leu Ser Lys Ala Leu Phe Ala Thr Leu Phe Arg Glu Glu Leu
      50      55      60
Ser Gly Leu Thr Pro Ala Leu Val Ser Ser Tyr Gln Val Ser Glu Asp
      65      70      75      80
Gly Arg Phe Tyr Arg Phe Cys Ile Arg Lys Asp Ala Lys Trp Ser Asp
      85      90      95
Gly Ser Leu Leu Leu Ala Glu Asp Val Ile Ala Ala Trp Glu His Thr
      100      105      110
Lys Gln Ala Gly Arg Tyr Ser Leu Leu Phe Glu Lys Leu Ser Phe Arg
      115      120      125
Ala Ser Ser Ser Ser Glu Ile Leu Ile Glu Leu Lys Glu Pro Glu Pro
      130      135      140
Gln Leu Leu Ala Ile Leu Ala Ser Pro Phe Phe Ala Val Tyr Arg Pro
      145      150      155
Glu Asn Pro Phe Leu Ser Ser Gly Pro Phe Met Pro Lys Thr Tyr Val
      160      165      170      175
Gln Gly Gln Thr Leu Val Leu Gln Lys Asn Pro Tyr Tyr Tyr Asp His
      180      185      190
Ala His Val Glu Leu His Ser Ile Asp Phe Arg Ile Ile Pro Asn Ile

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195 200 205
 Tyr Thr Ala Leu His Leu Leu Arg Arg Gly Asp Val Asp Trp Val Gly
 210 215 220
 Gln Pro Trp His Gln Gly Ile Pro Phe Glu Leu Arg Thr Thr Ser Ala
 225 230 235 240
 Leu Tyr Thr His Tyr Ser Val Asp Gly Thr Phe Trp Leu Ile Leu Asn
 245 250 255
 Pro Lys Asp Pro Val Leu Ser Ser Leu Ser Asn Arg Gln Arg Leu Ile
 260 265 270
 Ala Ala Val Gln Lys Glu Lys Leu Val Lys Gln Ala Leu Gly Thr Gln
 275 280 285
 Tyr Arg Val Ala Glu Ser Ser Pro Ser Pro Glu Gly Ile Ile Ala His
 290 295 300
 Gln Glu Ala Ser Thr Pro Phe Pro Gly Lys Ile Thr Leu Ile Tyr Pro
 305 310 315 320
 Asn Asn Ile Thr Arg Cys Gln Arg Leu Ala Glu Val Leu Gln Glu Gln
 325 330 335
 Cys Arg Asp Ala Gly Ile Gln Leu Thr Leu Glu Gly Leu Glu Tyr His
 340 345 350
 Val Phe Val Gln Lys Arg Ala Thr Gln Asp Phe Ser Val Ser Thr Ala
 355 360 365
 Thr Ser Ile Ala Phe His Pro Leu Ala Lys Ser Lys Phe Asp Gln Thr
 370 375 380
 Ala Leu Asp Asn Phe Thr Cys Leu Pro Leu Tyr His Ile Glu Tyr Asp
 385 390 395 400
 Tyr Ile Leu Ser Arg Pro Leu Asp Gln Ile Val His Tyr Pro Ser Gly
 405 410 415
 Ser Val Asp Leu Thr Tyr Ala His Phe His
 420 425

<210> 574

<211> 605

<212> PRT

<213> C. Trachomatis D serovar

<400> 574

Met Gln Asn Ile Leu Arg Thr Ser Ser Cys Arg Tyr Met Phe Leu Leu
 1 5 10 15
 Gly Ile Arg Ser Val Trp Asn Arg Val Ala Val Val Asn Asn Phe Arg
 20 25 30
 Gly Ser Ser Trp Lys Ile Val Ala Ile Pro Ser Cys Ile Leu Phe Thr
 35 40 45
 Leu Ile Phe His Leu Pro Arg Trp Leu Ile Asp Phe Gly Val Cys Thr
 50 55 60
 Asn Leu Ala Cys Ser Leu Ser Ile Ile Phe Trp Val Phe Ser Leu Arg
 65 70 75 80
 Ser Ser Ala Ser Ala Arg Ile Phe Pro Ser Leu Leu Leu Tyr Leu Cys
 85 90 95
 Leu Leu Arg Leu Gly Leu Asn Leu Ala Ser Thr Arg Trp Ile Leu Ser
 100 105 110
 Ser Gly Trp Ala Ser Pro Leu Ile Phe Ala Leu Gly Asn Phe Phe Ser
 115 120 125
 Leu Gly Ser Ile Pro Val Ala Leu Thr Val Cys Leu Leu Phe Leu
 130 135 140
 Val Asn Phe Leu Val Ile Thr Lys Gly Ala Glu Arg Ile Ala Glu Val
 145 150 155 160
 Arg Ala Arg Phe Ser Leu Glu Ala Leu Pro Gly Lys Gln Met Ser Leu
 165 170 175
 Asp Ala Asp Ile Ala Ala Gly Arg Ile Gly Tyr Ser Arg Ala Ser Val
 180 185 190
 Lys Lys Ser Ser Leu Leu Glu Glu Ser Asp Tyr Phe Ser Ala Met Glu

195 200 205
 Gly Val Phe Arg Phe Val Lys Gly Asp Ala Ile Met Ser Trp Val Leu
 210 215 220
 Leu Gly Val Asn Ile Leu Ala Ala Leu Phe Leu Gly Arg Ala Thr His
 225 230 235
 Val Gly Asp Leu Trp Leu Thr Val Leu Gly Asp Ala Leu Val Ser Gln
 245 250 255
 Ile Pro Ala Leu Leu Thr Ser Cys Ala Ala Thr Leu Ile Ala Lys
 260 265 270
 Val Gly Glu Lys Glu Ser Leu Ala Gln His Leu Leu Asp Tyr Tyr Glu
 275 280 285
 Gln Ser Arg Gln Ser Phe Leu Phe Ile Ala Leu Ile Leu Cys Gly Met
 290 295 300
 Ala Cys Ile Pro Gly Ala Pro Lys Ala Leu Ile Leu Gly Phe Ser Val
 305 310 315
 Leu Leu Phe Leu Gly Tyr Lys Asn Pro Ser Ser Gly Glu Thr Leu Leu
 325 330 335
 Phe Gln Lys Glu Arg Val Glu Phe Val Leu Pro Asp Glu Gly Val Gly
 340 345 350
 Asn Pro Ala Asn Leu Tyr Lys Asp Ala Arg Asn Gln Ile Tyr Gln Glu
 355 360 365
 Leu Gly Val Val Phe Pro Glu Ala Ile Val Val Arg His Val Thr Gly
 370 375 380
 Ser Ser Pro Arg Leu Ile Phe Ser Gly Gln Glu Val Ala Leu Arg Glu
 385 390 395
 Leu Ser Cys Pro Ala Ile Leu Glu Ser Ile Arg Gln Leu Ala Pro Glu
 405 410 415
 Thr Ile Ser Glu Arg Phe Val Thr Arg Leu Val Asp Glu Phe Arg Glu
 420 425 430
 His Ala Phe Leu Ser Ile Glu Glu Ile Leu Pro Leu Lys Ile Ser Glu
 435 440 445
 Asn Ser Leu Ile Phe Leu Leu Arg Ala Leu Val Arg Glu Arg Val Ser
 450 455 460
 Leu His Leu Phe Pro Lys Ile Leu Glu Ala Ile Asp Val Tyr Gly Ser
 465 470 475
 Gln Pro Lys Asn Ser Gln Glu Leu Val Glu Cys Val Arg Lys Tyr Leu
 485 490 495
 Gly Lys Gln Ile Gly Leu Ser Leu Trp Asn Arg Gln Asp Val Leu Glu
 500 505 510
 Val Ile Thr Ile Asp Ser Leu Val Glu Gln Phe Val Arg Asp Ser Gln
 515 520 525
 Glu Lys Val Val Leu Asp Leu Asn Glu Lys Val Val Ala Gln Val Lys
 530 535 540
 His Leu Leu Arg Val Gly Glu Gly Asn Phe Arg Ala Ile Val Thr Gly
 545 550 555
 Ser Glu Thr Arg Lys Glu Leu Lys Arg Ile Val Asp Pro Tyr Phe Pro
 565 570 575
 Asp Leu Leu Val Leu Ala His Ser Glu Leu Pro Glu Glu Ile Pro Ile
 580 585 590
 Thr Leu Leu Gly Ala Val Ser Asp Glu Val Leu Leu Ser
 595 600 605

<210> 575

<211> 173

<212> PRT

<213> C. Trachomatis D serovar

<400> 575

Met Lys Lys Phe Leu Leu Ser Leu Met Ser Leu Ser Ser Leu Pro
 1 5 10 15
 Thr Phe Ala Ala Asn Ser Thr Gly Thr Ile Gly Ile Val Asn Leu Arg

Arg	Cys	Leu	20	Glu	Glu	Ser	Ala	Leu	25	Gly	Lys	Lys	Glu	Ser	Ala	Glu	Phe
		35						40					45				
Glu	Lys	Met	Lys	Asn	Gln	Phe	Ser	Asn	Ser	Met	Gly	Lys	Met	Glu	Glu		
		50				55						60					
Glu	Leu	Ser	Ser	Ile	Tyr	Ser	Lys	Leu	Gln	Asp	Asp	Asp	Tyr	Met	Glu	Glu	
		65			70					75						80	
Gly	Leu	Ser	Glu	Thr	Ala	Ala	Ala	Glu	Leu	Arg	Lys	Lys	Phe	Glu	Asp		
				85					90						95		
Leu	Ser	Ala	Glu	Tyr	Asn	Thr	Ala	Gln	Gly	Gln	Tyr	Tyr	Gln	Ile	Leu		
			100					105					110				
Asn	Gln	Ser	Asn	Leu	Lys	Arg	Met	Gln	Lys	Ile	Met	Glu	Glu	Val	Lys		
			115				120					125					
Lys	Ala	Ser	Glu	Thr	Val	Arg	Ile	Gln	Glu	Gly	Leu	Ser	Val	Leu	Leu		
		130				135					140						
Asn	Glu	Asp	Ile	Val	Leu	Ser	Ile	Asp	Ser	Ser	Ala	Asp	Lys	Thr	Asp		
		145			150				155						160		
Ala	Val	Ile	Lys	Val	Leu	Asp	Asp	Ser	Phe	Gln	Asn	Asn					
				165					170								

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<210> 576
<211> 354
<212> PRT
<213> C. Trachomatis D serovar
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Met	Ser	Gln	Ser	Thr	Tyr	Ser	Leu	Glu	Gln	Leu	Ala	Asp	Phe	Leu	Lys
1				5					10					15	
Val	Glu	Phe	Gln	Gly	Asn	Gly	Ala	Thr	Leu	Leu	Ser	Gly	Val	Glu	Glu
			20					25					30		
Ile	Glu	Glu	Ala	Lys	Thr	Ala	His	Ile	Thr	Phe	Leu	Asp	Asn	Glu	Lys
		35					40					45			
Tyr	Ala	Lys	His	Leu	Lys	Ser	Ser	Glu	Ala	Gly	Ala	Ile	Ile	Ile	Ser
	50					55					60				
Arg	Thr	Gln	Phe	Gln	Lys	Tyr	Arg	Asp	Leu	Asn	Lys	Asn	Phe	Leu	Ile
	65				70				75					80	
Thr	Ser	Glu	Ser	Pro	Ser	Leu	Val	Phe	Gln	Lys	Cys	Leu	Glu	Leu	Phe
			85					90					95		
Ile	Thr	Pro	Val	Asp	Ser	Gly	Phe	Pro	Gly	Ile	His	Pro	Thr	Ala	Val
			100					105					110		
Ile	His	Pro	Thr	Ala	Ile	Ile	Glu	Asp	His	Val	Cys	Ile	Glu	Pro	Tyr
		115					120					125			
Ala	Val	Val	Cys	Gln	His	Ala	His	Val	Gly	Ser	Ala	Cys	His	Ile	Gly
	130					135					140				
Ser	Gly	Ser	Val	Ile	Gly	Ala	Tyr	Ser	Thr	Val	Gly	Gly	His	Ser	Tyr
	145				150					155				160	
Ile	His	Pro	Arg	Val	Val	Ile	Arg	Glu	Arg	Val	Ser	Ile	Gly	Lys	Arg
			165					170					175		
Val	Ile	Ile	Gln	Pro	Gly	Ala	Val	Ile	Gly	Ser	Cys	Gly	Phe	Gly	Tyr
		180						185					190		
Val	Thr	Ser	Ala	Phe	Gly	Gln	His	Lys	His	Leu	Lys	His	Leu	Gly	Lys
		195					200					205			
Val	Ile	Ile	Glu	Asp	Asp	Val	Glu	Ile	Gly	Ala	Asn	Thr	Thr	Ile	Asp
	210					215					220				
Arg	Gly	Arg	Phe	Lys	His	Ser	Val	Val	Arg	Glu	Gly	Ser	Lys	Ile	Asp
	225				230					235				240	
Asn	Leu	Val	Gln	Ile	Ala	His	Gln	Val	Glu	Val	Gly	Gln	His	Ser	Met
			245					250					255		
Ile	Val	Ala	Gln	Ala	Gly	Ile	Ala	Gly	Ser	Thr	Lys	Ile	Gly	Asn	His
		260						265					270		
Val	Ile	Ile	Gly	Gly	Gln	Ala	Gly	Ile	Thr	Gly	His	Ile	Cys	Ile	Ala

275	280	285
Asp His Val Ile Met Met Ala Gln Thr Gly Val Thr Lys Ser Ile Thr		
290	295	300
Ser Pro Gly Ile Tyr Gly Gly Ala Pro Ala Arg Pro Tyr Gln Glu Ile		
305	310	315
His Arg Gln Val Ala Lys Val Arg Asn Leu Pro Arg Leu Glu Glu Arg		
	325	330
Ile Ala Ala Leu Glu Lys Leu Val Gln Lys Leu Glu Ala Leu Ser Glu		
	340	345
		350
Gln His		

<210> 577

<211> 421

<212> PRT

<213> C. Trachomatis D serovar

<400> 577

Met Thr Ala Ser Gly Gly Ala Gly Gly Leu Gly Ser Thr Gln Thr Val	
1	5
Asp Val Ala Arg Ala Gln Ala Ala Ala Ala Thr Gln Asp Ala Gln Glu	
	20
Val Ile Gly Ser Gln Glu Ala Ser Glu Ala Ser Met Leu Lys Gly Cys	
	35
Glu Asp Leu Ile Asn Pro Ala Ala Ala Thr Arg Ile Lys Lys Lys Gly	
	50
Glu Lys Phe Glu Ser Leu Glu Ala Arg Arg Lys Pro Thr Ala Asp Lys	
	65
Ala Glu Lys Lys Ser Glu Ser Thr Glu Glu Lys Gly Asp Thr Pro Leu	
	85
Glu Asp Arg Phe Thr Glu Asp Leu Ser Glu Val Ser Gly Glu Asp Phe	
	100
Arg Gly Leu Lys Asn Ser Phe Asp Asp Asp Ser Ser Pro Asp Glu Ile	
	115
Leu Asp Ala Leu Thr Ser Lys Phe Ser Asp Pro Thr Ile Lys Asp Leu	
	130
Ala Leu Asp Tyr Leu Ile Gln Thr Ala Pro Ser Asp Gly Lys Leu Lys	
	145
Ser Thr Leu Ile Gln Ala Lys His Gln Leu Met Ser Gln Asn Pro Gln	
	165
Ala Ile Val Gly Gly Arg Asn Val Leu Leu Ala Ser Glu Thr Phe Ala	
	180
Ser Arg Ala Asn Thr Ser Pro Ser Ser Leu Arg Ser Leu Tyr Phe Gln	
	195
Val Thr Ser Ser Pro Ser Asn Cys Ala Asn Leu His Gln Met Leu Ala	
	210
Ser Tyr Leu Pro Ser Glu Lys Thr Ala Val Met Glu Phe Leu Val Asn	
	225
Gly Met Val Ala Asp Leu Lys Ser Glu Gly Pro Ser Ile Pro Pro Ala	
	245
Lys Leu Gln Val Tyr Met Thr Glu Leu Ser Asn Leu Gln Ala Leu His	
	260
Ser Val Asn Ser Phe Phe Asp Arg Asn Ile Gly Asn Leu Glu Asn Ser	
	275
Leu Lys His Glu Gly His Ala Pro Ile Pro Ser Leu Thr Thr Gly Asn	
	290
Leu Thr Lys Thr Phe Leu Gln Leu Val Glu Asp Lys Phe Pro Ser Ser	
	305
Ser Lys Ala Gln Lys Ala Leu Asn Glu Leu Val Gly Pro Asp Thr Gly	
	325
Pro Gln Thr Glu Val Leu Asn Leu Phe Phe Arg Ala Leu Asn Gly Cys	
	340
	350

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          340          345          350
Ser Pro Arg Ile Phe Ser Gly Ala Glu Lys Lys Gln Gln Leu Ala Ser
      355          360          365
Val Ile Thr Asn Thr Leu Asp Ala Ile Asn Ala Asp Asn Glu Asp Tyr
      370          375          380
Pro Lys Pro Gly Asp Phe Pro Arg Ser Ser Phe Ser Ser Thr Pro Pro
      385          390          395          400
His Ala Pro Val Pro Gln Ser Glu Ile Pro Thr Ser Pro Thr Ser Thr
          405          410          415
Gln Pro Pro Ser Pro
          420

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<210> 578
 <211> 231
 <212> PRT
 <213> C. Trachomatis D serovar

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<400> 578
Met Met Glu Val Phe Met Asn Phe Leu Asp Gln Leu Asp Leu Ile Ile
  1          5          10          15
Gln Asn Lys His Met Leu Glu His Thr Phe Tyr Val Lys Trp Ser Lys
      20          25          30
Gly Glu Leu Thr Lys Glu Gln Leu Gln Ala Tyr Ala Lys Asp Tyr Tyr
      35          40          45
Leu His Ile Lys Ala Phe Pro Lys Tyr Leu Ser Ala Ile His Ser Arg
      50          55          60
Cys Asp Asp Leu Glu Ala Arg Lys Leu Leu Leu Asp Asn Leu Met Asp
      65          70          75          80
Glu Glu Asn Gly Tyr Pro Asn His Ile Asp Leu Trp Lys Gln Phe Val
      85          90          95
Phe Ala Leu Gly Val Thr Pro Glu Glu Leu Glu Ala His Gln Pro Ser
      100          105          110
Glu Ala Ala Lys Ala Lys Val Ala Thr Phe Met Arg Trp Cys Thr Gly
      115          120          125
Asp Ser Leu Ala Ala Gly Val Ala Ala Leu Tyr Ser Tyr Glu Ser Gln
      130          135          140
Ile Pro Arg Ile Ala Arg Glu Lys Ile Arg Gly Leu Thr Glu Tyr Phe
      145          150          155          160
Gly Phe Ser Asn Pro Glu Asp Tyr Ala Tyr Phe Thr Glu His Glu Glu
      165          170          175
Ala Asp Val Arg His Ala Arg Glu Glu Lys Ala Leu Ile Glu Met Leu
      180          185          190
Leu Lys Asp Asp Ala Asp Lys Val Leu Glu Ala Ser Gln Glu Val Thr
      195          200          205
Gln Ser Leu Tyr Gly Phe Leu Asp Ser Phe Leu Asp Pro Gly Thr Cys
      210          215          220
Cys Ser Cys His Gln Ser Tyr
      225          230

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<210> 579
 <211> 243
 <212> PRT
 <213> C. Trachomatis D serovar

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<400> 579
Met Lys Ile Thr Pro Ile Lys Thr Arg Lys Val Phe Ala His Asp Ser
  1          5          10          15
Leu Gln Glu Ile Leu Gln Glu Ala Leu Pro Pro Leu Gln Glu Arg Ser
      20          25          30
Val Val Val Val Ser Ser Lys Ile Val Ser Leu Cys Glu Gly Ala Val
      35          40          45

```

Ala Asp Ala Arg Met Cys Lys Ala Glu Leu Ile Lys Lys Glu Ala Asp
 50 55 60
 Ala Tyr Leu Phe Cys Glu Lys Ser Gly Ile Tyr Leu Thr Lys Lys Glu
 65 70 75 80
 Gly Ile Leu Ile Pro Ser Ala Gly Ile Asp Glu Ser Asn Thr Asp Gln
 85 90 95
 Pro Phe Val Leu Tyr Pro Lys Asp Ile Leu Gly Ser Cys Asn Arg Ile
 100 105 110
 Gly Glu Trp Leu Arg Asn Tyr Phe Arg Val Lys Glu Leu Gly Val Ile
 115 120 125
 Ile Thr Asp Ser His Thr Thr Pro Met Arg Arg Gly Val Leu Gly Ile
 130 135 140
 Gly Leu Cys Trp Tyr Gly Phe Ser Pro Leu His Asn Tyr Ile Gly Ser
 145 150 155 160
 Leu Asp Cys Phe Gly Arg Pro Leu Gln Met Thr Gln Ser Asn Leu Val
 165 170 175
 Asp Ala Leu Ala Val Ala Val Val Cys Met Gly Glu Gly Asn Glu
 180 185 190
 Gln Thr Pro Leu Ala Val Ile Glu Gln Ala Pro Asn Met Val Tyr His
 195 200 205
 Ser His Pro Thr Ser Arg Glu Glu Tyr Cys Ser Leu Arg Ile Asp Glu
 210 215 220
 Thr Glu Asp Leu Tyr Gly Pro Phe Leu Gln Ala Val Thr Trp Ser Gln
 225 230 235 240
 Glu Lys Lys

<210> 580

<211> 383

<212> PRT

<213> C. Trachomatis D serovar

<400> 580

Met Leu Pro His Gln Gln Asn Ser Ser Ser Glu Arg Ala Arg His His
 1 5 10 15
 Glu Ser Arg Ser His Arg His Ser Ser Ser Arg His His Val Thr
 20 25 30
 Arg Ser Gln Ser Ser Ala Leu Pro Gln Leu Gln Glu Arg Pro Val Pro
 35 40 45
 His Pro Leu Ala Glu Arg Glu Leu Ile Ile Phe His Ser Val His Gln
 50 55 60
 Gln Gln Asn Asn Asn Pro Leu Arg Met Ile Cys Asp Thr Ile Arg Gln
 65 70 75 80
 Ala Gln Arg Gly Ile Phe Met Arg Ile Tyr Thr Ile Ser Ser Asp Asp
 85 90 95
 Ile Ile Gln Ser Leu Ile Gln Thr Ser His His Val Pro Val Glu Val
 100 105 110
 Lys Tyr His Cys Gly Glu Ser Leu Pro Val Ala Cys Gln Asn Ser Arg
 115 120 125
 Val Val Leu Arg Leu Thr Asn Gly Arg Thr Leu Gln His Lys Lys Thr
 130 135 140
 Met Leu Ala Asp Phe Gln Thr Val Val Thr Gly Ser Ala Asn Tyr Thr
 145 150 155 160
 Asp Leu Ser Leu Asn His Asp Ala Asn Val Thr Ala Cys Ile Glu Ser
 165 170 175
 Ser Glu Leu His Asp Ala Val Phe Ser Glu Arg Pro Gln Leu Val His
 180 185 190
 Val Gly Pro Gln Leu Leu Asn Tyr Ile Pro Ile Gln Arg Leu Ile Pro
 195 200 205
 Asn Ala Ala Ser Lys Met Ile Leu Asn Ala Ile Asn Gln Ala Thr Asp
 210 215 220

Ser Ile Phe Val Leu Met Tyr Ile Phe Leu Ser Pro Glu Phe Phe Leu
 225 230 240
 Ala Leu Ala Gln Ala Met Arg Arg Gly Val Arg Val Lys Val Ile Ile
 245 250 255
 Asp Asn His Ser Lys Gln Asp Thr Cys Lys Leu Leu Ser Lys Leu Gly
 260 265 270
 Ile Gln Leu Pro Ile Tyr Glu Arg Lys Thr Glu Gly Val Leu His Thr
 275 280 285
 Lys Ile Cys Cys Ile Asp Asn Lys Thr Leu Ile Phe Gly Ser Ala Asn
 290 295 300
 Trp Ser Gly Ala Gly Met Ile Lys Asn Phe Glu Asp Leu Phe Ile Leu
 305 310 315
 Arg Pro Ile Thr Glu Thr Gln Leu Gln Ala Phe Met Asp Val Trp Ser
 320 325 330
 Leu Leu Glu Thr Asn Ser Ser Tyr Leu Ser Pro Glu Ser Val Leu Thr
 335 340 345
 Ala Pro Thr Pro Ser Ser Arg Pro Thr Gln Gln Asp Thr Ser Ser Asp
 350 355 360
 Asp Glu Gln Pro Ser Thr Ser Gln Gln Asp Ile Arg Met Arg Lys
 365 370 375 380

<210> 581

<211> 193

<212> PRT

<213> C. Trachomatis D serovar

<400> 581

Met Trp Phe Phe Leu Gly Ser Pro Ser Ala Ile Thr Asn Phe Ser Arg
 1 5 10 15
 Val Asp Val Ala Leu Asn Leu Arg Ile Asn Arg Gln Ile Arg Ala Pro
 20 25 30
 Arg Val Arg Val Ile Gly Ser Ala Gly Glu Gln Leu Gly Ile Leu Ser
 35 40 45
 Ile Lys Glu Ala Leu Asp Leu Ala Lys Glu Ala Asn Leu Asp Leu Val
 50 55 60
 Glu Val Ala Ser Asn Ser Glu Pro Pro Val Cys Lys Ile Met Asp Tyr
 65 70 75 80
 Gly Lys Tyr Arg Tyr Asp Val Thr Lys Lys Glu Lys Asp Ser Lys Lys
 85 90 95
 Ala Gln His Gln Val Arg Ile Lys Glu Val Lys Leu Lys Pro Asn Ile
 100 105 110
 Asp Asp Asn Asp Phe Leu Thr Lys Ala Lys Gln Ala Arg Ala Phe Ile
 115 120 125
 Glu Lys Gly Asn Lys Val Lys Val Ser Cys Met Phe Arg Gly Arg Glu
 130 135 140
 Leu Ala Tyr Pro Glu His Gly Tyr Lys Val Ile Gln Arg Met Cys Gln
 145 150 155 160
 Gly Leu Glu Asp Ile Gly Phe Val Glu Ser Glu Pro Lys Leu Asn Gly
 165 170 175
 Arg Ser Leu Ile Cys Val Ile Ala Pro Gly Thr Leu Lys Thr Lys Lys
 180 185 190
 Lys

<210> 582

<211> 264

<212> PRT

<213> C. Trachomatis D serovar

<400> 582

Met Gly Asn Ser Gly Phe Tyr Leu Tyr Asn Thr Glu Asn Cys Val Phe

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1           5           10           15
Ala Asp Asn Ile Lys Val Gly Gln Met Thr Glu Pro Leu Lys Asp Gln
20
Gln Ile Ile Leu Gly Thr Lys Ser Thr Pro Val Ala Ala Lys Met Thr
35
Ala Ser Asp Gly Ile Ser Leu Thr Val Ser Asn Asn Ser Ser Thr Asn
50
Ala Ser Ile Thr Ile Gly Leu Asp Ala Glu Lys Ala Tyr Gln Leu Ile
65
Leu Glu Lys Leu Gly Asn Gln Ile Leu Asp Gly Ile Ala Asp Thr Ile
85
Val Asp Ser Thr Val Gln Asp Ile Leu Asp Lys Ile Thr Thr Asp Pro
100
Ser Leu Gly Leu Leu Lys Ala Phe Asn Asn Phe Pro Ile Thr Asn Lys
115
Ile Gln Cys Asn Gly Leu Phe Thr Pro Ser Asn Ile Glu Thr Leu Leu
130
Gly Gly Thr Glu Ile Gly Lys Phe Thr Val Thr Pro Lys Ser Ser Gly
145
Ser Met Phe Leu Val Ser Ala Asp Ile Ile Ala Ser Arg Met Glu Gly
165
Gly Val Val Leu Ala Leu Val Arg Glu Gly Asp Ser Lys Pro Cys Ala
180
Ile Ser Tyr Gly Tyr Ser Ser Gly Val Pro Asn Leu Cys Ser Leu Arg
195
Thr Ser Ile Thr Asn Thr Gly Leu Thr Pro Thr Thr Tyr Ser Leu Arg
210
Val Gly Gly Leu Glu Ser Gly Val Val Trp Val Asn Ala Leu Ser Asn
225
Gly Asn Asp Ile Leu Gly Ile Thr Asn Thr Ser Asn Val Ser Phe Leu
245
Glu Val Ile Pro Gln Thr Asn Ala
260

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<210> 583

<211> 1053

<212> PRT

<213> C. Trachomatis D serovar

<400> 583

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Met Phe Thr Arg Ile Val Met Val Asp Leu Gln Glu Lys Gln Cys Thr
1           5           10           15
Ile Val Lys Arg Asn Gly Met Phe Val Pro Phe Asp Arg Asn Arg Ile
20
Phe Gln Ala Leu Glu Ala Ala Phe Arg Asp Thr Arg Arg Ile Asp Asp
35
His Met Pro Leu Pro Glu Asp Leu Glu Ser Ser Ile Arg Ser Ile Thr
50
His Gln Val Val Lys Glu Val Val Gln Lys Ile Thr Asp Gly Gln Val
65
Val Thr Val Glu Arg Ile Gln Asp Met Val Glu Ser Gln Leu Tyr Val
85
Asn Gly Leu Gln Asp Val Ala Arg Asp Tyr Ile Val Tyr Arg Asp Asp
100
Arg Lys Ala His Arg Lys Lys Ser Trp Gln Ser Leu Ser Val Val Arg
115
Arg Cys Gly Thr Val Val His Phe Asn Pro Met Lys Ile Ser Ala Ala
130
Leu Glu Lys Ala Phe Arg Ala Thr Asp Lys Thr Glu Gly Met Thr Pro
145
Ser Ser Val Arg Glu Glu Ile Asn Ala Leu Thr Gln Asn Ile Val Ala
160

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Glu	Ile	Glu	Glu	Cys	Cys	Pro	Gln	Gln	Asp	Arg	Arg	Ile	Asp	Ile	Glu
Lys	Ile	Gln	Gln	Ile	Val	Glu	Gln	Gln	Leu	Met	Val	Val	Asp	Gly	Tyr
Ala	Val	Ala	Lys	Asn	Tyr	Ile	Leu	Tyr	Arg	Glu	Ala	Arg	Ala	Arg	Val
Arg	Asp	Asn	Arg	Glu	Glu	Asp	Gly	Ser	Thr	Gly	Lys	Thr	Ile	Ala	Glu
Glu	Ala	Val	Glu	Val	Leu	Ser	Lys	Asp	Gly	Ser	Thr	Tyr	Thr	Met	Thr
His	Ser	Gln	Leu	Leu	Ala	His	Leu	Ala	Arg	Ala	Cys	Ser	Arg	Phe	Pro
Glu	Thr	Thr	Asp	Ala	Ala	Leu	Leu	Thr	Asp	Met	Ala	Fhe	Ala	Asn	Phe
Tyr	Ser	Gly	Ile	Lys	Glu	Ser	Glu	Val	Val	Leu	Ala	Cys	Ile	Met	Ala
Ala	Arg	Ala	Asn	Ile	Glu	Lys	Glu	Pro	Asp	Tyr	Ala	Fhe	Val	Ala	Ala
Glu	Leu	Leu	Leu	Asp	Val	Val	Tyr	Lys	Glu	Ala	Leu	Gly	Lys	Ser	Lys
Tyr	Ala	Glu	Asp	Leu	Glu	Gln	Ala	His	Arg	Asp	His	Fhe	Lys	Arg	Tyr
Ile	Ala	Glu	Gly	Asp	Thr	Tyr	Arg	Leu	Asn	Ala	Glu	Leu	Lys	His	Leu
Phe	Asp	Leu	Asp	Ala	Leu	Ala	Asp	Ala	Met	Asp	Leu	Ser	Arg	Asp	Leu
Gln	Phe	Ser	Tyr	Met	Gly	Ile	Gln	Asn	Leu	Tyr	Asp	Arg	Tyr	Phe	Asn
His	His	Glu	Gly	Cys	Arg	Leu	Glu	Thr	Pro	Gln	Ile	Phe	Trp	Met	Arg
Val	Ala	Met	Gly	Leu	Ala	Leu	Asn	Glu	Gln	Asp	Lys	Thr	Ser	Trp	Ala
Ile	Thr	Phe	Tyr	Asn	Leu	Leu	Ser	Thr	Phe	Arg	Tyr	Thr	Pro	Ala	Thr
Pro	Thr	Leu	Phe	Asn	Ser	Gly	Met	Arg	His	Ser	Gln	Leu	Ser	Ser	Cys
Tyr	Leu	Ser	Thr	Val	Gln	Asp	Asn	Leu	Val	Asn	Ile	Tyr	Lys	Val	Ile
Ala	Asp	Asn	Ala	Met	Leu	Ser	Lys	Trp	Ala	Gly	Gly	Ile	Gly	Asn	Asp
Trp	Thr	Ala	Ile	Arg	Ala	Thr	Gly	Ala	Leu	Ile	Lys	Gly	Thr	Asn	Gly
Arg	Ser	Gln	Gly	Val	Ile	Pro	Phe	Ile	Lys	Val	Thr	Asn	Asp	Thr	Ala
Val	Ala	Val	Asn	Gln	Gly	Gly	Lys	Arg	Lys	Gly	Ala	Val	Cys	Val	Tyr
Glu	Glu	Val	Trp	His	Leu	Asp	Tyr	Glu	Asp	Phe	Leu	Glu	Leu	Arg	Lys
Asn	Thr	Gly	Asp	Glu	Arg	Arg	Arg	Ala	His	Asp	Val	Asn	Ile	Ala	Ser
Trp	Ile	Pro	Asp	Leu	Phe	Phe	Lys	Arg	Leu	Gln	Gln	Lys	Gly	Thr	Trp
Thr	Leu	Phe	Ser	Pro	Asp	Asp	Val	Pro	Gly	Leu	His	Asp	Ala	Tyr	Gly
Glu	Glu	Phe	Glu	Arg	Leu	Tyr	Glu	Glu	Tyr	Glu	Arg	Lys	Val	Asp	Thr
Gly	Glu	Ile	Arg	Leu	Phe	Lys	Lys	Val	Glu	Ala	Glu	Asp	Leu	Trp	Arg
Lys	Met	Leu	Ser	Met	Leu	Phe	Glu	Thr	Gly	His	Pro	Trp	Met	Thr	Phe

Lys Asp Pro Ser Asn Ile Arg Ser Ala Gln Asp His Lys Gly Val Val
 660 665 670
 Arg Cys Ser Asn Leu Cys Thr Glu Ile Leu Leu Asn Cys Ser Glu Thr
 675 680 685
 Glu Thr Ala Val Cys Asn Leu Gly Ser Ile Asn Leu Val Gln His Ile
 690 700
 Val Gly Asp Gly Leu Asp Glu Glu Lys Leu Ser Glu Thr Ile Ser Ile
 705 710 715 720
 Ala Val Arg Met Leu Asp Asn Val Ile Asp Ile Asn Phe Tyr Pro Thr
 725 730 735
 Lys Glu Ala Lys Glu Ala Asn Phe Ala His Arg Ala Ile Gly Leu Gly
 740 745 750
 Val Met Gly Phe Gln Asp Ala Leu Tyr Lys Leu Asp Ile Ser Tyr Ala
 755 760 765
 Ser Gln Glu Ala Val Glu Phe Ala Asp Tyr Ser Ser Glu Leu Ile Ser
 770 775 780
 Tyr Tyr Ala Ile Gln Ala Ser Cys Leu Leu Ala Lys Glu Arg Gly Thr
 785 790 795 800
 Tyr Ser Ser Tyr Lys Gly Ser Lys Trp Asp Arg Gly Leu Leu Pro Ile
 805 810 815
 Asp Thr Ile Gln Leu Leu Ala Asn Tyr Arg Gly Glu Ala Asn Leu Gln
 820 825 830
 Met Asp Thr Ser Ser Arg Lys Asp Trp Glu Pro Ile Arg Ser Leu Val
 835 840 845
 Lys Glu His Gly Met Arg His Cys Gln Leu Met Ala Ile Ala Pro Thr
 850 855 860
 Ala Thr Ile Ser Asn Ile Ile Gly Val Thr Gln Ser Ile Glu Pro Thr
 865 870 875 880
 Tyr Lys His Leu Phe Val Lys Ser Asn Leu Ser Gly Glu Phe Thr Ile
 885 890 895 900
 Pro Asn Val Tyr Leu Ile Glu Lys Leu Lys Lys Leu Gly Ile Trp Asp
 905 910 915 920
 Ala Asp Met Leu Asp Asp Leu Lys Tyr Phe Asp Gly Ser Leu Leu Glu
 925 930 935 940
 Ile Glu Arg Ile Pro Asp His Leu Lys His Ile Phe Leu Thr Ala Phe
 945 950 955 960
 Glu Ile Glu Pro Glu Trp Ile Ile Glu Cys Ala Ser Arg Arg Gln Lys
 965 970 975 980
 Trp Ile Asp Met Gly Gln Ser Leu Asn Leu Tyr Leu Ala Gln Pro Asp
 985 990 995 1000
 Gly Lys Lys Leu Ser Asn Met Tyr Leu Thr Ala Trp Lys Lys Gly Leu
 1005 1010 1015 1020
 Lys Thr Thr Tyr Tyr Leu Arg Ser Ser Ala Thr Thr Val Glu Lys
 1025 1030 1035 1040
 Ser Phe Val Asp Ile Asn Lys Arg Gly Ile Gln Pro Arg Trp Met Lys
 1045 1050
 Asn Lys Ser Ala Ser Ala Gly Ile Ile Val Glu Arg Ala Lys Lys Ala
 Pro Val Cys Ser Leu Glu Glu Gly Cys Glu Ala Cys Gln

<210> 584

<211> 346

<212> PRT

<213> C. Trachomatis D serovar

<400> 584

Met Gln Ala Asp Ile Leu Asp Gly Lys Gln Lys Arg Val Asn Leu Asn
 1 5 10 15
 Ser Lys Arg Leu Val Asn Cys Asn Gln Val Asp Val Asn Gln Leu Val
 20 25 30

Pro Ile Lys Tyr Lys Trp Ala Trp Glu His Tyr Leu Asn Gly Cys Ala
 35 40
 Asn Asn Trp Leu Pro Thr Glu Ile Pro Met Gly Lys Asp Ile Glu Leu
 50 55
 Trp Lys Ser Asp Arg Leu Ser Glu Asp Glu Arg Val Ile Leu Leu
 65 70
 Asn Leu Gly Phe Phe Ser Thr Ala Glu Ser Leu Val Gly Asn Asn Ile
 85 90
 Val Leu Ala Ile Phe Lys His Val Thr Asn Pro Glu Ala Arg Gln Tyr
 100 105
 Leu Leu Arg Gln Ala Phe Glu Glu Ala Val His Thr His Thr Phe Leu
 115 120
 Tyr Ile Cys Glu Ser Leu Gly Leu Asp Glu Lys Glu Ile Phe Asn Ala
 130 135
 Tyr Asn Glu Arg Ala Ala Ile Lys Ala Lys Asp Asp Phe Gln Met Glu
 145 150
 Ile Thr Gly Lys Val Leu Asp Pro Asn Phe Arg Thr Asp Ser Val Glu
 165 170
 Gly Leu Gln Glu Phe Val Lys Asn Leu Val Gly Tyr Tyr Ile Ile Met
 180 185
 Glu Gly Ile Phe Phe Tyr Ser Gly Phe Val Met Ile Leu Ser Phe His
 195 200
 Arg Gln Asn Lys Met Ile Gly Ile Gly Glu Gln Tyr Gln Tyr Ile Leu
 210 215
 Arg Asp Glu Thr Ile His Leu Asn Phe Gly Ile Asp Leu Ile Asn Gly
 225 230
 Ile Lys Glu Glu Asn Pro Glu Ile Trp Thr Pro Glu Leu Gln Gln Glu
 245 250
 Ile Val Glu Leu Ile Lys Arg Ala Val Asp Leu Glu Ile Glu Tyr Ala
 260 265
 Gln Asp Cys Leu Pro Arg Gly Ile Leu Gly Leu Arg Ala Ser Met Phe
 275 280
 Ile Asp Tyr Val Gln His Ile Ala Asp Arg Arg Leu Glu Arg Ile Gly
 290 295
 Leu Lys Pro Ile Tyr His Thr Lys Asn Pro Phe Pro Trp Met Ser Glu
 305 310
 Thr Ile Asp Leu Asn Lys Glu Lys Asn Phe Phe Glu Thr Arg Val Ile
 325 330
 Glu Tyr Gln His Ala Ala Ser Leu Thr Trp
 340 345

<210> 585

<211> 326

<212> PRT

<213> C. Trachomatis D serovar

<400> 585

Met Ser Phe Phe His Thr Arg Lys Tyr Lys Leu Ile Leu Arg Gly Leu
 1 10
 Leu Cys Leu Ala Gly Cys Phe Leu Met Asn Ser Cys Ser Ser Ser Arg
 20 25
 Gly Asn Gln Pro Ala Asp Glu Ser Ile Tyr Val Leu Ser Met Asn Arg
 35 40
 Met Ile Cys Asp Cys Val Ser Arg Ile Thr Gly Asp Arg Val Lys Asn
 50 55
 Ile Val Leu Ile Asp Gly Ala Ile Asp Pro His Ser Tyr Glu Met Val
 65 70
 Lys Gly Asp Glu Asp Arg Met Ala Met Ser Gln Leu Ile Phe Cys Asn
 85 90
 Gly Leu Gly Leu Glu His Ser Ala Ser Leu Arg Lys His Leu Glu Gly
 100 105 110

Asn Pro Lys Val Val Asp Leu Gly Gln Arg Leu Leu Asn Lys Asn Cys
 115 120 125
 Phe Asp Leu Leu Ser Glu Glu Gly Phe Pro Asp Pro His Ile Trp Thr
 130 135 140
 Asp Met Arg Val Trp Gly Ala Ala Val Lys Glu Met Ala Ala Ala Leu
 145 150 155
 Ile Gln Gln Phe Pro Gln Tyr Glu Glu Asp Phe Gln Lys Asn Ala Asp
 165 170 175
 Gln Ile Leu Ser Glu Met Glu Glu Leu Asp Arg Trp Ala Ala Arg Ser
 180 185 190
 Leu Ser Thr Ile Pro Glu Lys Asn Arg Tyr Leu Val Thr Gly His Asn
 195 200 205
 Ala Phe Ser Tyr Phe Thr Arg Arg Tyr Leu Ser Ser Asp Ala Glu Arg
 210 215 220
 Val Ser Gly Glu Trp Arg Ser Arg Cys Ile Ser Pro Glu Gly Leu Ser
 225 230 235
 Pro Glu Ala Gln Ile Ser Ile Arg Asp Ile Met Arg Val Val Glu Tyr
 245 250 255
 Ile Ser Ala Asn Asp Val Glu Val Val Phe Leu Glu Asp Thr Leu Asn
 260 265 270
 Gln Asp Ala Leu Arg Lys Ile Val Ser Cys Ser Lys Ser Gly Gln Lys
 275 280 285
 Ile Arg Leu Ala Lys Ser Pro Leu Tyr Ser Asp Asn Val Cys Asp Asn
 290 295 300
 Tyr Phe Ser Thr Phe Gln His Asn Val Arg Thr Ile Thr Glu Glu Leu
 305 310 315 320
 Gly Gly Thr Val Leu Glu
 325

<210> 586

<211> 102

<212> PRT

<213> C. Trachomatis D serovar

<400> 586

Met Gln Asn Lys Arg Lys Val Arg Asp Asp Phe Ile Lys Ile Val Lys
 1 5 10 15
 Asp Val Lys Lys Asp Phe Pro Glu Leu Asp Leu Lys Ile Arg Val Asn
 20 25 30
 Lys Glu Lys Val Thr Phe Leu Asn Ser Pro Leu Glu Leu Tyr His Lys
 35 40 45
 Ser Val Ser Leu Ile Leu Gly Leu Leu Gln Gln Ile Glu Asn Ser Leu
 50 55 60
 Gly Leu Phe Pro Asp Ser Pro Val Leu Glu Lys Leu Glu Asp Asn Ser
 65 70 75 80
 Leu Lys Leu Lys Lys Ala Leu Ile Met Leu Ile Leu Ser Arg Lys Asp
 85 90 95
 Met Phe Ser Lys Ala Glu
 100

<210> 587

<211> 243

<212> PRT

<213> C. Trachomatis D serovar

<400> 587

Val Gly Cys Asn Leu Ala Gln Phe Leu Gly Lys Lys Val Leu Leu Ala
 1 5 10 15
 Asp Leu Asp Pro Gln Ser Asn Leu Ser Ser Gly Leu Gly Ala Ser Val
 20 25 30
 Arg Asn Asn Gln Lys Gly Leu His Asp Ile Val Tyr Lys Ser Asn Asp

```

      35              40              45
Leu Lys Ser Ile Ile Cys Glu Thr Lys Lys Asp Ser Val Asp Leu Ile
 50      55      60
Pro Ala Ser Phe Leu Ser Glu Gln Phe Arg Glu Leu Asp Ile His Arg
 65      70      75      80
Gly Pro Ser Asn Asn Leu Lys Leu Phe Leu Asn Glu Tyr Cys Ala Pro
      85      90      95
Phe Tyr Asp Ile Cys Ile Ile Asp Thr Pro Pro Ser Leu Gly Gly Leu
 100      105      110
Thr Lys Glu Ala Phe Val Ala Gly Asp Lys Leu Ile Ala Cys Leu Thr
 115      120      125
Pro Glu Pro Phe Ser Ile Leu Gly Leu Gln Lys Ile Arg Glu Phe Leu
 130      135      140
Ser Ser Val Gly Lys Pro Glu Glu Glu His Ile Leu Gly Ile Ala Leu
 145      150      155      160
Ser Phe Trp Asp Asp Arg Asn Ser Thr Asn Gln Met Tyr Ile Asp Ile
      165      170      175
Ile Glu Ser Ile Tyr Lys Asn Lys Leu Phe Ser Thr Lys Ile Arg Arg
 180      185      190
Asp Ile Ser Leu Ser Arg Ser Leu Leu Lys Glu Asp Ser Val Ala Asn
 195      200      205
Val Tyr Pro Asn Ser Arg Ala Ala Glu Asp Ile Leu Lys Leu Thr His
 210      215      220
Glu Ile Ala Asn Ile Leu His Ile Glu Tyr Glu Arg Asp Tyr Ser Gln
 225      230      235      240
Arg Thr Thr

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<210> 588

<211> 527

<212> PRT

<213> C. Trachomatis D serovar

<400> 588

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Met Pro Ser Leu Ser Gln Ser Arg Arg Ile Ile Gln Gln Ser Ser Ile
 1      5      10      15
Arg Lys Ile Trp Asn Gln Ile Asp Thr Ser Pro Lys His Gly Val Cys
 20      25      30
Val Pro Leu Phe Ser Leu Tyr Thr Gln Glu Ser Cys Gly Ile Gly Glu
 35      40      45
Phe Leu Asp Leu Ile Pro Met Ile Asp Trp Cys Ile Ser Cys Gly Phe
 50      55      60
Gln Ile Leu Gln Ile Leu Pro Ile Asn Asp Thr Gly Ser Cys Ser Ser
 65      70      75      80
Pro Tyr Asn Ser Ile Ser Ser Ile Ala Leu Asn Pro Leu His Leu Ser
      85      90      95
Ile Ser Ala Leu Pro Tyr Lys Glu Glu Val Pro Ala Ala Glu Thr Arg
 100      105      110
Ile Arg Glu Met Gln Gln Leu Ser Gln Leu Pro Gln Val His Tyr Glu
 115      120      125
Lys Val Arg Ser Met Lys Arg Asp Phe Phe Gln Glu Tyr Tyr Arg Val
 130      135      140
Cys Lys Gln Lys Lys Leu Thr Asp His Pro Asp Phe Tyr Ala Phe Cys
 145      150      155      160
Glu Gln Glu Lys Tyr Trp Leu His Pro Tyr Ala Leu Phe Arg Ser Ile
      165      170      175
Arg Glu His Leu Asp Asn Leu Pro Ile Asn His Trp Pro Thr Thr Tyr
 180      185      190
Thr Asp Leu Ser Gln Ile Thr Glu His Glu Arg Thr Phe Ala Glu Asp
 195      200      205
Ile Gln Phe His Ser Tyr Leu Gln Tyr Leu Cys Phe Gln Gln Met Thr

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210 215 220
 Gln Val Arg Glu His Ala Asn Cys Lys Ser Cys Leu Ile Lys Gly Asp
 225 230 235 240
 Ile Pro Ile Leu Ile Ser Lys Asp Ser Cys Asp Val Trp Phe Tyr Arg
 245 250 255
 His Tyr Phe Ser Ser Ser Glu Ser Val Gly Ala Pro Pro Asp Leu Tyr
 260 265 270 275
 Asn Ala Glu Gly Gln Asn Trp His Leu Pro Ile Cys Asn Met Lys Thr
 280 285
 Leu Gln Gln Asp Asn Tyr Leu Trp Trp Lys Glu Arg Leu Arg Tyr Ala
 290 295 300 305
 Glu Asn Phe Tyr Ser Leu Tyr Arg Leu Asp His Val Val Gly Leu Phe
 310 315 320
 Arg Phe Trp Val Trp Asp Glu Ser Gly Cys Gly Arg Phe Glu Pro His
 325 330 335
 Asp Pro Lys Asn Tyr Leu Ala Gln Gly Gln Asp Ile Leu Ser His Leu
 340 345 350
 Leu Thr Ser Ser Ser Met Leu Pro Ile Gly Glu Asp Leu Gly Thr Ile
 355 360 365
 Pro Ser Asp Val Lys Arg Met Leu Glu Ser Phe Ala Val Cys Gly Thr
 370 375 380
 Arg Ile Pro Arg Trp Glu Arg Asn Trp Glu Gly Asn Gly Ala Tyr Thr
 385 390 395 400
 Pro Phe Asp Gln Tyr Asp Pro Leu Ser Val Thr Ser Leu Ser Thr His
 405 410 415
 Asp Ser Ser Thr Leu Ala Ser Trp Trp Lys Glu Ser Pro Gln Glu Ser
 420 425 430
 Lys Leu Phe Ala Gln Phe Leu Gly Leu Pro Tyr Ser Ser Thr Leu Ser
 435 440 445
 Leu His Asn His Thr Glu Ile Leu Lys Leu Ser His Lys Thr Ser Ser
 450 455 460
 Ile Phe Arg Ile Asn Leu Ile Asn Asp Tyr Leu Ala Leu Phe Pro Asp
 465 470 475 480
 Leu Ile Ser Lys Thr Pro Arg Tyr Glu Arg Ile Asn Leu Pro Gly Thr
 485 490 495
 Ile Ser Lys Asn Asn Trp Val Tyr Arg Val Lys Pro Ser Ile Glu Asp
 500 505 510
 Leu Ser Ser His Ser Lys Leu Asn Ser Leu Leu Glu Ala Leu Phe
 515 520 525

<210> 589

<211> 146

<212> FRT

<213> C. Trachomatis D serovar

<400> 589

Met Gln Asn Gln Phe Glu Gln Leu Leu Thr Glu Leu Gly Thr Gln Ile
 1 5 10 15
 Asn Ser Pro Leu Thr Pro Asp Ser Asn Asn Ala Cys Ile Val Arg Phe
 20 25 30
 Gly Tyr Asn Asn Val Ala Val Gln Ile Glu Glu Asp Gly Asn Ser Gly
 35 40 45
 Phe Leu Val Ala Gly Val Met Leu Gly Lys Leu Pro Glu Asn Thr Phe
 50 55 60
 Arg Gln Lys Ile Phe Lys Ala Ala Leu Ser Ile Asn Gly Ser Pro Gln
 65 70 75 80
 Ser Asn Ile Lys Gly Thr Leu Gly Tyr Gly Glu Ile Ser Asn Gln Leu
 85 90 95
 Tyr Leu Cys Asp Arg Leu Asn Met Thr Tyr Leu Asn Gly Glu Lys Leu
 100 105 110
 Ala Arg Tyr Leu Val Leu Phe Ser Gln His Ala Asn Ile Trp Met Gln

115
 Ser Ile Ser Lys Gly Ala Leu 120
 130 Pro Asp Leu His Ala 125
 His Leu 140
 145

<210> 590
 <211> 650
 <212> FRT
 <213> C. Trachomatis D serovar

<400> 590
 Met Thr Ile Pro Ile His Glu Asn Lys Tyr Ser Met Ile Ser Phe Thr
 1 5 10 15
 Arg Thr Ile Gly Phe Arg Leu Trp Leu Ile Cys Val Ala Ala Ile Met
 20 25 30
 Phe Pro Leu Gly Ile Asn Ile Leu Gln Leu Asn Leu Gln Tyr Lys
 35 40 45
 Lys Thr Leu Ser Ser Ile Thr Ser Asp Leu Arg Glu Asn Ala Leu Phe
 50 55 60
 Lys Ala His Thr Leu Gln Gln Thr Ile Pro Leu Asn Ile Asp Ile Leu
 65 70 75 80
 Ala Leu Phe Ser Glu Ile Phe Asp Leu Asp Arg Gly Val Pro Ala Glu
 85 90 95
 Pro Asp Leu Ala Leu Ser Lys Glu Met Glu Lys Ile Phe His Ser Thr
 100 105 110
 Tyr Lys Glu Ile Ser Leu Val Lys Lys Glu Ala Asp Gly Asn Phe Arg
 115 120 125
 Val Val Ala Ser Ser Arg Ile Glu Gln Leu Gly Lys Asn Tyr Asn Gln
 130 135 140
 Glu Ile Phe Leu Ser Asp Ser Gln Pro Phe Leu Ala Thr Leu Arg His
 145 150 155 160
 Ser Gly Ser Asp Ser Gln Val Leu Ala Val Leu Gln Thr Asn Ile Phe
 165 170 175
 Asp Ile Ser Ser Gln Glu Val Leu Gly Val Leu Tyr Thr Leu Ser Asp
 180 185 190
 Thr Asn Tyr Leu Leu Asn Gly Leu Leu Ala Ala Lys Asp Pro Leu Ser
 195 200 205
 Val Lys Thr Ala Ile Leu Ser Lys Asn Gly Ile Ile Leu Gln Ala Thr
 210 215 220
 Asp Ser Ser Leu Asp Leu Val Ser Ile His Lys Thr Val Ser Lys Glu
 225 230 235 240
 Gln Phe Cys Asp Val Phe Leu Arg Asp Asp Ile Cys Pro Pro His Leu
 245 250 255
 Leu Leu Arg Pro Pro Leu Asn Leu Asp Pro Leu Pro Tyr Gly Glu Asn
 260 265 270
 Phe Val Ser Phe Cys Ile Gly Asn Thr Glu Met Trp Gly Tyr Ile His
 275 280 285
 Ser Leu Pro Glu Met Asp Phe Arg Ile Leu Thr Tyr Glu Glu Lys Ser
 290 295 300
 Ile Ile Phe Ala Ser Leu Trp Arg Arg Thr Leu Leu Tyr Phe Ala Tyr
 305 310 315 320
 Phe Cys Cys Val Leu Leu Gly Ser Ile Thr Ala Phe Leu Val Ala Lys
 325 330 335
 Arg Leu Ser Lys Pro Ile Arg Lys Leu Ala Thr Ala Met Met Glu Thr
 340 345 350
 Arg Arg Asn Gln His His Pro Tyr Glu Pro Asp Ser Leu Gly Phe Glu
 355 360 365
 Ile Asn His Leu Gly Glu Ile Phe Asn Ser Met Val Gln Ser Leu Leu
 370 375 380
 Gln Gln Gln Ser Leu Ala Glu Lys Asn Phe Glu Ile Lys Gln His Ala

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385          390          395          400
Gln Asn Ala Leu Arg Leu Gly Glu Glu Ala Gln Gln Cys Leu Leu Pro
      405      410      415
Asn Gln Leu Pro Asp Ser Pro Thr Thr Glu Ile Ala Lys Ala Tyr Ile
      420      425      430
Pro Ala Ile Thr Val Gly Gly Asp Phe Phe Asp Ile Phe Val Ile Gly
      435      440      445
Glu Gly Pro Gln Ala Lys Leu Phe Leu Ile Val Ala Asp Ala Ser Gly
      450      455      460
Lys Gly Val Asn Ala Cys Ala Tyr Ser Leu Phe Leu Lys Asn Met Leu
      465      470      475      480
His Thr Phe Leu Ser Glu Leu Ser Ser Ile Gln Glu Ala Val Gln Gln
      485      490      495
Thr Ala Ala Leu Phe Tyr Gln Gln Thr Ala Glu Ser Gly Met Phe Val
      500      505
Thr Leu Cys Ile Tyr Cys Tyr His Tyr Ala Thr Arg Glu Leu Glu Tyr
      515      520      525
Tyr Ser Cys Gly His Asn Pro Ala Cys Leu Arg Ala Pro Asn Gly Asp
      530      535      540
Ile Ser Phe Leu Ser His Pro Gly Met Ala Leu Gly Phe Leu Pro Glu
      545      550      555      560
Val Pro Pro His Pro Ala Tyr Thr Leu Val Leu Glu Glu Glu Ser Leu
      565      570      575
Leu Val Leu Tyr Thr Asp Gly Val Thr Glu Ala Ser Asn Lys His Gly
      580      585      590
Glu Met Phe Gly Glu Glu Arg Leu Lys Ala Leu Val Ala Ser Leu Thr
      595      600      605
Lys Gln Ser Ala Glu Glu Ala Ile Gln Ser Ile Met Phe Ser Ile Lys
      610      615      620
Ser Phe Val Lys Asp Cys Pro Gln His Asp Asp Ile Thr Leu Leu Val
      625      630      635      640
Leu Lys Ile Pro Lys Glu Pro Ser Ala Tyr
      645      650

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<210> 591
<211> 313
<212> PRT
<213> C. Trachomatis D serovar

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<400> 591
Met Leu Ser Tyr Ile Lys Arg Arg Leu Leu Phe Asn Leu Leu Ser Leu
  1          5          10          15
Trp Val Val Val Thr Leu Thr Phe Phe Ile Ile Lys Thr Ile Pro Gly
  20          25          30
Asp Pro Phe Asn Asp Glu Asn Gly Asn Ile Leu Ser Ser Glu Thr Leu
  35          40          45
Ala Leu Leu Lys Asn Arg Tyr Gly Leu Asp Lys Pro Leu Phe Thr Gln
  50          55          60
Tyr Leu Ile Tyr Leu Lys Cys Leu Leu Thr Leu Asp Phe Gly Glu Ser
  65          70          75          80
Leu Ile Tyr Lys Asp Arg Thr Val Ile Ser Ile Ile Ala Ala Leu
  85          90          95
Pro Ser Ser Ala Ile Leu Gly Leu Glu Ser Leu Cys Leu Ser Leu Phe
  100         105         110
Gly Gly Ile Thr Leu Gly Ile Leu Ala Ala Phe Tyr Lys Lys Ser Cys
  115         120         125
Gly Arg Thr Ile Phe Phe Ser Ser Val Ile Gln Ile Ser Val Pro Ala
  130         135         140
Phe Val Ile Gly Ala Phe Leu Gln Tyr Val Phe Ala Ile Lys Tyr Ser
  145         150         155         160
Cys Leu Pro Ile Ala Cys Trp Gly Asn Phe Ser His Thr Leu Leu Pro

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          165          170          175
Ser Ile Ala Leu Ala Ile Thr Pro Met Ala Phe Ile Thr Gln Leu Thr
      180          185          190
Cys Ala Ser Val Ser Ala Asn Leu Lys Lys Asp Tyr Val Leu Leu Ala
      195          200          205
Tyr Ala Lys Gly Leu Ser Pro Phe Lys Val Leu Ile Lys His Ile Leu
      210          215          220
Pro Tyr Ala Leu Phe Pro Val Ile Ser Tyr Ser Ala Phe Leu Ile Thr
      225          230          235          240
Thr Leu Met Thr Gly Thr Phe Ser Ile Glu Asn Leu Phe Cys Ile Pro
      245          250          255
Gly Leu Gly Lys Trp Phe Ile Cys Ser Ile Lys Gln Arg Asp Tyr Pro
      260          265          270
Ile Thr Leu Gly Leu Ser Val Phe Tyr Gly Ala Phe Phe Met Leu Thr
      275          280          285
Ser Leu Cys Cys Asp Leu Leu Gln Ala Trp Ile Asp Pro Gln Ile Arg
      290          295          300
Tyr Ser Tyr Gly Lys Glu Arg Ser Lys
      305          310

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<210> 592

<211> 1237

<212> PRT

<213> C. Trachomatis D serovar

<400> 592

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Met Thr Trp Ile Pro Leu His Cys His Ser Gln Tyr Ser Ile Leu Asp
  1          5          10          15
Ala Thr Cys Ser Ile Lys Lys Phe Val Ala Lys Ala Val Glu Tyr Gln
      20          25          30
Ile Pro Ala Leu Ala Leu Thr Asp His Gly Asn Leu Phe Gly Ala Val
      35          40          45
Glu Phe Tyr Lys Thr Cys Lys Gln Asn Ala Ile Lys Pro Ile Ile Gly
      50          55          60
Cys Glu Leu Tyr Val Ala Pro Ser Ser Arg Phe Asp Lys Lys Lys Glu
      65          70          75          80
Arg Lys Ser Arg Val Ala Asn His Leu Ile Leu Leu Cys Lys Asp Glu
      85          90          95
Glu Gly Tyr Arg Asn Leu Cys Leu Leu Ser Ser Leu Ala Tyr Thr Glu
      100          105          110
Gly Phe Tyr Tyr Val Pro Arg Ile Asp Arg Asp Leu Leu Ser Gln His
      115          120          125
Ser Lys Gly Leu Ile Cys Leu Ser Ala Cys Leu Ser Gly Ser Val Ala
      130          135          140
Gln Ala Ala Leu Glu Ser Glu Glu Asp Leu Glu Lys Asp Leu Leu Trp
      145          150          155          160
Tyr Gln Asp Leu Phe Gln Glu Asp Phe Phe Ser Glu Val Gln Leu His
      165          170          175
Lys Ser Ser Glu Glu Lys Val Ala Leu Phe Glu Glu Thr Trp Leu Lys
      180          185          190
Gln Asn Tyr Tyr Gln Phe Ile Glu Lys Gln Leu Lys Val Asn Glu Ala
      195          200          205
Val Leu Ala Thr Ser Lys Arg Leu Gly Ile Pro Ser Val Ala Thr Asn
      210          215          220
Asp Ile His Tyr Leu Asn Pro Asp Asp Trp Leu Ala His Glu Ile Leu
      225          230          235          240
Leu Asn Val Gln Ser Arg Glu Pro Ile Arg Thr Ala Lys Gln Asn Thr
      245          250          255
Tyr Ile Pro Asn Pro Lys Arg Lys Thr Tyr Pro Ser Arg Glu Phe Tyr
      260          265          270
Phe Lys Ser Pro Gln Glu Ile Ala Glu Leu Phe Ala Ala His Pro Glu

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[illegible]

Ala Ala Ala Asn Gly Ile Asp Pro Ser Ile Ala Thr Thr Ile Phe Asp
 770 775 780
 Lys Met Glu Lys Phe Ala Ser Tyr Gly Phe Asn Lys Ser His Ala Ala
 785 790 795 800
 Ala Tyr Gly Leu Ile Thr Tyr Thr Thr Ala Tyr Leu Lys Ala Leu Tyr
 805 810 815
 Pro Lys Glu Trp Leu Ala Ala Leu Leu Thr Cys Asp Tyr Asp Asp Ile
 820 825 830
 Glu Lys Val Gly Lys Leu Ile Gln Glu Ala His Ser Met Asn Ile Leu
 835 840 845
 Val Leu Pro Pro Asp Ile Asn Glu Ser Gly Gln Asp Phe Glu Ala Thr
 850 855 860
 Gln Lys Gly Ile Arg Phe Ser Leu Gly Ala Val Lys Gly Val Gly Met
 865 870 875 880
 Ser Ile Val Asp Ser Ile Val Glu Glu Arg Glu Lys Asn Gly Pro Tyr
 885 890 895
 Lys Ser Leu Gln Asp Phe Val Gln Arg Ala Asp Phe Lys Lys Val Thr
 900 905 910
 Lys Lys Gln Leu Glu Asn Leu Val Asp Ala Gly Thr Phe Asp Cys Phe
 915 920 925
 Glu Pro Asn Lys Asp Leu Ala Leu Ala Ile Leu Asn Asp Leu Tyr Asp
 930 935 940
 Thr Phe Ser Arg Glu Lys Lys Glu Ala Ala Thr Gly Val Leu Thr Phe
 945 950 955 960
 Phe Ser Leu Asp Ser Met Ala Arg Asp Pro Val Lys Ile Thr Val Ser
 965 970 975
 Pro Glu Asn Val Ile Gln Arg Ser Pro Lys Glu Leu Leu Lys Arg Glu
 980 985 990
 Lys Glu Leu Leu Gly Val Tyr Leu Thr Ala His Pro Met Asp Ala Val
 995 1000 1005
 Glu His Met Leu Pro Phe Leu Ser Val Val Pro Ala Arg Asp Phe Glu
 1010 1015 1020
 Gly Leu Pro His Gly Thr Ile Ile Arg Thr Val Phe Leu Ile Asp Lys
 1025 1030 1035 1040
 Val Thr Thr Lys Ile Ser Ser Ala Glu Gln Lys Lys Phe Ala Leu Leu
 1045 1050 1055
 Gln Val Ser Asp Glu Val Asp Ser Tyr Glu Leu Pro Ile Trp Ala Asp
 1060 1065 1070
 Met Tyr Ala Glu Tyr Arg Asp Leu Leu Glu Glu Asp Arg Leu Ile Tyr
 1075 1080 1085
 Ala Ile Leu Ala Ile Asp Arg Arg Ser Asp Ser Leu Arg Leu Ser Cys
 1090 1095 1100
 Arg Trp Met Arg Asp Leu Ser Thr Val Asn Asp Ser Val Ile Ala Glu
 1105 1110 1115 1120
 Cys Asp Glu Val Tyr Asp Arg Leu Lys Ser Gln Lys Val Tyr Ser Ser
 1125 1130 1135
 Thr Lys Lys Ser Thr Gly Ala Gln Ser Ser Ala Met Ile Lys Lys Val
 1140 1145 1150
 Glu Thr Arg Glu Ile Ser Pro Val Thr Ile Ser Leu Asp Leu Asn Lys
 1155 1160 1165
 Leu Arg His Ser His Leu Phe Ile Leu Lys Gly Leu Ile Arg Lys Tyr
 1170 1175 1180
 Ser Gly Ser Gln Ala Leu Ser Leu Val Phe Thr Lys Asp Asn Gln Arg
 1185 1190 1195 1200
 Phe Ala Ser Ile Ser Pro Asp Ala Asp Phe Phe Val Thr Asp Asp Ile
 1205 1210 1215
 Ser Ser Leu Leu Gln Glu Ile Glu Ala Thr Asn Ile Pro Ala Arg Val
 1220 1225 1230
 Leu Ala Thr Thr Val
 1235

<210> 593

<211> 563

<212> PRT

<213> C. Trachomatis D serovar

<400> 593

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Met Val Tyr Phe Arg Ala His Gln Pro Arg His Thr Pro Lys Thr Phe
1      5      10
Pro Leu Glu Val His His Ser Phe Ser Asp Lys His Pro Gln Ile Ala
20      25
Lys Ala Met Arg Ile Thr Gly Ile Ala Leu Ala Ala Leu Ser Leu Leu
35      40      45
Ala Val Val Ala Cys Val Ile Ala Val Ser Ala Gly Gly Ala Ala Ile
50      55      60
Pro Leu Ala Val Ile Ser Gly Ile Ala Val Met Ser Gly Leu Leu Ser
65      70      75
Ala Ala Thr Ile Ile Cys Ser Ala Lys Lys Ala Leu Ala Gln Arg Lys
85      90      95
Gln Lys Gln Leu Glu Glu Ser Leu Pro Leu Asp Asn Ala Thr Glu His
100     105     110
Val Ser Tyr Leu Thr Ser Asp Thr Ser Tyr Phe Asn Gln Trp Glu Ser
115     120     125
Leu Gly Ala Leu Asn Lys Gln Leu Ser Gln Ile Asp Leu Thr Ile Gln
130     135     140
Ala Pro Glu Lys Lys Leu Leu Lys Glu Val Leu Gly Ser Arg Tyr Asp
145     150     155
Ser Ile Asn His Ser Ile Glu Glu Ile Ser Asp Arg Phe Thr Lys Met
165     170     175
Leu Ser Leu Leu Arg Leu Arg Glu His Phe Tyr Arg Gly Glu Glu Arg
180     185     190
Tyr Ala Pro Tyr Leu Ser Pro Pro Leu Leu Asn Lys Asn Arg Leu Leu
195     200     205
Thr Gln Ile Thr Ser Asn Met Ile Arg Met Leu Pro Lys Ser Gly Gly
210     215     220
Val Phe Ser Leu Lys Ala Asn Thr Leu Ser His Ala Ser Arg Thr Leu
225     230     235
Tyr Thr Val Leu Lys Val Ala Leu Ser Leu Gly Val Leu Ala Gly Val
245     250     255
Ala Ala Leu Ile Ile Phe Leu Pro Pro Ser Leu Pro Phe Ile Ala Val
260     265     270
Ile Gly Val Ser Ser Leu Ala Leu Gly Met Ala Ser Phe Leu Met Ile
275     280     285
Arg Gly Ile Lys Tyr Leu Leu Glu His Ser Pro Leu Asn Arg Lys Gln
290     295     300
Leu Ala Lys Asp Ile Gln Lys Thr Ile Gly Pro Asp Val Leu Ala Ser
305     310     315
Met Val His Tyr Gln His Gln Leu Leu Ser His Leu His Glu Thr Leu
325     330     335
Leu Asp Glu Ala Ile Thr Ala Arg Trp Ser Glu Pro Phe Ile Glu
340     345     350
His Ala Asn Leu Lys Ala Lys Ile Glu Asp Leu Thr Lys Gln Tyr Asp
355     360     365
Ile Leu Asn Ala Ala Phe Asn Lys Ser Leu Gln Gln Asp Glu Ala Leu
370     375     380
Arg Ser Gln Leu Glu Lys Arg Ala Tyr Leu Phe Pro Ile Pro Asn Asn
385     390     395
Asp Glu Asn Ala Lys Thr Lys Glu Ser Gln Leu Leu Asp Ser Glu Asn
405     410     415
Asp Ser Asn Ser Glu Phe Gln Glu Ile Ile Asn Lys Gly Leu Glu Ala
420     425     430
Ala Asn Lys Arg Arg Ala Asp Ala Lys Ser Lys Phe Tyr Thr Glu Asp

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      435      440      445
Glu Thr Ser Asp Lys Ile Phe Ser Ile Trp Lys Pro Thr Lys Asn Leu
450      455      460
Ala Leu Glu Asp Leu Trp Arg Val His Glu Ala Cys Asn Glu Glu Gln
465      470      475
Gln Ala Leu Leu Glu Asp Tyr Met Ser Tyr Lys Thr Ser Glu Cys
      485      490      495
Gln Ala Ala Leu Gln Lys Val Ser Gln Glu Leu Lys Ala Ala Gln Lys
      500      505      510
Ser Phe Ala Val Leu Glu Lys His Ala Leu Asp Arg Ser Tyr Glu Ser
      515      520      525
Ser Val Ala Thr Met Asp Leu Ala Arg Ala Asn Gln Glu Thr His Arg
      530      535      540
Leu Leu Asn Ile Leu Ser Glu Leu Gln Gln Leu Ala Gln Tyr Leu Leu
545      550      555      560
Asp Asn His

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<210> 594
<211> 1751
<212> PRT
<213> C. Trachomatis D serovar

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<400> 594
Met Lys Trp Leu Ser Ala Thr Ala Val Phe Ala Ala Val Leu Pro Ser
1      5      10      15
Val Ser Gly Phe Cys Phe Pro Glu Pro Lys Glu Leu Asn Phe Ser Arg
      20      25      30
Val Gly Thr Ser Ser Thr Thr Phe Thr Glu Thr Val Gly Glu Ala
      35      40      45
Gly Ala Glu Tyr Ile Val Ser Gly Asn Ala Ser Phe Thr Lys Phe Thr
      50      55      60
Asn Ile Pro Thr Thr Asp Thr Thr Pro Thr Asn Ser Asn Ser Ser
      65      70      75      80
Ser Ser Asn Gly Glu Thr Ala Ser Val Ser Glu Asp Ser Asp Ser Thr
      85      90      95
Thr Thr Thr Pro Asp Pro Lys Gly Gly Gly Ala Phe Tyr Asn Ala His
      100      105      110
Ser Gly Val Leu Ser Phe Met Thr Arg Ser Gly Thr Glu Gly Ser Leu
      115      120      125
Thr Leu Ser Glu Ile Lys Ile Thr Gly Glu Gly Glu Ala Ile Phe Ser
      130      135      140
Gln Gly Glu Leu Leu Phe Thr Asp Leu Thr Gly Leu Thr Ile Gln Asn
      145      150      155      160
Asn Leu Ser Gln Leu Ser Gly Gly Ala Ile Phe Gly Glu Ser Thr Ile
      165      170      175
Ser Leu Ser Gly Ile Thr Lys Ala Thr Phe Ser Ser Asn Ser Ala Glu
      180      185      190
Val Pro Ala Pro Val Lys Lys Pro Thr Glu Pro Lys Ala Gln Thr Ala
      195      200      205
Ser Glu Thr Ser Gly Ser Ser Ser Ser Gly Asn Asp Ser Val Ser
      210      215      220
Ser Pro Ser Ser Ser Arg Ala Glu Pro Ala Ala Ala Asn Leu Gln Ser
      225      230      235      240
His Phe Ile Cys Ala Thr Ala Thr Pro Ala Ala Gln Thr Asp Thr Glu
      245      250      255
Thr Ser Thr Pro Ser His Lys Pro Gly Ser Gly Gly Ala Ile Tyr Ala
      260      265      270
Lys Gly Asp Leu Thr Ile Ala Asp Ser Gln Glu Val Leu Phe Ser Ile
      275      280      285
Asn Lys Ala Thr Lys Asp Gly Gly Ala Ile Phe Ala Glu Lys Asp Val

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290 295 300
 Ser Phe Glu Asn Ile Thr Ser Leu Lys Val Gln Thr Asn Gly Ala Glu
 305 310 315 320
 Glu Lys Gly Gly Ile Tyr Ala Lys Gly Asp Leu Ser Ile Gln Ser
 325 330 335
 Ser Lys Gln Ser Leu Phe Asn Ser Asn Tyr Ser Lys Gln Gly Gly
 340 345 350
 Ala Leu Tyr Val Glu Gly Asp Ile Asn Phe Gln Asp Leu Glu Glu Ile
 355 360 365
 Arg Ile Lys Tyr Asn Lys Ala Gly Thr Phe Glu Thr Lys Lys Ile Thr
 370 375 380
 Leu Pro Lys Ala Gln Ala Ser Ala Gly Asn Ala Asp Ala Trp Ala Ser
 385 390 395 400
 Ser Ser Pro Gln Ser Gly Ser Gly Ala Thr Thr Val Ser Asn Ser Gly
 405 410 415
 Asp Ser Ser Ser Gly Ser Asp Ser Asp Thr Ser Glu Thr Val Pro Ala
 420 425 430
 Thr Ala Lys Gly Gly Gly Leu Tyr Thr Asp Lys Asn Leu Ser Ile Thr
 435 440 445
 Asn Ile Thr Gly Ile Ile Glu Ile Ala Asn Asn Lys Ala Thr Asp Val
 450 455 460
 Gly Gly Gly Ala Tyr Val Lys Gly Thr Leu Thr Cys Glu Asn Ser His
 465 470 475 480
 Arg Leu Gln Phe Leu Lys Asn Ser Ser Asp Lys Gln Gly Gly Gly Ile
 485 490 495
 Tyr Gly Glu Asp Asn Ile Thr Leu Ser Asn Leu Thr Gly Lys Thr Leu
 500 505 510
 Phe Gln Glu Asn Thr Ala Lys Glu Glu Gly Gly Leu Phe Ile Lys
 515 520 525
 Gly Thr Asp Lys Ala Leu Thr Met Thr Gly Leu Asp Ser Phe Cys Leu
 530 535 540
 Ile Asn Asn Thr Ser Glu Lys His Gly Gly Gly Ala Phe Val Thr Lys
 545 550 555 560
 Glu Ile Ser Gln Thr Tyr Thr Ser Asp Val Glu Thr Ile Pro Gly Ile
 565 570 575
 Thr Pro Val His Gly Glu Thr Val Ile Thr Gly Asn Lys Ser Thr Gly
 580 585 590
 Gly Asn Gly Gly Gly Val Cys Thr Lys Arg Leu Ala Leu Ser Asn Leu
 595 600 605
 Gln Ser Ile Ser Ile Ser Gly Asn Ser Ala Ala Glu Asn Gly Gly Gly
 610 615 620
 Ala His Thr Cys Pro Asp Ser Phe Pro Thr Ala Asp Thr Ala Glu Gln
 625 630 635 640
 Pro Ala Ala Ala Ser Ala Ala Thr Ser Thr Pro Glu Ser Ala Pro Val
 645 650 655
 Val Ser Thr Ala Leu Ser Thr Pro Ser Ser Ser Thr Val Ser Ser Leu
 660 665 670
 Thr Leu Leu Ala Ala Ser Ser Gln Ala Ser Pro Ala Thr Ser Asn Lys
 675 680 685
 Glu Thr Gln Asp Pro Asn Ala Asp Thr Asp Leu Leu Ile Asp Tyr Val
 690 695 700
 Val Asp Thr Thr Ile Ser Lys Asn Thr Ala Lys Lys Gly Gly Gly Ile
 705 710 715 720
 Tyr Ala Lys Lys Ala Lys Met Ser Arg Ile Asp Gln Leu Asn Ile Ser
 725 730 735
 Glu Asn Ser Ala Thr Glu Ile Gly Gly Gly Ile Cys Cys Lys Gly Ser
 740 745 750
 Leu Glu Leu Asp Ala Leu Val Ser Leu Ser Val Thr Glu Asn Leu Val
 755 760 765
 Gly Lys Glu Gly Gly Gly Leu His Ala Lys Thr Val Asn Ile Ser Asn
 770 775 780

Leu Lys Ser Gly Phe Ser Phe Ser Asn Asn Lys Ala Asn Ser Ser Ser
 785 790 795 800
 Thr Gly Val Ala Thr Thr Ala Ser Ala Pro Ala Ala Ala Ala Ala Ser
 805 810 815
 Leu Gln Ala Ala Ala Ala Val Pro Ser Ser Pro Ala Thr Pro Thr
 820 825 830
 Tyr Ser Gly Val Val Gly Gly Ala Ile Tyr Gly Glu Lys Val Thr Phe
 835 840 845
 Ser Gln Cys Ser Gly Thr Cys Gln Phe Ser Gly Asn Gln Ala Ile Asp
 850 855 860
 Asn Asn Pro Ser Gln Ser Ser Leu Asn Val Gln Gly Gly Ala Ile Tyr
 865 870 875
 Ala Lys Thr Ser Leu Ser Ile Gly Ser Ser Asp Ala Gly Thr Ser Tyr
 885 890 895
 Ile Phe Ser Gly Asn Ser Val Ser Thr Gly Lys Ser Gln Thr Thr Gly
 900 905 910
 Gln Ile Ala Gly Gly Ala Ile Tyr Ser Pro Thr Val Thr Leu Asn Cys
 915 920 925
 Pro Ala Thr Phe Ser Asn Asn Thr Ala Ser Met Ala Thr Pro Lys Thr
 930 935 940
 Ser Ser Glu Asp Gly Ser Ser Gly Asn Ser Ile Lys Asp Thr Ile Gly
 945 950 955 960
 Gly Ala Ile Ala Gly Thr Ala Ile Thr Leu Ser Gly Val Ser Arg Phe
 965 970 975
 Ser Gly Asn Thr Ala Asp Leu Gly Ala Ala Ile Gly Thr Leu Ala Asn
 980 985 990
 Ala Asn Thr Pro Ser Ala Thr Ser Gly Ser Gln Asn Ser Ile Thr Glu
 995 1000 1005
 Lys Ile Thr Leu Glu Asn Gly Ser Phe Ile Phe Glu Arg Asn Gln Ala
 1010 1015 1020
 Asn Lys Arg Gly Ala Ile Tyr Ser Pro Ser Val Ser Ile Lys Gly Asn
 1025 1030 1035 1040
 Asn Ile Thr Phe Asn Gln Asn Thr Ser Thr His Asp Gly Ser Ala Ile
 1045 1050 1055
 Tyr Phe Thr Lys Asp Ala Thr Ile Glu Ser Leu Gly Ser Val Leu Phe
 1060 1065 1070
 Thr Gly Asn Asn Val Thr Ala Thr Gln Ala Ser Ser Ala Thr Ser Gly
 1075 1080 1085
 Gln Asn Thr Asn Thr Ala Asn Tyr Gly Ala Ala Ile Phe Gly Asp Pro
 1090 1095 1100
 Gly Thr Thr Gln Ser Ser Gln Thr Asp Ala Ile Leu Thr Leu Leu Ala
 1105 1110 1115 1120
 Ser Ser Gly Asn Ile Thr Phe Ser Asn Asn Ser Leu Gln Asn Asn Gln
 1125 1130 1135
 Gly Asp Thr Pro Ala Ser Lys Phe Cys Ser Ile Ala Gly Tyr Val Lys
 1140 1145 1150
 Leu Ser Leu Gln Ala Ala Lys Gly Lys Thr Ile Ser Phe Phe Asn Cys
 1155 1160 1165
 Val His Thr Ser Thr Lys Lys Ile Gly Ser Thr Gln Asn Val Tyr Glu
 1170 1175 1180
 Thr Leu Asp Ile Asn Lys Glu Glu Asn Ser Asn Pro Tyr Thr Gly Thr
 1185 1190 1195 1200
 Ile Val Phe Ser Ser Glu Leu His Glu Asn Lys Ser Tyr Ile Pro Gln
 1205 1210 1215
 Asn Ala Ile Leu His Asn Gly Thr Leu Val Leu Lys Glu Lys Thr Glu
 1220 1225 1230
 Leu His Val Val Ser Phe Glu Gln Lys Glu Gly Ser Lys Leu Ile Met
 1235 1240 1245
 Lys Pro Gly Ala Val Leu Ser Asn Gln Asn Ile Ala Asn Gly Ala Leu
 1250 1255 1260
 Val Ile Asn Gly Leu Thr Ile Asp Leu Ser Ser Met Gly Thr Pro Gln

1265 1270 1275 1280
 Ala Gly Glu Ile Phe Ser Pro Pro Glu Leu Arg Ile Val Ala Thr Thr
 1285 1290 1295
 Ser Ser Ala Ser Gly Gly Ser Gly Val Ser Ser Ser Ile Pro Thr Asn
 1300 1305 1310
 Pro Lys Arg Ile Ser Ala Ala Ala Pro Ser Gly Ser Ala Ala Thr Thr
 1315 1320 1325
 Pro Thr Met Ser Glu Asn Lys Val Phe Leu Thr Gly Asp Leu Thr Leu
 1330 1335 1340
 Ile Asp Pro Asn Gly Asn Phe Tyr Gln Asn Pro Met Leu Gly Ser Asp
 1345 1350 1355 1360
 Leu Asp Val Pro Leu Ile Lys Leu Pro Thr Asn Thr Ser Asp Val Gln
 1365 1370 1375
 Val Tyr Asp Leu Thr Leu Ser Gly Asp Leu Phe Pro Gln Lys Gly Tyr
 1380 1385 1390
 Met Gly Thr Trp Thr Leu Asp Ser Asn Pro Gln Thr Gly Lys Leu Gln
 1395 1400 1405
 Ala Arg Trp Thr Phe Asp Thr Tyr Arg Arg Trp Val Tyr Ile Pro Arg
 1410 1415 1420
 Asp Asn His Phe Tyr Ala Asn Ser Ile Leu Gly Ser Gln Asn Ser Met
 1425 1430 1435 1440
 Ile Val Val Lys Gln Gly Leu Ile Asn Asn Met Leu Asn Asn Ala Arg
 1445 1450 1455
 Phe Asp Asp Ile Ala Tyr Asn Asn Phe Trp Val Ser Gly Val Gly Thr
 1460 1465 1470
 Phe Leu Ala Gln Gln Gly Thr Pro Leu Ser Glu Glu Phe Ser Tyr Tyr
 1475 1480 1485
 Ser Arg Gly Thr Ser Val Ala Ile Asp Ala Lys Pro Arg Gln Asp Phe
 1490 1495 1500
 Ile Leu Gly Ala Ala Phe Ser Lys Met Val Gly Lys Thr Lys Ala Ile
 1505 1510 1515 1520
 Lys Lys Met His Asn Tyr Phe His Lys Gly Ser Glu Tyr Ser Tyr Gln
 1525 1530 1535
 Ala Ser Val Tyr Gly Gly Lys Phe Leu Tyr Phe Leu Leu Asn Lys Gln
 1540 1545 1550
 His Gly Trp Ala Leu Pro Phe Leu Ile Gln Gly Val Val Ser Tyr Gly
 1555 1560 1565
 His Ile Lys His Asp Thr Thr Thr Leu Tyr Pro Ser Ile His Glu Arg
 1570 1575 1580
 Asn Lys Gly Asp Trp Glu Asp Leu Gly Trp Leu Ala Asp Leu Arg Ile
 1585 1590 1595 1600
 Ser Met Asp Leu Lys Glu Pro Ser Lys Asp Ser Ser Lys Arg Ile Thr
 1605 1610 1615
 Val Tyr Gly Glu Leu Glu Tyr Ser Ser Ile Arg Gln Lys Gln Phe Thr
 1620 1625 1630
 Glu Ile Asp Tyr Asp Pro Arg His Phe Asp Asp Cys Ala Tyr Arg Asn
 1635 1640 1645
 Leu Ser Leu Pro Val Gly Cys Ala Val Glu Gly Ala Ile Met Asn Cys
 1650 1655 1660
 Asn Ile Leu Met Tyr Asn Lys Leu Ala Leu Ala Tyr Met Pro Ser Ile
 1665 1670 1675 1680
 Tyr Arg Asn Asn Pro Val Cys Lys Tyr Arg Val Leu Ser Ser Asn Glu
 1685 1690 1695
 Ala Gly Gln Val Ile Cys Gly Val Pro Thr Arg Thr Ser Ala Arg Ala
 1700 1705 1710
 Glu Tyr Ser Thr Gln Leu Tyr Leu Gly Pro Phe Trp Thr Leu Tyr Gly
 1715 1720 1725
 Asn Tyr Thr Ile Asp Val Gly Met Tyr Thr Leu Ser Gln Met Thr Ser
 1730 1735 1740
 Cys Gly Ala Arg Met Ile Phe
 1745 1750

<210> 595
 <211> 900
 <212> DNA
 <213> *Chlamydia pneumoniae*

<400> 595
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 ggatatggct ggggtattgc taaactctct gcagaaagc gagctacgat tattgttagga 120
 acatgggtac cgatttcaaa aattttctct cagctctggg aattaggaaa attcaaatgaa 180
 tctagaaatg tctcgaatgg cactctctta gagattgcta agatctatcc catggagcga 240
 agttttgata gccctgaaga tgttctcgaa gatattgctg aaaaataaac ttacaaagggc 300
 attacgggat tcacgatatc agaagtcgca gaacaggtaa aaaaagattt tgggtcatatt 360
 gacattcttg tccactcgct ggcaaatagt cctgaaattt ctaagctctct attagaaca 420
 tcaagaaaaa gttacttagc ggctctcagt gcctctagtt attcttttgg tagcctcttc 480
 tctcactttg gaagtatcat gaaccggtgg ggatcgacaa tatcgctcac ctatttggct 540
 tctatgcgag ctgttctctg atacggaggg ggcatgagtt cggcaaaaag agctttggaa 600
 agtgacacca aaactcttgc ttgggaagcg ggacgcggtt ggggcatatc tgtcaatacc 660
 tctctgagag cagccttagc aagccgagct ggaaaagcaa ttggttttat tgaagaagt 720
 gtacactatt accaagagtg ggcgcctatt cccgagcgta tgaatgccga gcaggtgggt 780
 gccgttcgag ctttcttagc atcactctta gcttcagcaa ttactgtgga gcacttatac 840
 gtatgatacag gagccaatgt gatgggaatt ggtcctgaga tgttccctaa agactcataa 900

<210> 596
 <211> 1743
 <212> DNA
 <213> *Chlamydia pneumoniae*

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 ctccagagaag agcttgcgga atttaagat ttgctttata oggcaacag aattactctg 120
 agcgagaagc aatctgtata cgaataacag cctggcgcca tctcaaaagg tacctagtct 180
 gatatttaata aagactttgt cgtagttgat ttgtgtctga agtctgagg agaatgctat 240
 atgtcagagt tcatagactc ttccagaagg tttagtgctt gagctgaagt agaatgctat 300
 ctccagcaag ccgaagcaga agagggcaaa gttgtctctt ctgagagaaa agccacaaga 360
 caacgtcaat ggggaatcat cttagctcat ttgtgaagaag gtctctattgt taaggtgcaa 420
 attacacgta aagtcaaaag cggccttatt gtatgatatt gaatggaagt cttcctactct 480
 ggatcacaaa ttgacaacaa gaaaatcaaa aattttagat attatgtcgg aagaaatttgt 540
 gaattcaaaa ttttaaaaaa taacgttgaa cgttgcgaata ttgtttgtct aagaagagaa 600
 ctcttagaag ctgagagaat ctctaaagaa gccgaactta ttgaaacaaa ttctctcggg 660
 gaataccgca aaggagttgt taaaaacatt actgactttt gtgtattctt agatctcgat 720
 ggtattgacg gcttctccca cattaccgat atgacctgga agcgcatacg acatcctctc 780
 gaaatgggtg aatttgaata agagtggaa gtaatttttt taagcgtaga taaagaaaaa 840
 ggacgagttg ccttaggtct caaacaaaaa gagcataatc ctggggaaga tattgagaag 900
 aaaaatctct ctggaaaacg agttcttggg aaaaatttga agcttctccc ctaccgggct 960
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 aacttaacca attacgggtc ttctgttgaa ttgaaacag gaattggagg ttgatctaat 1260
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 gggattgaag gattgattca cgttccagaa ctttctgaca agccctttgc aaaaattgaa 1560
 gatattatct ccaattggaga aatgtttctt gcaaaaagta ttaagctgat tccagatgat 1620
 aaaaagttt ctctttctgt aaaaagaata ttagctgaca atgcttatga tcaagactct 1680
 aggactgaat tagatttcaa gatttctcaa gccctaaag agagaaagaa aaaaagaaaa 1740
 tag 1743

290

<210> 598
<211> 580
<212> PRT
<213> Chlamydia pneumoniae

<400> 598

Met Pro Lys Gln Ala Glu Tyr Thr Trp Gly Ser Lys Lys Ile Leu Asp
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Asn Ile Glu Cys Leu Thr Glu Asp Val Ala Glu Phe Lys Asp Leu Leu
20 25 30

Tyr Thr Ala His Arg Ile Thr Ser Ser Glu Glu Glu Ser Asp Asn Glu
35 40 45

Ile Gln Pro Gly Ala Ile Leu Lys Gly Thr Val Val Asp Ile Asn Lys
50 55 60

Asp Phe Val Val Val Asp Val Gly Leu Lys Ser Glu Gly Val Ile Pro
65 70 75 80

Met Ser Glu Phe Ile Asp Ser Ser Glu Gly Leu Val Leu Gly Ala Glu
85 90 95

Val Glu Val Tyr Leu Asp Gln Ala Glu Asp Glu Glu Gly Lys Val Val
100 105 110

Leu Ser Arg Glu Lys Ala Thr Arg Gln Arg Gln Trp Glu Tyr Ile Leu
115 120 125

Ala His Cys Glu Glu Gly Ser Ile Val Lys Gly Gln Ile Thr Arg Lys
130 135 140

Val Lys Gly Gly Leu Ile Val Asp Ile Gly Met Glu Ala Phe Leu Pro
145 150 155 160

Gly Ser Gln Ile Asp Asn Lys Lys Ile Lys Asn Leu Asp Asp Tyr Val
165 170 175

Gly Lys Val Cys Glu Phe Lys Ile Leu Lys Ile Asn Val Glu Arg Arg
180 185 190

Asn Ile Val Val Ser Arg Arg Glu Leu Leu Glu Ala Glu Arg Ile Ser
195 200 205

Lys Lys Ala Glu Leu Ile Glu Gln Ile Ser Ile Gly Glu Tyr Arg Lys
210 215 220

Gly Val Val Lys Asn Ile Thr Asp Phe Gly Val Phe Leu Asp Leu Asp
225 230 235 240

Gly Ile Asp Gly Leu Leu His Ile Thr Asp Met Thr Trp Lys Arg Ile
245 250 255

Arg His Pro Ser Glu Met Val Glu Leu Asn Gln Glu Leu Glu Val Ile
260 265 270

Ile Leu Ser Val Asp Lys Glu Lys Gly Arg Val Ala Leu Gly Leu Lys
275 280 285

295

Gln Lys Glu His Asn Pro Trp Glu Asp Ile Glu Lys Lys Tyr Pro Pro
 290 295 300
 Gly Lys Arg Val Leu Gly Lys Ile Val Lys Leu Leu Pro Tyr Gly Ala
 305 310 315 320
 Phe Ile Glu Ile Glu Glu Gly Ile Glu Gly Leu Ile His Ile Ser Glu
 325 330 335
 Met Ser Trp Val Lys Asn Ile Val Asp Pro Ser Glu Val Val Asn Lys
 340 345 350
 Gly Asp Glu Val Glu Ala Ile Val Leu Ser Ile Gln Lys Asp Glu Gly
 355 360 365
 Lys Ile Ser Leu Gly Leu Lys Gln Thr Glu Arg Asn Pro Trp Asp Asn
 370 375 380
 Ile Glu Glu Lys Tyr Pro Ile Gly Leu His Val Asn Ala Glu Ile Lys
 385 390 395 400
 Asn Leu Thr Asn Tyr Gly Ala Phe Val Glu Leu Glu Pro Gly Ile Glu
 405 410 415
 Gly Leu Ile His Ile Ser Asp Met Ser Trp Ile Lys Lys Val Ser His
 420 425 430
 Pro Ser Glu Leu Phe Lys Lys Gly Asn Ser Val Glu Ala Val Ile Leu
 435 440 445
 Ser Val Asp Lys Glu Ser Lys Lys Ile Thr Leu Gly Val Lys Gln Leu
 450 455 460
 Ser Ser Asn Pro Trp Asn Glu Ile Glu Ala Met Phe Pro Ala Gly Thr
 465 470 475 480
 Val Ile Ser Gly Val Val Thr Lys Ile Thr Ala Phe Gly Ala Phe Val
 485 490 495
 Glu Leu Gln Asn Gly Ile Glu Gly Leu Ile His Val Ser Glu Leu Ser
 500 505 510
 Asp Lys Pro Phe Ala Lys Ile Glu Asp Ile Ile Ser Ile Gly Glu Asn
 515 520 525
 Val Ser Ala Lys Val Ile Lys Leu Asp Pro Asp His Lys Lys Val Ser
 530 535 540
 Leu Ser Val Lys Glu Tyr Leu Ala Asp Asn Ala Tyr Asp Gln Asp Ser
 545 550 555 560
 Arg Thr Glu Leu Asp Phe Lys Asp Ser Gln Gly Pro Lys Glu Arg Lys
 565 570 575
 Lys Lys Gly Lys
 580

<210> 599

<211> 358

<212> PRT

<213> Chlamydia trachomatis serovar D

<400> 599

Met Arg Lys Thr Val Ile Val Ala Met Ser Gly Gly Val Asp Ser Ser
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Val Val Ala Tyr Leu Leu Lys Lys Gln Gly Glu Tyr Asn Val Val Gly
 20 25 30

Leu Phe Met Lys Asn Trp Gly Glu Gln Asp Glu Asn Gly Glu Cys Thr
 35 40 45

Ala Thr Lys Asp Phe Arg Asp Val Glu Arg Ile Ala Glu Gln Leu Ser
 50 55 60

Ile Pro Tyr Tyr Thr Val Ser Phe Ser Lys Glu Tyr Lys Glu Arg Val
 65 70 75 80

Phe Ser Arg Phe Leu Arg Glu Tyr Ala Asn Gly Tyr Thr Pro Asn Pro
 85 90 95

Asp Val Leu Cys Asn Arg Glu Ile Lys Phe Asp Leu Leu Gln Lys Lys
 100 105 110

Val Arg Glu Leu Lys Gly Asp Phe Leu Ala Thr Gly His Tyr Cys Arg
 115 120 125

Gly Gly Ala Asp Gly Thr Gly Leu Ser Arg Gly Ile Asp Pro Asn Lys
 130 135 140

Asp Gln Ser Tyr Phe Leu Cys Gly Thr Pro Lys Asp Ala Leu Ser Asn
 145 150 155 160

Val Leu Phe Pro Leu Gly Gly Met Tyr Lys Thr Glu Val Arg Arg Ile
 165 170 175

Ala Gln Glu Ala Gly Leu Ala Thr Ala Thr Lys Lys Asp Ser Thr Gly
 180 185 190

Ile Cys Phe Ile Gly Lys Arg Pro Phe Lys Ser Phe Leu Glu Gln Phe
 195 200 205

Val Ala Asp Ser Pro Gly Asp Ile Ile Asp Phe Asp Thr Gln Gln Val
 210 215 220

Val Gly Arg His Glu Gly Ala His Tyr Tyr Thr Ile Gly Gln Arg Arg
 225 230 235 240

Gly Leu Asn Ile Gly Gly Met Glu Lys Pro Cys Tyr Val Leu Ser Lys
 245 250 255

Asn Met Glu Lys Asn Ile Val Tyr Ile Val Arg Gly Glu Asp His Pro
 260 265 270

Leu Leu Tyr Arg Gln Glu Leu Leu Ala Lys Glu Leu Asn Trp Phe Val
 275 280 285

Pro Leu Gln Glu Pro Met Ile Cys Ser Ala Lys Val Arg Tyr Arg Ser
 290 295 300

Pro Asp Glu Lys Cys Ser Val Tyr Pro Leu Glu Asp Gly Thr Val Lys
305 310 315 320

Val Ile Phe Asp Val Pro Val Lys Ala Val Thr Pro Gly Gln Thr Val
325 330 335

Ala Phe Tyr Gln Gly Asp Ile Cys Leu Gly Gly Gly Val Ile Glu Val
340 345 350

Pro Met Ile His Gln Leu
355